FILE 'REGISTRY' ENTERED AT 15:58:21 ON 12 AUG 2005
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STRUCTURE FILE UPDATES: 11 AUG 2005 HIGHEST RN 859751-76-1
DICTIONARY FILE UPDATES: 11 AUG 2005 HIGHEST RN 859751-76-1

New CAS Information Use Policies, enter HELP USAGETERMS for details.

TSCA INFORMATION NOW CURRENT THROUGH JANUARY 18, 2005

Please note that search-term pricing does apply when
conducting SmartSELECT searches.

```
**********************************************************************
*                                                                    *
* The CA roles and document type information have been removed from *
* the IDE default display format and the ED field has been added,    *
* effective March 20, 2005.  A new display format, IDERL, is now     *
* available and contains the CA role and document type information.  *
*                                                                    *
**********************************************************************
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Structure search iteration limits have been increased. See HELP SLIMITS
for details.

Experimental and calculated property data are now available. For more
information enter HELP PROP at an arrow prompt in the file or refer
to the file summary sheet on the web at:
http://www.cas.org/ONLINE/DBSS/registryss.html

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             0 GCATGTTACAGGTAGAAAAGCC/SQEP
        123660 SQL=22
L1           0 GCATGTTACAGGTAGAAAAGCC/SQEP
                 (GCATGTTACAGGTAGAAAAGCC/SQEP AND SQL=22)


             0 CTGGCGTATCTGAAGAGTCTG/SQEP
        335042 SQL=21
L2           0 CTGGCGTATCTGAAGAGTCTG/SQEP
                 (CTGGCGTATCTGAAGAGTCTG/SQEP AND SQL=21)


             0 GACCGCATAGACTTCTCAGA/SQEP
        452450 SQL=20
L3           0 GACCGCATAGACTTCTCAGA/SQEP
                 (GACCGCATAGACTTCTCAGA/SQEP AND SQL=20)
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FILE 'HOME' ENTERED AT 15:58:30 ON 12 AUG 2005

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     (FILE 'HOME' ENTERED AT 15:22:24 ON 12 AUG 2005)
               DEL HIS Y

     FILE 'REGISTRY' ENTERED AT 15:58:21 ON 12 AUG 2005
L1             0 SEA ABB=ON  PLU=ON  GCATGTTACAGGTAGAAAAGCC/SQEP
L2             0 SEA ABB=ON  PLU=ON  CTGGCGTATCTGAAGAGTCTG/SQEP
L3             0 SEA ABB=ON  PLU=ON  GACCGCATAGACTTCTCAGA/SQEP

     FILE 'HOME' ENTERED AT 15:58:30 ON 12 AUG 2005


     FILE REGISTRY
     Property values tagged with IC are from the ZIC/VINITI data file
     provided by InfoChem.

     STRUCTURE FILE UPDATES:   11 AUG 2005  HIGHEST RN 859751-76-1
     DICTIONARY FILE UPDATES:  11 AUG 2005  HIGHEST RN 859751-76-1

     New CAS Information Use Policies, enter HELP USAGETERMS for details.

     TSCA INFORMATION NOW CURRENT THROUGH JANUARY 18, 2005

       Please note that search-term pricing does apply when
       conducting SmartSELECT searches.

     ******************************************************************
     *                                                                *
     * The CA roles and document type information have been removed from *
     * the IDE default display format and the ED field has been added,  *
     * effective March 20, 2005.  A new display format, IDERL, is now   *
     * available and contains the CA role and document type information. *
     *                                                                *
     ******************************************************************

     Structure search iteration limits have been increased.  See HELP SLIMI
     for details.

     Experimental and calculated property data are now available. For more
     information enter HELP PROP at an arrow prompt in the file or refer
     to the file summary sheet on the web at:
     http://www.cas.org/ONLINE/DBSS/registryss.html

     FILE HOME
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Davis, M.
09/743825
Seq IDs 7, 8 & 10

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 12, 2005, 05:00:31 ; Search time 1565 Seconds
(without alignments)
681.160 Million cell updates/sec

Title: US-09-743-825-7
Perfect score: 22
Sequence: 1 gcatgttacaggtagaaaagcc 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 952800

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
c	1	15.2	69.1	20	6	AR314796	AR314796 Sequence
	2	13.2	60.0	21	6	AR374844	AR374844 Sequence
	3	13.2	60.0	21	6	AX139516	AX139516 Sequence
	4	13.2	60.0	21	6	BD014939	BD014939 Lawsonia
c	5	12.8	58.2	19	6	BD231604	BD231604 Chromosom
c	6	12.8	58.2	20	6	AX405008	AX405008 Sequence
c	7	12.8	58.2	21	6	CQ876341	CQ876341 Sequence
	8	12.2	55.5	18	6	AR139875	AR139875 Sequence
	9	12.2	55.5	18	6	AR167519	AR167519 Sequence
	10	12.2	55.5	18	6	AR234243	AR234243 Sequence
	11	12.2	55.5	18	6	AR293044	AR293044 Sequence
	12	12.2	55.5	18	6	AR476160	AR476160 Sequence
	13	12.2	55.5	18	6	AR488045	AR488045 Sequence
	14	12.2	55.5	18	6	BD084547	BD084547 Recombina
c	15	12.2	55.5	20	6	AR207150	AR207150 Sequence
	16	12.2	55.5	20	6	AR271107	AR271107 Sequence
c	17	12.2	55.5	21	6	AX378485	AX378485 Sequence
	18	12	54.5	20	6	AR118897	AR118897 Sequence
c	19	12	54.5	20	6	CQ763548	CQ763548 Sequence
c	20	12	54.5	20	6	AR297958	AR297958 Sequence
c	21	12	54.5	20	6	AX405002	AX405002 Sequence
c	22	12	54.5	21	6	AX133296	AX133296 Sequence
	23	12	54.5	22	6	CQ848304	CQ848304 Sequence
	24	11.8	53.6	17	6	BD063649	BD063649 Nucleotid
	25	11.8	53.6	19	6	AR294337	AR294337 Sequence
c	26	11.8	53.6	20	6	A33496	A33496 Synthetic P
	27	11.8	53.6	20	6	AR162418	AR162418 Sequence
c	28	11.8	53.6	20	6	I42395	I42395 Sequence 27
c	29	11.8	53.6	20	6	AX405006	AX405006 Sequence
c	30	11.8	53.6	20	6	AX405010	AX405010 Sequence
c	31	11.8	53.6	21	6	CQ854109	CQ854109 Sequence
	32	11.8	53.6	21	6	CQ854110	CQ854110 Sequence
	33	11.8	53.6	22	6	BD089416	BD089416 A method
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	36	11.8	53.6	22	12	AB068145	AB068145 Synthetic
	37	11.6	52.7	19	6	AR292809	AR292809 Sequence
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	40	11.6	52.7	20	6	BD012454	BD012454 A novel g
c	41	11.4	51.8	14	6	BD199416	BD199416 Method an
	42	11.4	51.8	14	6	AX587242	AX587242 Sequence
c	43	11.4	51.8	17	6	BD199179	BD199179 Method an
	44	11.4	51.8	17	6	AR186046	AR186046 Sequence
	45	11.4	51.8	17	6	AR322677	AR322677 Sequence
	46	11.4	51.8	17	6	AR326882	AR326882 Sequence
	47	11.4	51.8	17	6	AR402362	AR402362 Sequence
	48	11.4	51.8	17	6	AR402363	AR402363 Sequence
	49	11.4	51.8	17	6	AR402364	AR402364 Sequence
	50	11.4	51.8	17	6	AR402365	AR402365 Sequence
	51	11.4	51.8	17	6	BD067862	BD067862 Enzymatic
	52	11.4	51.8	17	6	BD067863	BD067863 Enzymatic
	53	11.4	51.8	17	6	BD067864	BD067864 Enzymatic
	54	11.4	51.8	17	6	BD067865	BD067865 Enzymatic
	55	11.4	51.8	18	6	A59434	A59434 Sequence 27
	56	11.4	51.8	18	6	AR182188	AR182188 Sequence
	57	11.4	51.8	19	6	AR235508	AR235508 Sequence
	58	11.4	51.8	19	6	AR235535	AR235535 Sequence
	59	11.4	51.8	19	6	AR235539	AR235539 Sequence
	60	11.4	51.8	19	6	AR294949	AR294949 Sequence
c	61	11.4	51.8	20	6	AR136599	AR136599 Sequence
	62	11.4	51.8	20	6	BD196199	BD196199 Antisense
	63	11.4	51.8	20	6	AR199824	AR199824 Sequence
c	64	11.4	51.8	20	6	AR312888	AR312888 Sequence
	65	11.4	51.8	20	6	AR336983	AR336983 Sequence
	66	11.4	51.8	20	6	AR353685	AR353685 Sequence
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c	69	11.4	51.8	20	6	AR489905	AR489905 Sequence
c	70	11.4	51.8	20	6	AX115518	AX115518 Sequence
c	71	11.4	51.8	21	6	AR212918	AR212918 Sequence
c	72	11.4	51.8	21	6	AR294892	AR294892 Sequence
	73	11.4	51.8	21	6	AX146202	AX146202 Sequence
c	74	11.4	51.8	22	6	BD260883	BD260883 PCR cloni
c	75	11.4	51.8	22	6	BD269905	BD269905 Tumor nec
c	76	11.4	51.8	22	6	E14592	E14592 PCR primer
c	77	11.4	51.8	22	6	AR287736	AR287736 Sequence
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	79	11.2	50.9	17	6	AX215699	AX215699 Sequence
	80	11.2	50.9	17	6	AX217091	AX217091 Sequence
	81	11.2	50.9	17	6	AX727595	AX727595 Sequence
	82	11.2	50.9	17	6	AX729770	AX729770 Sequence
c	83	11.2	50.9	18	6	I40592	I40592 Sequence 20
c	84	11.2	50.9	18	6	I40863	I40863 Sequence 20
c	85	11.2	50.9	18	6	I40891	I40891 Sequence 20
c	86	11.2	50.9	18	6	I56833	I56833 Sequence 20
	87	11.2	50.9	18	6	AX785422	AX785422 Sequence
	88	11.2	50.9	20	6	A46320	A46320 Sequence 9
c	89	11.2	50.9	20	6	A70786	A70786 Sequence 10
c	90	11.2	50.9	20	6	A79270	A79270 Sequence 10
	91	11.2	50.9	20	6	AR112896	AR112896 Sequence
	92	11.2	50.9	20	6	CQ876370	CQ876370 Sequence

93	11.2	50.9	20	6	I43991	I43991 Sequence 9
94	11.2	50.9	20	6	AR493229	AR493229 Sequence
95	11.2	50.9	20	6	AX010205	AX010205 Sequence
c 96	11.2	50.9	20	6	AX405000	AX405000 Sequence
c 97	11.2	50.9	20	6	AX405004	AX405004 Sequence
c 98	11.2	50.9	20	6	AX412214	AX412214 Sequence
c 99	11.2	50.9	20	6	AX613528	AX613528 Sequence
c 100	11.2	50.9	20	6	AX937895	AX937895 Sequence

ALIGNMENTS

RESULT 1
AR314796/c
LOCUS AR314796 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 5333 from patent US 6559294.
ACCESSION AR314796
VERSION AR314796.1 GI:31708222
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A., Sankaran,B. and Fletcher,L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 5333 06-MAY-2003;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

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Best Local Similarity 85.0%; Pred. No. 1.2e+04;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCATGTTACAGGTAGAAAAG 20
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Db 20 GCCTGTTCCAGATAGAAAAG 1

RESULT 2
AR374844
LOCUS AR374844 21 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 50 from patent US 6605696.
ACCESSION AR374844
VERSION AR374844.1 GI:40077832
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 21)
AUTHORS Rosey,E.L.
TITLE Lawsonia intracellularis proteins, and related methods and materials
JOURNAL Patent: US 6605696-A 50 12-AUG-2003;
FEATURES Location/Qualifiers
source 1. .21
/organism="unknown"
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Query Match 60.0%; Score 13.2; DB 6; Length 21;
Best Local Similarity 83.3%; Pred. No. 1.3e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 2 TGGTACAGCAAGAAAAGC 19

RESULT 3
AX139516
LOCUS AX139516 21 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 50 from Patent EP1094070.
ACCESSION AX139516
VERSION AX139516.1 GI:14275153
KEYWORDS .
SOURCE Lawsonia intracellularis
ORGANISM Lawsonia intracellularis
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae; Lawsonia.
REFERENCE 1
AUTHORS Rosey,E.L.
TITLE Lawsonia intracellularis proteins, and related methods and materials
JOURNAL Patent: EP 1094070-A 50 25-APR-2001;
Pfizer Products Inc. (US)
FEATURES Location/Qualifiers
source 1. .21
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/mol_type="unassigned DNA"
/db_xref="taxon:29546"
ORIGIN

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Best Local Similarity 83.3%; Pred. No. 1.3e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 2 TGGTACAGCAAGAAAAGC 19

RESULT 4
BD014939
LOCUS BD014939 21 bp DNA linear PAT 27-AUG-2002
DEFINITION Lawsonia intracellularis protein and methods and materials relating thereto.
ACCESSION BD014939
VERSION BD014939.1 GI:22555746
KEYWORDS JP 2001169787-A/43.
SOURCE Lawsonia intracellularis
ORGANISM Lawsonia intracellularis
Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae; Lawsonia.
REFERENCE 1 (bases 1 to 21)
AUTHORS Rosi,I.L.
TITLE Lawsonia intracellularis protein and methods and materials relating thereto
JOURNAL Patent: JP 2001169787-A 43 26-JUN-2001;
PFIZER PRODUCTS INC
COMMENT OS Lawsonia intracellularis
PN JP 2001169787-A/43
PD 26-JUN-2001
PF 20-OCT-2000 JP 2000320736
PR 22-OCT-1999 US 60/160922
PI IBURETTO LEE ROSI
PC C12N15/09,A61K38/00,A61K39/106,A61K48/00,A61P31/04,C07K14/205,
PC C07K16/12,
PC C12N1/15,C12N1/19,C12N1/21,C12N5/10,G01N33/53,G01N33/569// PC C12P21/02,
PC C12P21/08,(C12P21/02,C12R1:19),C12N15/00,A61K37/02,C12N5/00 CC Lawsonia intracellularis protein and methods and materials CC relating thereto
FH Key Location/Qualifiers
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              || |||||  ||||||||
Db          2 TGGTACAGCAAGAAAAGC 19


RESULT 5
BD231604/c
LOCUS       BD231604                 19 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Chromosome 17q-linked prostate cancer susceptibility gene.
ACCESSION   BD231604
VERSION     BD231604.1  GI:33041374
KEYWORDS    JP 2002529065-A/156.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Tavtigian,S.V., Teng,D.H.F., Simard,J. and Rommens,J.M.
  TITLE     Chromosome 17q-linked prostate cancer susceptibility gene
  JOURNAL   Patent: JP 2002529065-A 156 10-SEP-2002;
            MYRIAD GENETICS INC,THE HOSPITAL FOR SICK CHILDREN
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002529065-A/156
            PD   10-SEP-2002
            PF   05-NOV-1999 JP 2000581041
            PR   06-NOV-1998 US    60/107468
            PI   SEAN V TAVTIGIAN,DAVID H F TENG,JACQUES SIMARD,JOHANNA M  PI
            ROMMENS
            PC   C12N15/09,A61K31/713,A61K38/00,A61K39/395,A61K45/00,A61K48/00,
            PC   A61P35/00,
            PC
            C07K14/47,C07K16/18,C07K16/44,C12N1/15,C12N1/19,C12N1/21,C12N5/ PC
             10,
            PC   C12P21/02,C12Q1/68,G01N33/15,G01N33/50,G01N33/53,G01N33/566,
            PC   G01N33/577,
            PC   G01N37/00,C12N15/00,A61K37/02,C12N5/00
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Qy          3 ATGTTACAGGTAGAAA 18
              |||| ||||| |||||
Db         19 ATGTCACAGGCAGAAA 4


RESULT 6
AX405008/c
LOCUS       AX405008                 20 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 25 from Patent WO0222634.
ACCESSION   AX405008
VERSION     AX405008.1  GI:21438223
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Choo,Y. and Isalan,M.
  TITLE     Method for the preparation of selectively randomised nucleic acid
            molecules
  JOURNAL   Patent: WO 0222634-A 25 21-MAR-2002;
            Sangamo Biosciences Inc. (US)
FEATURES            Location/Qualifiers
     source         1. .20
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                    /db_xref="taxon:32630"
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ORIGIN

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Qy          4 TGTTACAGGTAGAAAAGC 21
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Db         19 TSYKCGAGKYAGAAAAGC 2


RESULT 7
CQ876341/c
LOCUS       CQ876341                 21 bp    DNA     linear   PAT 04-OCT-2004
DEFINITION  Sequence 191 from Patent WO2004065583.
ACCESSION   CQ876341
VERSION     CQ876341.1  GI:53789945
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Cobleigh,M.A., Shak,S., Baker,J.B. and Cronin,M.T.
  TITLE     Gene expression markers for breast cancer prognosis
  JOURNAL   Patent: WO 2004065583-A 191 05-AUG-2004;
            Genomic Health, Inc. (US); Rush University Medical Center (US)
FEATURES            Location/Qualifiers
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ORIGIN

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Qy          7 TACAGGTAGAAAAGCC 22
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Db         21 TTCTGGTAGAAAAGCC 6


RESULT 8
AR139875
LOCUS       AR139875                 18 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 53 from patent US 6207416.
ACCESSION   AR139875
VERSION     AR139875.1  GI:14482371
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Tsarev,S.A., Emerson,S.U. and Purcell,R.H.
  TITLE     Recombinant proteins of a Pakistani strain of hepatitis E and their
            use in diagnostic methods and vaccines
  JOURNAL   Patent: US 6207416-A 53 27-MAR-2001;
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ORIGIN
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Qy          5 GTTACAGGTAGAAAAGC 21
              |||||||  ||||||  |
Db          2 GTTACAGCCAGAAAACC 18

.
RESULT 9
AR167519
LOCUS       AR167519                  18 bp    DNA     linear   PAT 17-DEC-2001
DEFINITION  Sequence 53 from patent US 6287759.
ACCESSION   AR167519
VERSION     AR167519.1  GI:17903303
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Tsarev,S.A., Emerson,S.U. and Purcell,R.H.
  TITLE     Recombinant proteins of a Pakistani strain of hepatitis E and their
            use in diagnostic methods and vaccines
  JOURNAL   Patent: US 6287759-A 53 11-SEP-2001;
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             55.5%;  Score 12.2;  DB 6;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 4.2e+05;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 GTTACAGGTAGAAAAGC 21
              |||||||  ||||||  |
Db          2 GTTACAGCCAGAAAACC 18


RESULT 10
AR234243
LOCUS       AR234243                  18 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 53 from patent US 6458562.
ACCESSION   AR234243
VERSION     AR234243.1  GI:27276915
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Emerson,S.U., Purcell,R.H., Tsarev,S.A. and Robinson,R.A.
  TITLE     Recombinant proteins of a Pakistani strain of hepatitis E and their
            use in diagnostic methods and vaccines
  JOURNAL   Patent: US 6458562-A 53 01-OCT-2002;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             55.5%;  Score 12.2;  DB 6;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 4.2e+05;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 GTTACAGGTAGAAAAGC 21
              |||||||  ||||||  |
Db          2 GTTACAGCCAGAAAACC 18


RESULT 11
AR293044
LOCUS       AR293044                  18 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 4779 from patent US 6537751.
ACCESSION   AR293044
VERSION     AR293044.1  GI:31680328
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 4779 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             55.5%;  Score 12.2;  DB 6;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 4.2e+05;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 TGTTACAGGTAGAAAAG 20
              ||| | |||||||  |||
Db          1 TGTGAGAGGTAGAGAAG 17


RESULT 12
AR476160
LOCUS       AR476160                  18 bp    DNA     linear   PAT 14-MAY-2004
DEFINITION  Sequence 53 from patent US 6696242.
ACCESSION   AR476160
VERSION     AR476160.1  GI:47233050
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Tsarev,S.A., Emerson,S.U. and Purcell,R.H.
  TITLE     Recombinant proteins of a Pakistani strain of hepatitis E and their
            use in diagnostic methods and vaccines
  JOURNAL   Patent: US 6696242-A 53 24-FEB-2004;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             55.5%;  Score 12.2;  DB 6;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 4.2e+05;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 GTTACAGGTAGAAAAGC 21
              |||||||  ||||||  |
Db          2 GTTACAGCCAGAAAACC 18


RESULT 13
AR488045
LOCUS       AR488045                  18 bp    DNA     linear   PAT 15-MAY-2004
DEFINITION  Sequence 53 from patent US 6706873.
ACCESSION   AR488045
VERSION     AR488045.1  GI:47253790
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Tsarev,S.A., Emerson,S.U. and Purcell,R.H.
  TITLE     Recombinant proteins of a pakistani strain of hepatitis E and their
            use in diagnostic methods and vaccines
  JOURNAL   Patent: US 6706873-A 53 16-MAR-2004;
FEATURES             Location/Qualifiers
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     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             55.5%;  Score 12.2;  DB 6;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 4.2e+05;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 GTTACAGGTAGAAAAGC 21
              |||||||  ||||||  |
Db          2 GTTACAGCCAGAAAACC 18


RESULT 14
BD084547
LOCUS       BD084547                  18 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Recombinant proteins of a pakistani strain of hepatitis E and their
            use in diagnostic methods and vaccines.
ACCESSION   BD084547
VERSION     BD084547.1  GI:22630157
KEYWORDS    JP 2001524821-A/50.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Emerson,S.U., Purcell,R.H., Tsarev,S.A. and Robinson,R.A.
  TITLE     Recombinant proteins of a pakistani strain of hepatitis E and their
            use in diagnostic methods and vaccines
  JOURNAL   Patent: JP 2001524821-A 50 04-DEC-2001;
            THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY
            THE BIO ORIENTED TECHNOLOGY RESEARCH ADVANCEMENT INSTITUTION
            SECRETARY DEPARTMENT OF HEALTH AND HUMAN SERVICES
COMMENT     OS   Unidentified
            PN   JP 2001524821-A/50
            PD   04-DEC-2001
            PF   09-APR-1998 JP 1998544174
            PR   11-APR-1997 US    08/840316
            PI   SUZANNE U EMERSON,ROBERT H PURCELL,SERGEI A TSAREV,ROBIN A  PI
              ROBINSON
            PC   C12N15/51,C07K14/08,C07K16/10,A61K39/29,G01N33/576 CC
            Strandedness: Single;
            CC   Topology: Linear;
            CC   Recombinant proteins of a pakistani strain of hepatitis E and
            CC            their use in
            CC   diagnostic methods and vaccines
            FH   Key             Location/Qualifiers
            FT   source          1. .18
            FT                   /organism='Unidentified'.
FEATURES            Location/Qualifiers
     source         1. .18
                    /organism="unidentified"
                    /mol_type="genomic DNA"
                    /db_xref="taxon:32644"
ORIGIN

  Query Match             55.5%;  Score 12.2;  DB 6;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 4.2e+05;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 GTTACAGGTAGAAAAGC 21
              |||||||  ||||||  |
Db          2 GTTACAGCCAGAAAACC 18


RESULT 15
AR207150/c
LOCUS       AR207150                  20 bp    DNA     linear   PAT 20-JUN-2002
DEFINITION  Sequence 44 from patent US 6372492.
ACCESSION   AR207150
VERSION     AR207150.1  GI:21505970
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Bennett,C.Frank. and Cowsert,L.M.
  TITLE     Antisense modulation of talin expression
  JOURNAL   Patent: US 6372492-A 44 16-APR-2002;
FEATURES            Location/Qualifiers
     source         1. .20
                    /organism="unknown"
                    /mol_type="unassigned DNA"
ORIGIN

  Query Match             55.5%;  Score 12.2;  DB 6;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 4.2e+05;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 TGTTACAGGTAGAAAAG 20
              |||| |||| || ||||
Db         19 TGTTGCAGGCAGCAAAG 3


RESULT 16
AR271107
LOCUS       AR271107                  20 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 50 from patent US 6503152.
ACCESSION   AR271107
VERSION     AR271107.1  GI:29702410
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Pelz,D.T.
  TITLE     Putting trainer
  JOURNAL   Patent: US 6503152-A 50 07-JAN-2003;
FEATURES            Location/Qualifiers
     source         1. .20
                    /organism="unknown"
                    /mol_type="genomic DNA"
ORIGIN

  Query Match             55.5%;  Score 12.2;  DB 6;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 4.2e+05;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 GTTACAGGTAGAAAAGC 21
              || ||||||  |||||  |
Db          1 GTCACAGGTGGAAAATC 17


RESULT 17
AX378485/c
LOCUS       AX378485                  21 bp    DNA     linear   PAT 18-MAR-2002
DEFINITION  Sequence 274 from Patent WO0206525.
ACCESSION   AX378485
VERSION     AX378485.1  GI:19574338
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Cohen,D., Blumenfeld,M., Chumakov,I., Abderrahim,H. and Bihain,B.
  TITLE     Obesity associated biallelic marker maps
  JOURNAL   Patent: WO 0206525-A 274 24-JAN-2002;
            GENSET (FR)
FEATURES            Location/Qualifiers
     source         1. .21
                    /organism="Homo sapiens"
                    /mol_type="unassigned DNA"
                    /db_xref="taxon:9606"
     primer_bind    1. .21
                    /note="upstream amplification primer 99-44259 for SEQ 103"
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ORIGIN

  Query Match             55.5%;  Score 12.2;  DB 6;  Length 21;
  Best Local Similarity   82.4%;  Pred. No. 4.2e+05;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 GTTACAGGTAGAAAAGC 21
              ||| ||| || ||||||
Db         19 GTTTCAGATAAAAAAGC 3


RESULT 18
AR118897
LOCUS       AR118897                  20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 23 from patent US 6150092.
ACCESSION   AR118897
VERSION     AR118897.1  GI:14100807
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Uchida,K., Uchida,T., Tanaka,Y., Matsuda,Y. and Kondo,S.
  TITLE     Antisense nucleic acid compound targeted to VEGF
  JOURNAL   Patent: US 6150092-A 23 21-NOV-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             54.5%;  Score 12;  DB 6;  Length 20;
  Best Local Similarity   75.0%;  Pred. No. 5.3e+05;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GCATGTTACAGGTAGAAAAG 20
              ||||| | ||||||| ||
Db          1 GCATGGTGGAGGTAGAGCAG 20


RESULT 19
CQ763548/c
LOCUS       CQ763548                  20 bp    DNA     linear   PAT 03-MAR-2004
DEFINITION  Sequence 2166 from Patent WO2004003201.
ACCESSION   CQ763548
VERSION     CQ763548.1  GI:44906784
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kane,C.D.
  TITLE     Antisense modulation of lrh1 expression
  JOURNAL   Patent: WO 2004003201-A 2166 08-JAN-2004;
            Pharmacia Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Human LRH1 antisense"
ORIGIN

  Query Match             54.5%;  Score 12;  DB 6;  Length 20;
  Best Local Similarity   75.0%;  Pred. No. 5.3e+05;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 ATGTTACAGGTAGAAAAGCC 22
              |||  |||||||  |||| |
Db         20 ATGCCACAGGTATGAAAGTC 1


RESULT 20
AR297958/c
LOCUS       AR297958                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 9693 from patent US 6537751.
ACCESSION   AR297958
VERSION     AR297958.1  GI:31685242
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 9693 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             54.5%;  Score 12;  DB 6;  Length 20;
  Best Local Similarity   75.0%;  Pred. No. 5.3e+05;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GCATGTTACAGGTAGAAAAG 20
              | ||||   ||||| |||||
Db         20 GTATGTCTGAGGTATAAAAG 1


RESULT 21
AX405002/c
LOCUS       AX405002                  20 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 19 from Patent WO0222634.
ACCESSION   AX405002
VERSION     AX405002.1  GI:21438217
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Choo,Y. and Isalan,M.
  TITLE     Method for the preparation of selectively randomised nucleic acid
            molecules
  JOURNAL   Patent: WO 0222634-A 19 21-MAR-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"
ORIGIN

  Query Match             54.5%;  Score 12;  DB 6;  Length 20;
  Best Local Similarity   66.7%;  Pred. No. 5.3e+05;
  Matches   12;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 TGTTACAGGTAGAAAAGC 21
              ||:   ||::|||||||||
Db         19 TGKCCGAGKYAGAAAAGC 2


RESULT 22
AX133296/c
LOCUS       AX133296                  21 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 4514 from Patent WO0130362.
ACCESSION   AX133296
VERSION     AX133296.1  GI:14139606
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 4514 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="VEGF hammerhead ribozyme recognition site"
ORIGIN

  Query Match             54.5%;  Score 12;  DB 6;  Length 21;
  Best Local Similarity   75.0%;  Pred. No. 5.3e+05;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 CATGTTACAGGTAGAAAAGC 21
              |||| |  |||||||  |||
Db         21 CATGGTGGAGGTAGAGCAGC 2


RESULT 23
CQ848304
LOCUS       CQ848304                  22 bp    DNA     linear   PAT 19-AUG-2004
DEFINITION  Sequence 9 from Patent WO2004063366.
ACCESSION   CQ848304
VERSION     CQ848304.1  GI:51469805
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Steiger,S. and Sandmann,G.
  TITLE     Method for producing ketocarotenoids by cultivating genetically
            modified organisms
  JOURNAL   Patent: WO 2004063366-A 9 29-JUL-2004;
            BASF AKTIENGESELLSCHAFT (DE)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             54.5%;  Score 12;  DB 6;  Length 22;
  Best Local Similarity   75.0%;  Pred. No. 5.3e+05;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 ATGTTACAGGTAGAAAAGCC 22
              ||| | ||| ||||| | ||
Db          1 ATGATCCAGTTAGAACAACC 20


RESULT 24
BD063649
LOCUS       BD063649                  17 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Nucleotide and protein sequences of liver activin/inhibin and
            methods based thereon.
ACCESSION   BD063649
VERSION     BD063649.1  GI:22609252
KEYWORDS    JP 2001505420-A/14.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Bonadio,J. and Fang,J.
  TITLE     Nucleotide and protein sequences of liver activin/inhibin and
            methods based thereon
  JOURNAL   Patent: JP 2001505420-A 14 24-APR-2001;
            THE REGENTS OF THE UNIVERSITY OF MICHIGAN
COMMENT     OS   Artificial Sequence
            PN   JP 2001505420-A/14
            PD   24-APR-2001
            PF   20-NOV-1997 JP 1998523766
            PR   20-NOV-1996 US    08/752919
            PI   JEFFREY BONADIO,JIANMING FANG
            PC   C07H21/04,C12N15/00,C12N5/10,C12N5/16
            CC   Synthetic oligonucleotide
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             53.6%;  Score 11.8;  DB 6;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 6.8e+05;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CATGTTACAGGTAGA 16
              |||| | ||||||||
Db          1 CATGCTCCAGGTAGA 15


RESULT 25
AR294337
LOCUS       AR294337                  19 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 6072 from patent US 6537751.
ACCESSION   AR294337
VERSION     AR294337.1  GI:31681621
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 6072 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             53.6%;  Score 11.8;  DB 6;  Length 19;
  Best Local Similarity   86.7%;  Pred. No. 6.8e+05;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 GTTACAGGTAGAAAA 19
              |||| |||| |||||
Db          1 GTTAGAGGTTGAAAA 15


RESULT 26
A33496/c
LOCUS       A33496                    20 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Synthetic P.falciparum 155 gene PCR primer RIT34.
ACCESSION   A33496
VERSION     A33496.1  GI:1567941
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Holmes,M.J. and Uhlen,M.
  TITLE     SOLID PHASE DIAGNOSIS OF MEDICAL CONDITIONS
  JOURNAL   Patent: WO 9011369-A 21 04-OCT-1990;
            CEMU BIOTEKNIK (SE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
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                     /db_xref="taxon:32630"
ORIGIN

  Query Match            53.6%;  Score 11.8;  DB 6;  Length 20;
  Best Local Similarity  86.7%;  Pred. No. 6.8e+05;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 TGTTACAGGTAGAAA 18
              || |||||| |||||
Db         19 TGGTACAGGCAGAAA 5


RESULT 27
AR162418
LOCUS       AR162418                  20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 98 from patent US 6258600.
ACCESSION   AR162418
VERSION     AR162418.1  GI:16229597
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Zhang,H. and Cowsert,L.M.
  TITLE     Antisense modulation of caspase 8 expression
  JOURNAL   Patent: US 6258600-A 98 10-JUL-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            53.6%;  Score 11.8;  DB 6;  Length 20;
  Best Local Similarity  86.7%;  Pred. No. 6.8e+05;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 ACAGGTAGAAAAGCC 22
              | |||||||| ||||
Db          4 AGAGGTAGAAGAGCC 18


RESULT 28
I42395/c
LOCUS       I42395                    20 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 27 from patent US 5629158.
ACCESSION   I42395
VERSION     I42395.1  GI:2467890
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Uhlen,M.
  TITLE     Solid phase diagnosis of medical conditions
  JOURNAL   Patent: US 5629158-A 27 13-MAY-1997;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            53.6%;  Score 11.8;  DB 6;  Length 20;
  Best Local Similarity  86.7%;  Pred. No. 6.8e+05;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 TGTTACAGGTAGAAA 18
              || |||||| |||||
Db         19 TGGTACAGGCAGAAA 5


RESULT 29
AX405006/c
LOCUS       AX405006                  20 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 23 from Patent WO0222634.
ACCESSION   AX405006
VERSION     AX405006.1  GI:21438221
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Choo,Y. and Isalan,M.
  TITLE     Method for the preparation of selectively randomised nucleic acid
            molecules
  JOURNAL   Patent: WO 0222634-A 23 21-MAR-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"
ORIGIN

  Query Match            53.6%;  Score 11.8;  DB 6;  Length 20;
  Best Local Similarity  58.8%;  Pred. No. 6.8e+05;
  Matches   10;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 GTTACAGGTAGAAAAGC 21
              :::  ||::||||||||
Db         18 SYKCGAGKYAGAAAAGC 2


RESULT 30
AX405010/c
LOCUS       AX405010                  20 bp    DNA     linear   PAT 14-JUN-2002
DEFINITION  Sequence 27 from Patent WO0222634.
ACCESSION   AX405010
VERSION     AX405010.1  GI:21438225
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Choo,Y. and Isalan,M.
  TITLE     Method for the preparation of selectively randomised nucleic acid
            molecules
  JOURNAL   Patent: WO 0222634-A 27 21-MAR-2002;
            Sangamo Biosciences Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"
ORIGIN

  Query Match            53.6%;  Score 11.8;  DB 6;  Length 20;
  Best Local Similarity  58.8%;  Pred. No. 6.8e+05;
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Qy          5 GTTACAGGTAGAAAAGC 21
              :::  ||::||||||||
Db         18 SYKCGAGKYAGAAAAGC 2


RESULT 31
CQ854109/c
LOCUS       CQ854109                  21 bp    DNA     linear   PAT 23-AUG-2004
DEFINITION  Sequence 11 from Patent WO2004067564.
ACCESSION   CQ854109
VERSION     CQ854109.1  GI:51510136
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
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REFERENCE   1
  AUTHORS   Law,D., Gish,K.C., Murray,R. and Culp,P.
  TITLE     Compositions against cancer antigen liv-1 and uses thereof
  JOURNAL   Patent: WO 2004067564-A 11 12-AUG-2004;
            PROTEIN DESIGN LABS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="BCR4-53 sense siRNA"
ORIGIN

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  Best Local Similarity   86.7%;  Pred. No. 6.7e+05;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 TACAGGTAGAAAAGC 21
              ||  ||||||||||
Db         17 TAGCGGTAGAAAAGC 3


RESULT 32
CQ854110
LOCUS       CQ854110                  21 bp    DNA     linear   PAT 23-AUG-2004
DEFINITION  Sequence 12 from Patent WO2004067564.
ACCESSION   CQ854110
VERSION     CQ854110.1  GI:51510137
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Law,D., Gish,K.C., Murray,R. and Culp,P.
  TITLE     Compositions against cancer antigen liv-1 and uses thereof
  JOURNAL   Patent: WO 2004067564-A 12 12-AUG-2004;
            PROTEIN DESIGN LABS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="BCR4-53 antisense siRNA"
ORIGIN

  Query Match             53.6%;  Score 11.8;  DB 6;  Length 21;
  Best Local Similarity   86.7%;  Pred. No. 6.7e+05;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 TACAGGTAGAAAAGC 21
              ||  ||||||||||
Db          3 TAGCGGTAGAAAAGC 17


RESULT 33
BD089416
LOCUS       BD089416                  22 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  A method of arraying genome clone.
ACCESSION   BD089416
VERSION     BD089416.1  GI:22635026
KEYWORDS    JP 2001321190-A/1660.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Soeda,E.
  TITLE     A method of arraying genome clone
  JOURNAL   Patent: JP 2001321190-A 1660 20-NOV-2001;
            THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
            GENOTECHS
COMMENT     OS   Artificial Sequence
            PN   JP 2001321190-A/1660
            PD   20-NOV-2001
            PF   12-MAR-2001 JP 2001068285
            PI   EIICHI SOEDA
            PC   C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
              C12N15/00,
            PC   C12N15/00
            CC   Description of Artificial Sequence:Synthetic DNA FH   Key
                   Location/Qualifiers
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            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
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ORIGIN

  Query Match             53.6%;  Score 11.8;  DB 6;  Length 22;
  Best Local Similarity   86.7%;  Pred. No. 6.7e+05;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CATGTTACAGGTAGA 16
              |||||||| ||| |
Db          8 CATGTTACATGTACA 22


RESULT 34
BD089578
LOCUS       BD089578                  22 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  A method of arraying genome clone.
ACCESSION   BD089578
VERSION     BD089578.1  GI:22635188
KEYWORDS    JP 2001321190-A/1822.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Soeda,E.
  TITLE     A method of arraying genome clone
  JOURNAL   Patent: JP 2001321190-A 1822 20-NOV-2001;
            THE INSTITUTE OF PHYSICAL AND CHEMICAL RESEARCH, YUGENKAISHA
            GENOTECHS
COMMENT     OS   Artificial Sequence
            PN   JP 2001321190-A/1822
            PD   20-NOV-2001
            PF   12-MAR-2001 JP 2001068285
            PI   EIICHI SOEDA
            PC   C12N15/09,C12N15/09,C12M1/00,C12Q1/68,G01N33/53,G01N33/566, PC
              C12N15/00,
            PC   C12N15/00
            CC   Description of Artificial Sequence:Synthetic DNA FH   Key
                   Location/Qualifiers
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            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             53.6%;  Score 11.8;  DB 6;  Length 22;
  Best Local Similarity   86.7%;  Pred. No. 6.7e+05;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CATGTTACAGGTAGA 16
              |||||||| ||| |
Db          8 CATGTTACATGTACA 22


RESULT 35
AB068139
LOCUS       AB068139                  22 bp    DNA     linear   SYN 21-MAY-2003
DEFINITION  Synthetic construct DNA, reverse primer for human STS
```

```
            sts-stGDB443043 at 1p36.
ACCESSION   AB068139
VERSION     AB068139.1  GI:15128943
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
            Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
            Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
            and Soeda,E.
  TITLE     A BAC-based STS-content map spanning a 35-Mb region of human
            chromosome 1p35-p36
  JOURNAL   Genomics 74 (1), 55-70 (2001)
  MEDLINE   21269192
   PUBMED   11374902
REFERENCE   2  (bases 1 to 22)
  AUTHORS   Horii,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
            Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
            Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
            Tel:81-22-717-8042, Fax:81-22-717-8047)
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
     misc_feature    1. .22
                     /note="reverse primer for human STS sts-stGDB443043 at
                     1p36
                     sts-stGDB443043 obtained from clones B58A11, B239M20,
                     B215H8, B239P22, B239P22, B88A11, Human BAC library
                     RPCI-11"
ORIGIN

  Query Match             53.6%;  Score 11.8;  DB 12;  Length 22;
  Best Local Similarity   86.7%;  Pred. No. 6.7e+05;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CATGTTACAGGTAGA 16
              ||||||||| ||| |
Db          8 CATGTTACATGTACA 22


RESULT 36
AB068145
LOCUS       AB068145                 22 bp    DNA     linear   SYN 21-MAY-2003
DEFINITION  Synthetic construct DNA, reverse primer for human STS sts-A002O35
            at 1p36.
ACCESSION   AB068145
VERSION     AB068145.1  GI:15128949
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Chen,Y.Z., Hayashi,Y., Wu,J.G., Takaoka,E., Maekawa,K.,
            Watanabe,N., Inazawa,J., Hosoda,F., Arai,Y., Mizushima,H.,
            Morohashi,A., Ohira,M., Nakagawara,A., Liu,S., Hoshi,M., Horii,A.
            and Soeda,E.
  TITLE     A BAC-based STS-content map spanning a 35-Mb region of human
            chromosome 1p35-p36
  JOURNAL   Genomics 74 (1), 55-70 (2001)
  MEDLINE   21269192
   PUBMED   11374902
REFERENCE   2  (bases 1 to 22)
  AUTHORS   Horii,A.
  TITLE     Direct Submission
  JOURNAL   Submitted (04-AUG-2001) Akira Horii, Tohoku University School of
            Medicine, Molecular Pathology; 2-1 Seiryomachi, Aoba-ku, Sendai,
            Miyagi 980-8575, Japan (E-mail:horii@mail.cc.tohoku.ac.jp,
            Tel:81-22-717-8042, Fax:81-22-717-8047)
FEATURES             Location/Qualifiers
     source          1. .22
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     misc_feature    1. .22
                     /note="reverse primer for human STS sts-A002O35 at 1p36
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                     B239P22, B239P22, B301O16, B262K21, Human BAC library
                     RPCI-11"
ORIGIN

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  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CATGTTACAGGTAGA 16
              ||||||||| ||| |
Db          8 CATGTTACATGTACA 22


RESULT 37
AR292809
LOCUS       AR292809                 19 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 4544 from patent US 6537751.
ACCESSION   AR292809
VERSION     AR292809.1  GI:31680093
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 4544 25-MAR-2003;
FEATURES             Location/Qualifiers
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ORIGIN

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  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 TGTTACAGGTAGAAAAGC 21
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Db          2 TGTCATAGTTAGAAAGGC 19


RESULT 38
CQ762779/c
LOCUS       CQ762779                 20 bp    DNA     linear   PAT 03-MAR-2004
DEFINITION  Sequence 1397 from Patent WO2004003201.
ACCESSION   CQ762779
VERSION     CQ762779.1  GI:44906015
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kane,C.D.
  TITLE     Antisense modulation of lrh1 expression
  JOURNAL   Patent: WO 2004003201-A 1397 08-JAN-2004;
            Pharmacia Corporation (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             52.7%;  Score 11.6;  DB 6;  Length 20;
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  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 ATGTTACAGGTAGAAAAG 20
              |||  |||||||  ||||
Db         19 ATGCCACAGGTATGAAAG 2


RESULT 39
CQ763112/c
LOCUS       CQ763112                  20 bp    DNA     linear   PAT 03-MAR-2004
DEFINITION  Sequence 1730 from Patent WO2004003201.
ACCESSION   CQ763112
VERSION     CQ763112.1  GI:44906348
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Kane,C.D.
  TITLE     Antisense modulation of lrh1 expression
  JOURNAL   Patent: WO 2004003201-A 1730 08-JAN-2004;
            Pharmacia Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .20
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Human LRH1 antisense"
ORIGIN

  Query Match             52.7%;  Score 11.6;  DB 6;  Length 20;
  Best Local Similarity   77.8%;  Pred. No. 8.6e+05;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 ATGTTACAGGTAGAAAAG 20
              |||  |||||||  ||||
Db         18 ATGCCACAGGTATGAAAG 1


RESULT 40
BD012454
LOCUS       BD012454                  20 bp    DNA     linear   PAT 02-AUG-2002
DEFINITION  A novel gene encoding TSP1-like protein.
ACCESSION   BD012454
VERSION     BD012454.1  GI:22092643
KEYWORDS    WO 0109321-A/38.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ota,T., Isogai,T., Nishikawa,T., Hayashi,K., Saito,K., Yamamoto,J.,
            Ishii,S., Sugiyama,T., Wakamatsu,A., Nagai,K., Otsuki,T.,
            Murakami,K., Yano,K., Kanzaki,K. and Inoue,Y.
  TITLE     A novel gene encoding TSP1-like protein
  JOURNAL   Patent: WO 0109321-A 38 08-FEB-2001;
            HELIX RESEARCH INSTITUTE,TOSHIO OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,
            KOJI HAYASHI,KAORU SAITO,JUNICHI YAMAMOTO,SHIZUKO ISHII, OMOYASU
            SUGIYAMA, AI WAKAMATSU,KEIICHI NAGAI,TETSUJI OTSUKI,KOJI MURAKAMI,
            AZUHIRO YANO, KOJI KANZAKI,YOSHIHISA INOUE
COMMENT     OS   Artificial Sequence
            PN   WO 0109321-A/38
            PD   08-FEB-2001
            PF   28-JUL-2000 WO 2000JP005068
            PR   29-JUL-1999 JP 99P   248036,27-AUG-1999 JP 99P   300253 PR
            11-JAN-2000 JP 00P   118776,02-MAY-2000 JP 00P   183767 PR
            18-OCT-1999 US    60/159590,17-FEB-2000 US    60/183322 PI   TOSHIO
            OTA,TAKAO ISOGAI,TETSUO NISHIKAWA,KOJI HAYASHI, PI   KAORU SAITO,
            PI   JUNICHI YAMAMOTO,SHIZUKO ISHII,TOMOYASU SUGIYAMA,AI WAKAMATSU,
            PI   KEIICHI NAGAI,TETSUJI OTSUKI,KOJI MURAKAMI,KAZUHIRO YANO, PI
            KOJI KANZAKI,
            PI   YOSHIHISA INOUE
            PC   C12N15/12,C07K14/47,C07K16/18,C12P21/08
            CC   Description of Artificial Sequence:an artificially synthesized
            primer
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            CC   sequence
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FEATURES             Location/Qualifiers
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  Best Local Similarity   77.8%;  Pred. No. 8.6e+05;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GCATGTTACAGGTAGAAA 18
              ||||||||||  | || |
Db          1 GCATGTTACATCTGGAGA 18


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GenCore version 5.1.6

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Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 2486036

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Post-processing: Minimum Match 0%
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Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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	4	13.2	60.0	21	9	ACA92364	Aca92364 Lawsonia
	5	13.2	60.0	21	10	ADG33930	Adg33930 L. intrac
	6	13.2	60.0	21	10	ADJ66835	Adj66835 Lawsonia
	7	13.2	60.0	21	13	ADR72987	Adr72987 Lawsonia
c	8	13	59.1	22	4	AAF85459	Aaf85459 Polynucle
c	9	12.8	58.2	19	3	AAA60336	Aaa60336 Human HPC
c	10	12.8	58.2	19	6	AAS99071	Aas99071 Human pro
c	11	12.8	58.2	20	2	AAT33010	Aat33010 Mouse SRY
c	12	12.8	58.2	20	6	ABK87666	Abk87666 Synthetic
c	13	12.8	58.2	20	10	ADA66516	Ada66516 Transform
c	14	12.8	58.2	21	10	ADG89282	Adg89282 Cancer de
c	15	12.8	58.2	21	12	ADP27751	Adp27751 PCR prime
c	16	12.8	58.2	21	13	ADR00153	Adr00153 COX2 prob
c	17	12.6	57.3	20	12	ADQ13916	Adq13916 DMD regio
	18	12.4	56.4	20	10	ADD18145	Add18145 Human G-p
	19	12.4	56.4	20	12	ADI41032	Adi41032 Human HGP
c	20	12.4	56.4	21	10	ABT16558	Abt16558 Ethylene
	21	12.2	55.5	18	2	AAQ61732	Aaq61732 HEV strai
	22	12.2	55.5	18	2	AAT27443	Aat27443 HEV strai
	23	12.2	55.5	18	2	AAV71653	Aav71653 HEV ORF p
	24	12.2	55.5	18	3	AAZ70423	Aaz70423 Human bia
c	25	12.2	55.5	20	6	ABN89231	Abn89231 Human Tal
c	26	12.2	55.5	20	6	ADG90494	Adg90494 Human tal
	27	12.2	55.5	20	10	ADC65754	Adc65754 Human TGF
	28	12.2	55.5	20	10	ADF90932	Adf90932 Microorga
c	29	12.2	55.5	20	10	ABZ86479	Abz86479 Human oli
c	30	12.2	55.5	20	11	ABD22709	Abd22709 Human myo
c	31	12.2	55.5	20	12	ADP85699	Adp85699 Human Tal
	32	12.2	55.5	21	3	AAC73052	Aac73052 Single nu
c	33	12.2	55.5	21	6	ABK41026	Abk41026 Human obe
	34	12.2	55.5	22	12	ADH56236	Adh56236 Yeast YFL
c	35	12	54.5	20	3	AAZ75337	Aaz75337 Human bia
c	36	12	54.5	20	6	ABK87660	Abk87660 Synthetic
c	37	12	54.5	20	12	ADJ17616	Adj17616 Antisense
	38	12	54.5	20	12	ADL01087	Adl01087 Human VEG
c	39	12	54.5	21	5	AAH62090	Aah62090 VEGF hamm
	40	12	54.5	22	12	ADO16516	Ado16516 4 synthes
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	42	11.8	53.6	17	2	AAV38248	Aav38248 Murine li
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c	44	11.8	53.6	20	2	AAZ04704	Aaz04704 PCR prime
	45	11.8	53.6	20	5	AAD12412	Aad12412 Mouse cas
c	46	11.8	53.6	20	6	ABK87668	Abk87668 Synthetic
c	47	11.8	53.6	20	6	ABK87664	Abk87664 Synthetic
	48	11.8	53.6	20	10	ADD25041	Add25041 Mouse cas
c	49	11.8	53.6	20	12	ADJ46478	Adj46478 Human PPP
	50	11.8	53.6	20	12	ADQ15482	Adq15482 Human thy
c	51	11.8	53.6	20	12	ADQ15323	Adq15323 Human thy
c	52	11.8	53.6	20	12	ADQ15336	Adq15336 Human thy
	53	11.8	53.6	20	12	ADQ15472	Adq15472 Human thy
	54	11.8	53.6	21	9	ADA89324	Ada89324 Human IBD
c	55	11.8	53.6	21	13	ADR87279	Adr87279 BCR4-53 s
	56	11.8	53.6	21	13	ADR87280	Adr87280 BCR4-53 a
	57	11.8	53.6	22	6	ABL44778	Abl44778 Human chr
	58	11.8	53.6	22	6	ABL44616	Abl44616 Human chr
	59	11.8	53.6	22	10	ADC39407	Adc39407 Novel hum
c	60	11.6	52.7	18	6	ABT05087	Abt05087 TNFR1 exp
c	61	11.6	52.7	18	13	ADR06117	Adr06117 Human TNF
	62	11.6	52.7	19	3	AAZ70188	Aaz70188 Human bia
c	63	11.6	52.7	19	6	ABT11816	Abt11816 E chaffee
	64	11.6	52.7	20	4	AAH77788	Aah77788 PCR prime
	65	11.6	52.7	20	9	ACC59349	Acc59349 Murine MI
c	66	11.6	52.7	20	10	ABZ91134	Abz91134 Human oli
	67	11.6	52.7	20	10	ABZ93362	Abz93362 Human oli
c	68	11.6	52.7	20	11	ABD27364	Abd27364 H05893-de
	69	11.6	52.7	20	11	ABD29592	Abd29592 H86812-de
c	70	11.6	52.7	20	12	ADI57114	Adi57114 Oryza min
c	71	11.6	52.7	20	12	ADJ17180	Adj17180 Antisense
c	72	11.6	52.7	20	12	ADJ16847	Adj16847 Antisense
c	73	11.6	52.7	21	2	ADG77351	Adg77351 Canine di
c	74	11.6	52.7	21	6	ABX09387	Abx09387 Arteriosc
	75	11.6	52.7	22	2	AAQ86462	Aaq86462 IFN-omega
c	76	11.4	51.8	13	5	ABC71407	Abc71407 Oligonucl
	77	11.4	51.8	13	5	ABC71406	Abc71406 Oligonucl
c	78	11.4	51.8	14	2	AAA19216	Aaa19216 Human TIE
	79	11.4	51.8	14	6	ABT13115	Abt13115 Fanconi a
	80	11.4	51.8	14	10	ADC42352	Adc42352 Human FAN
	81	11.4	51.8	17	2	AAX68784	Aax68784 Human flt
	82	11.4	51.8	17	2	AAV97923	Aav97923 Human EGF
	83	11.4	51.8	17	2	AAV97925	Aav97925 Human EGF
	84	11.4	51.8	17	2	AAV97922	Aav97922 Human EGF
	85	11.4	51.8	17	2	AAV97924	Aav97924 Human EGF
	86	11.4	51.8	18	2	AAQ57499	Aaq57499 Rat GAP-4
	87	11.4	51.8	18	2	AAQ57508	Aaq57508 Rat GAP-4
	88	11.4	51.8	19	2	AAX61172	Aax61172 Human chr
	89	11.4	51.8	19	2	AAX61168	Aax61168 Human chr
	90	11.4	51.8	19	2	AAX61141	Aax61141 Human chr
	91	11.4	51.8	19	3	AAZ72328	Aaz72328 Human bia
c	92	11.4	51.8	19	10	ADF36174	Adf36174 Human VEG
	93	11.4	51.8	19	10	ADF35747	Adf35747 Human VEG

c	94	11.4	51.8	19	12	ADQ62530	Adq62530 Anti-inte
	95	11.4	51.8	20	2	AAX58979	Aax58979 PCR prime
c	96	11.4	51.8	20	2	AAV84314	Aav84314 Human JAG
	97	11.4	51.8	20	2	AAX38517	Aax38517 E. coli S
c	98	11.4	51.8	20	2	AAX94099	Aax94099 PCR prime
c	99	11.4	51.8	20	4	AAH37845	Aah37845 SNP speci
	100	11.4	51.8	20	6	AAD35778	Aad35778 Human hIb

ALIGNMENTS

RESULT 1
AAZ50444
ID AAZ50444 standard; DNA; 22 BP.
XX
AC AAZ50444;
XX
DT 18-MAY-2000 (first entry)
XX
DE EST R00504-specific primer 1.
XX
KW PB39; human; prostate cancer; PC; chromosome 11p11.1-11.2; cancer;
KW prostate epithelium; splicing mechanism; early diagnosis; progression;
KW precancerous cell; metastatic potential; non-neoplastic prostate disease;
KW expressed sequence tag; EST; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200005376-A1.
XX
PD 03-FEB-2000.
XX
PF 23-JUL-1999; 99WO-US016831.
XX
PR 24-JUL-1998; 98US-0094137P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Chuaqui RF, Cole KA, Liotta LA;
XX
DR WPI; 2000-182700/16.
XX
PT Novel gene which is dysregulated in prostate cancer useful for diagnosing
PT cancer.
XX
PS Claim 5; Page 16; 51pp; English.
XX
CC The present sequence is the EST AAR00504-specific PCR primer, used for
CC amplification of sequences contained within the EST AAR00504. It is
CC useful to probe the gene overexpressed in prostate cancer epithelium and
CC to analyse the differential expression of the EST. The PB39 gene that is
CC dysregulated in prostate cancer is isolated from human pancreas cDNA
CC library and has homology to the EST AAR00504. PB39 gene is located on
CC chromosome 11p11.1-11.2. Abnormally high concentrations of PB39 are found
CC in prostate tissue derived from prostate cancer (PC) epithelium. PB39
CC sequence is useful for detection of precancerous or cancer cells in the
CC prostate. PB39 is useful for early diagnosis of the progression of
CC prostate cancer, especially in aggressive prostate carcinoma. It can also
CC distinguish PC from other non-neoplastic prostate disease. The diagnostic
CC method is selective and specific for various types of PC and also
CC facilitates identifying prostate cancer of differing aggressiveness and
CC metastatic potential
XX
SQ Sequence 22 BP; 8 A; 4 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 22; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.51;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATGTTACAGGTAGAAAAGCC 22
||||||||||||||||||||||
Db 1 GCATGTTACAGGTAGAAAAGCC 22

RESULT 2
AAX96007/c
ID AAX96007 standard; DNA; 20 BP.
XX
AC AAX96007;
XX
DT 13-SEP-1999 (first entry)
XX
DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX
KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW neutralising epitope; PCR primer; ss.
XX
OS Synthetic.
OS Chlamydophila pneumoniae.
XX
PN WO9927105-A2.
XX
PD 03-JUN-1999.
XX
PF 20-NOV-1998; 98WO-IB001890.
XX
PR 21-NOV-1997; 97FR-00014673.
PR 04-NOV-1998; 98US-0107078P.
XX
PA (GEST) GENSET.
XX
PI Griffais R;
XX
DR WPI; 1999-357842/30.
XX
PT Genome sequence of Chlamydia pneumoniae.
XX
PS Page 1792; Disclosure; 1912pp; English.
XX
CC AAX91991-X97517 represent PCR primers used to amplify open reading frames
CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC (see AAX91990). C. pneumoniae causes respiratory disease such as
CC pneumonia and bronchitis and is thought to be a contributing factor in
CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotides sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae
XX
SQ Sequence 20 BP; 4 A; 5 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 69.1%; Score 15.2; DB 2; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GCATGTTACAGGTAGAAAAG 20
|| |||| ||| ||||||||
Db 20 GCCTGTTCCAGATAGAAAAG 1

RESULT 3
AAI98006
ID AAI98006 standard; DNA; 21 BP.
XX
AC AAI98006;
XX
DT 20-NOV-2001 (first entry)
XX
DE Lawsonia intracellularis protein related oligonucleotide SEQ ID NO: 50.
XX
KW HtrA; PonA; HypC; YefW; ABC1; Omp100; Lawsonia intracellularis infection;
KW vaccine; PCR primer; probe; ss.

XX
OS Lawsonia intracellularis.
XX
PN JP2001169787-A.
XX
PD 26-JUN-2001.
XX
PF 20-OCT-2000; 2000JP-00320736.
XX
PR 22-OCT-1999; 99US-0160922P.
XX
PA (PFIZ) PFIZER PROD INC.
XX
DR WPI; 2001-592540/67.
XX
PT Lawsonia intracellularis polynucleotide and encoded protein, used to
PT prevent Lawsonia intracellularis infection.
XX
PS Example 2; Page 55; 67pp; Japanese.
XX
CC The present invention provides isolated polynucleotides encoding HtrA,
CC PonA, HypC, LysS, YefW, ABC1 or Omp100 protein of Lawsonia
CC intracellularis. The sequences can be used in vaccines for the prevention
CC of Lawsonia intracellularis infection. The present sequence is an
CC oligonucleotide described in the exemplification of the invention
XX
SQ Sequence 21 BP; 10 A; 3 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 60.0%; Score 13.2; DB 4; Length 21;
Best Local Similarity 83.3%; Pred. No. 1.2e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TGTTACAGGTAGAAAAGC 21
|| ||||| ||||||||
Db 2 TGGTACAGCAAGAAAAGC 19

RESULT 4
ACA92364
ID ACA92364 standard; DNA; 21 BP.
XX
AC ACA92364;
XX
DT 16-JUL-2003 (first entry)
XX
DE Lawsonia intracellularis DNA PCR primer #41.
XX
KW Primer; ss; antibacterial; HtrA; PonA; HypC; LysS; YcfW; ABC1; Omp100;
KW Lawsonia intracellularis infection; Orf1; pig; PCR.
XX
OS Lawsonia intracellularis.
XX
PN US2003021802-A1.
XX
PD 30-JAN-2003.
XX
PF 01-AUG-2002; 2002US-00210296.
XX
PR 22-OCT-1999; 99US-0160922P.
PR 05-NOV-1999; 99US-0163858P.
PR 12-OCT-2000; 2000US-00689065.
XX
PA (ROSE/) ROSEY E L.
XX
PI Rosey EL;
XX
DR WPI; 2003-416977/39.
XX
PT New isolated Lawsonia intracellularis polynucleotide and polypeptide,
PT useful for the prevention and diagnosis of Lawsonia infections in
PT susceptible animals, such as pigs.
XX
PS Example 2; Page 46; 64pp; English.
XX
CC The invention relates to an isolated polynucleotide molecule comprising a
CC sequence encoding Lawsonia intracellularis HtrA, PonA, HypC, LysS, YcfW,
CC ABC1 or Omp100 protein. The invention also relates to a genetic construct
CC comprising a polynucleotide molecule that can be used to alter a Lawsonia
CC gene, comprising a polynucleotide molecule comprising a sequence that is
CC otherwise the same as a nucleotide sequence of a htrA, ponA, hypC, lysS,
CC ycfW, abc1 or omp100 gene, or its homologue, a substantial portion, or
CC mutations capable of altering the above mentioned genes or a
CC polynucleotide molecule comprising a sequence that naturally flanks in
CC situ the ORF of the htrA, ponA, hypC, lysS, ycfW, abc1 or omp100 gene or
CC its homologue. The invention also relates to a fusion protein of a
CC polypeptide of the invention fused to another polypeptide or an analogue
CC or derivative. The invention further relates to a substantially pure
CC polypeptide comprising an epitope of HtrA, PonA, HypC, LysS, YcfW, ABC1
CC or Omp100 protein that is specifically reactive with anti-Lawsonia
CC antibodies. The methods and compositions of the present invention are
CC useful for the prevention and diagnosis of L. intracellularis infections
CC in susceptible animals, such as pigs. Sequences ACA92324-ACA92415
CC represent PCR primers used to amplify DNA encoding L. intracellularis
CC proteins of the invention
XX
SQ Sequence 21 BP; 10 A; 3 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 60.0%; Score 13.2; DB 9; Length 21;
Best Local Similarity 83.3%; Pred. No. 1.2e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TGTTACAGGTAGAAAAGC 21
|| ||||| ||||||||
Db 2 TGGTACAGCAAGAAAAGC 19

RESULT 5
ADG33930
ID ADG33930 standard; DNA; 21 BP.
XX
AC ADG33930;
XX
DT 26-FEB-2004 (first entry)
XX
DE L. intracellularis sequencing primer #26.
XX
KW Lawsonia intracellularis; HtrA; PonA; HypC; LysS; YcfW; ABC1; Omp100;
KW pig; ss; sequencing; primer.
XX
OS Lawsonia intracellularis.
XX
PN US2003202983-A1.
XX
PD 30-OCT-2003.
XX
PF 29-MAY-2003; 2003US-00449462.
XX
PR 22-OCT-1999; 99US-0160922P.
PR 05-NOV-1999; 99US-0163858P.
PR 12-OCT-2000; 2000US-00689065.
XX
PA (ROSE/) ROSEY E L.
XX
PI Rosey EL;
XX
DR WPI; 2003-900619/82.
XX
PT New isolated Lawsonia intracellularis polynucleotide and polypeptide,
PT useful for the prevention and diagnosis of Lawsonia infections in
PT susceptible animals, such as pigs.
XX
PS Example 2; SEQ ID NO 50; 66pp; English.
XX
CC The invention relates to a new isolated polynucleotide molecule which
CC encodes Lawsonia intracellularis HtrA, PonA, HypC, LysS, YcfW, ABC1 or
CC Omp100 protein. The methods and compositions of the present invention are

```
CC   useful for the prevention and diagnosis of L. intracellularis infections
CC   in susceptible animals, such as pigs. The present sequence is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 21 BP; 10 A; 3 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             60.0%;  Score 13.2;  DB 10;  Length 21;
  Best Local Similarity   83.3%;  Pred. No. 1.2e+04;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 TGTTACAGGTAGAAAAGC 21
              || |||||  ||||||||
Db          2 TGGTACAGCAAGAAAAGC 19


RESULT 6
ADJ66835
ID   ADJ66835 standard; DNA; 21 BP.
XX
AC   ADJ66835;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Lawsonia intracellularis PCR primer SeqID50.
XX
KW   antibacterial; vaccine; HtrA; PonA; HypC; LysS; YcfW; ABC1; Omp100;
KW   diagnostic agent; infection; pig; porcine proliferative enteropathy; PCR;
KW   primer; ss.
XX
OS   Lawsonia intracellularis.
XX
PN   US6605696-B1.
XX
PD   12-AUG-2003.
XX
PF   12-OCT-2000; 2000US-00689065.
XX
PR   22-OCT-1999;   99US-0160922P.
PR   05-NOV-1999;   99US-0163868P.
XX
PA   (PFIZ ) PFIZER INC.
PA   (PFIZ ) PFIZER PROD INC.
XX
PI   Rosey EL;
XX
DR   WPI; 2003-895290/82.
XX
PT   New Lawsonia intracellularis polypeptides, useful as vaccines, as
PT   diagnostic agents, or in preventing infections in susceptible animals
PT   such as pigs, e.g. porcine proliferative enteropathy.
XX
PS   Example 2; SEQ ID NO 50; 62pp; English.
XX
CC   This invention relates to a novel isolated polypeptide derived from
CC   Lawsonia intracellularis. The invention may be useful for the development
CC   of compounds with an antibacterial activity or a vaccine. Specifically
CC   claimed are L intracellularis proteins, such as HtrA, PonA, HypC, LysS,
CC   YcfW, ABC1 and Omp100 proteins. The invention may be useful for the
CC   development of vaccines, diagnostic agents, or in preventing L
CC   intracellularis infections in susceptible animals such as pigs, for
CC   example porcine proliferative enteropathy. The present sequence is that
CC   of a PCR primer which was used for amplification and/or sequencing of a
CC   region of L intracellularis DNA during the exemplification of the
CC   invention.
XX
SQ   Sequence 21 BP; 10 A; 3 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             60.0%;  Score 13.2;  DB 10;  Length 21;
  Best Local Similarity   83.3%;  Pred. No. 1.2e+04;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 TGTTACAGGTAGAAAAGC 21
              || |||||  ||||||||
Db          2 TGGTACAGCAAGAAAAGC 19


RESULT 7
ADR72987
ID   ADR72987 standard; DNA; 21 BP.
XX
AC   ADR72987;
XX
DT   04-NOV-2004  (first entry)
XX
DE   Lawsonia intracellularis DNA sequence #41.
XX
KW   HtrA; PonA; HypC; LysS; YcfW; ABC1; Omp100; infection; primer; probe; ss.
XX
OS   Lawsonia intracellularis.
XX
PN   JP2004229667-A.
XX
PD   19-AUG-2004.
XX
PF   26-MAR-2004; 2004JP-00092095.
XX
PR   22-OCT-1999;   99US-0160922P.
PR   20-OCT-2000; 2000JP-00320736.
XX
PA   (PFIZ ) PFIZER PROD INC.
XX
DR   WPI; 2004-597336/58.
XX
PT   Novel isolated polynucleotide comprising Lawsonia intracellularis
PT   nucleotide sequence that encodes HtrA, PonA, HypC, LysS, YcfW, ABC1 or
PT   Omp100 protein or its essential portion, useful as diagnostic agent.
XX
PS   Example 2; SEQ ID NO 50; 55pp; Japanese.
XX
CC   The invention comprises the amino acid and coding sequences of the
CC   Lawsonia intracellularis proteins: HtrA, PonA, HypC, LysS, YcfW, ABC1,
CC   and Omp100. The DNA and protein sequences of the invention are useful for
CC   preventing Lawsonia intracellularis infection of animals (e.g. pig). The
CC   present DNA sequence was used in the exemplification of the invention.
CC   NOTE: The present sequence is not shown in the specification but was
CC   obtained from the Japanese Patent Office.
XX
SQ   Sequence 21 BP; 10 A; 3 C; 5 G; 3 T; 0 U; 0 Other;

  Query Match             60.0%;  Score 13.2;  DB 13;  Length 21;
  Best Local Similarity   83.3%;  Pred. No. 1.2e+04;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 TGTTACAGGTAGAAAAGC 21
              || |||||  ||||||||
Db          2 TGGTACAGCAAGAAAAGC 19


RESULT 8
AAF85459/c
ID   AAF85459 standard; DNA; 22 BP.
XX
AC   AAF85459;
XX
DT   23-JUL-2001  (first entry)
XX
DE   Polynucleotide in unique region in exon 1 of rabbit motilin receptor.
XX
KW   Motilin receptor; gastrointestinal disease; gastric motility disorder;
KW   gastroparesis; irritable bowel syndrome; diarrhoea; ss.
XX
OS   Oryctolagus cuniculus.
XX
PN   WO200132710-A1.
XX
PD   10-MAY-2001.
```

XX
PF 25-OCT-2000; 2000WO-US029426.
XX
PR 29-OCT-1999; 99US-0162264P.
XX
PA (MERI) MERCK & CO INC.
XX
PI Tan C, Mckee K;
XX
DR WPI; 2001-343479/36.
XX
PT Novel polypeptides related to dog and rabbit motilin receptor
PT polypeptide, comprising unique regions from dog and motilin receptor
PT amino acid sequence, useful for identifying compounds for treating
PT diarrhea in humans.
XX
PS Claim 17; Page 22; 42pp; English.
XX
CC AAF85456-60 represent polynucleotide sequences from the unique region of
CC exon 1 of a rabbit motilin receptor gene. The specification describes an
CC unique sequence present in exon 1 of the motilin receptor, which is not
CC present in human or Sphaeroides nephelus 75E7 motilin receptor sequences.
CC The unique nucleic acid sequence is useful for measuring the ability of a
CC compound to affect motilin receptor activity. Motilin receptor
CC polynucleotides and polypeptides are used to identify therapeutic
CC compounds which are useful for treating gastrointestinal diseases and
CC disorders such as gastric motility disorders, gastroparesis, irritable
CC bowel syndrome, and diarrhoea
XX
SQ Sequence 22 BP; 2 A; 7 C; 5 G; 8 T; 0 U; 0 Other;

Query Match 59.1%; Score 13; DB 4; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.5e+04;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 CAGGTAGAAAAGC 21
||||||||||||||
Db 13 CAGGTAGAAAAGC 1

RESULT 9
AAA60336/c
ID AAA60336 standard; DNA; 19 BP.
XX
AC AAA60336;
XX
DT 07-DEC-2000 (first entry)
XX
DE Human HPC2 cDNA exon 18 mutation screening primer SEQ ID NO: 157.
XX
KW Human; mouse; prostate cancer predisposing gene; HPC2;
KW human chromosome 17p; gene therapy; peptide therapy; drug design;
KW PCR primer; sequencing primer; ss.
XX
OS Homo sapiens.
XX
PN WO200027864-A1.
XX
PD 18-MAY-2000.
XX
PF 05-NOV-1999; 99WO-US026055.
XX
PR 06-NOV-1998; 98US-0107468P.
XX
PA (MYRI-) MYRIAD GENETICS INC.
XX
PI Tavtigian SV, Teng DHF, Simard J, Rommens JM;
XX
DR WPI; 2000-376481/32.
XX
PT Human prostate cancer (HPC)2 nucleic acids, polypeptides, and antibodies,
PT useful for treatment and diagnosis of prostate cancer.
XX
PS Example 5; Page 61; 157pp; English.
XX
CC The present sequence is a primer used in the isolation of the human and
CC murine prostate cancer predisposing genes HPC2 and Mm.HPC2. The human
CC version of the gene is found on chromosome 17p. Some alleles cause a
CC predisposition to cancer, particularly prostate cancer. This gene and its
CC protein can be used in peptide and gene therapy for cancer patients, as
CC well as being useful as diagnostic tools (both for cancer sufferers and
CC those with a predisposition to the disease) and in the production of
CC cancer drugs
XX
SQ Sequence 19 BP; 2 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

Query Match 58.2%; Score 12.8; DB 3; Length 19;
Best Local Similarity 87.5%; Pred. No. 1.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 ATGTTACAGGTAGAAA 18
|||| ||||| |||||
Db 19 ATGTCACAGGCAGAAA 4

RESULT 10
AAS99071/c
ID AAS99071 standard; DNA; 19 BP.
XX
AC AAS99071;
XX
DT 12-MAR-2002 (first entry)
XX
DE Human prostate cancer predisposing gene (HPC2) PCR primer #67.
XX
KW Human; mouse; HPC2; prostate cancer; neoplastic growth; cytostatic; ss;
KW gene therapy; prostate cancer predisposing gene; chimpanzee; gorilla;
KW sequencing primer; PCR primer.
XX
OS Homo sapiens.
XX
PN WO200185911-A2.
XX
PD 15-NOV-2001.
XX
PF 07-MAY-2001; 2001WO-US014602.
XX
PR 05-MAY-2000; 2000US-00564805.
XX
PA (MYRI-) MYRIAD GENETICS INC.
PA (HOSP-) HOSPITAL FOR SICK CHILDREN.
XX
PI Tavtigian SV, Teng DHF, Simard J, Rommens JM;
XX
DR WPI; 2002-066599/09.
XX
PT Novel nucleic acid sequence encoding HPC2 polypeptide, which is marker
PT for prostate cancer, is useful in gene therapy techniques to restore HPC2
PT normal levels by which neoplastic growth is suppressed in recipient cell.
XX
PS Example 8; Page 74; 239pp; English.
XX
CC The invention relates to a human prostate cancer predisposing gene coding
CC for an HPC2 polypeptide. The DNA and protein sequences are useful as
CC diagnostic reagents for identifying a mutant HPC2 nucleotide sequence in
CC a suspected mutant HPC2 allele by comparing the sequence of the suspected
CC mutant HPC2 allele with a wild-type HPC2 sequence. The sequences are also
CC useful for detecting an alteration in HPC2, where the alteration is
CC associated with cancer in a human. The method involves analysing an HPC2
CC gene or an HPC2 gene expression product from a tissue of the human. The
CC HPC2 gene is useful as a marker for prostate cancer and can be used in
CC gene therapy techniques to suppress neoplastic growth of recipient cells
CC which carry the mutant HPC2 allele. The sequences represent primers used
CC in the methods of the invention, cDNA encoding human and mouse HPC2 and
CC cDNA encoding HPC2 paralogues and orthologues
XX

```
SQ   Sequence 19 BP; 2 A; 6 C; 4 G; 7 T; 0 U; 0 Other;

  Query Match             58.2%;  Score 12.8;  DB 6;  Length 19;
  Best Local Similarity   87.5%;  Pred. No. 1.9e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 ATGTTACAGGTAGAAA 18
              |||| ||||| ||||
Db         19 ATGTCACAGGCAGAAA 4


RESULT 11
AAT33010/c
ID   AAT33010 standard; DNA; 20 BP.
XX
AC   AAT33010;
XX
DT   23-OCT-1996  (first entry)
XX
DE   Mouse SRY-related gene primer 2.
XX
KW   Mouse; SRY; primer; PCR; polymerase chain reaction; amplification; probe;
KW   HMG box; human; bovine; sex; animal; birth; ss.
XX
OS   Synthetic.
XX
PN   JP08154685-A.
XX
PD   18-JUN-1996.
XX
PF   30-NOV-1994;   94JP-00319525.
XX
PR   30-NOV-1994;   94JP-00319525.
XX
PA   (KACH-) KACHIKU JUSEIRAN ISHOKU GIKUTSU KENKYUKU.
XX
DR   WPI; 1996-336575/34.
XX
PT   Bovine and mouse Sry-related DNA - useful for detecting e.g. the sex of
PT   unborn animals.
XX
PS   Example 2; Page 6; 21pp; Japanese.
XX
CC   The primers AAT33009-10 were used to amplify a fragment of the gene
CC   encoding a mouse SRY-related protein (AAT33007). This primer corresp. to
CC   bases 7156-7175 of the mouse gene. The amplified fragment was used to
CC   screen a mouse genomic library. The screen isolated 4 EcoRI fragments of
CC   2.3, 2.8, 3.5 and 1.5 kb covering the gene. Sequence analysis revealed a
CC   240 bp HMG box sequence between bases 7154-7393. Similarity with the
CC   human SRY HMG box sequence resulted in primers being generated to amplify
CC   the human SRY HMG box sequence for use as a probe to isolate the bovine
CC   SRY-related gene (AAT33008). The mouse and bovine genes are useful for
CC   determining the sex of an animal prior to birth
XX
SQ   Sequence 20 BP; 4 A; 6 C; 4 G; 6 T; 0 U; 0 Other;

  Query Match             58.2%;  Score 12.8;  DB 2;  Length 20;
  Best Local Similarity   87.5%;  Pred. No. 1.9e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 TACAGGTAGAAAAGCC 22
              | ||||| ||||||||
Db         20 TGCAGGTGGAAAAGCC 5


RESULT 12
ABK87666/c
ID   ABK87666 standard; DNA; 20 BP.
XX
AC   ABK87666;
XX
DT   24-SEP-2002  (first entry)
XX
DE   Synthetic oligo #21, for selective randomisation of zinc finger protein.
XX
KW   Selectively randomised synthetic oligonucleotide; NNN randomisation;
KW   resin-splitting; zinc finger; ss.
XX
OS   Synthetic.
XX
PN   WO200222634-A1.
XX
PD   21-MAR-2002.
XX
PF   12-SEP-2001; 2001WO-GB004084.
XX
PR   12-SEP-2000; 2000GB-00022330.
XX
PA   (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI   Choo Y,  Isalan M;
XX
DR   WPI; 2002-507792/54.
XX
PT   Making selectively randomized synthetic oligonucleotide by utilizing
PT   phosphoramidite dinucleotide and mononucleotide synthesis strategy, where
PT   a deprotecting step is performed after each coupling step.
XX
PS   Example 3; Fig 1B; 42pp; English.
XX
CC   The present invention relates to a new method of making selectively
CC   randomised synthetic oligonucleotides. The method involves deprotecting
CC   starting material at 3' position, which is coupled to support in nucleic
CC   acid synthesiser, coupling dinucleotide phosphoramidite to 3' position,
CC   deprotecting the new 3' position of extended oligonucleotide, coupling
CC   mononucleotide phosphoramidite to the 3' position and repeating coupling
CC   steps until desired length oligonucleotide is obtained. The method of the
CC   invention is useful for making selectively randomised synthetic
CC   oligonucleotides. Unlike prior art techniques, the method provides
CC   randomised oligonucleotides without the problems of NNN randomisation,
CC   without having to resort to complicated resin-splitting procedures or the
CC   use of low coupling efficiency trinucleotide phosphoramidites. The
CC   present nucleic acid sequence represents one of a collection (ABK87646-
CC   ABK87669 and ABK87671-ABK87676) of synthetic oligonucleotides that were
CC   used in the invention for selective randomisation of zinc finger protein
XX
SQ   Sequence 20 BP; 1 A; 5 C; 2 G; 6 T; 0 U; 6 Other;

  Query Match             58.2%;  Score 12.8;  DB 6;  Length 20;
  Best Local Similarity   61.1%;  Pred. No. 1.9e+04;
  Matches   11;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 TGTTACAGGTAGAAAAGC 21
              |:::  ||::||||||||
Db         19 TSYKCGAGKYAGAAAAGC 2


RESULT 13
ADA66516/c
ID   ADA66516 standard; DNA; 20 BP.
XX
AC   ADA66516;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Transforming growth factor-beta 3 antisense oligonucleotide, SEQ ID 75.
XX
KW   Cytostatic; antirheumatic; antiarthritic; gynecological;
KW   antiarteriosclerotic; Transforming Growth Factor beta-3; TGF beta-3;
KW   hyperproliferative disorder; cancers; atherosclerosis;
KW   rheumatoid arthritis; preeclampsia; fibrosis; phosphorothioate; ss.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base    1. .20
```

```
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "This oligonucleotide has a phosphorothioate
FT                   backbone and 2-'methyoxyethyl (2'-MOE) wings at the 5'
FT                   and 3' ends, which are 5 nucleotides in length. Also all
FT                   cytidine residues are 5-methylcytidines"
XX
PN   WO2003008544-A2.
XX
PD   30-JAN-2003.
XX
PF   12-JUL-2002; 2002WO-US022423.
XX
PR   14-JUL-2001; 2001US-00906158.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP,  Freier SM;
XX
DR   WPI; 2003-229569/22.
XX
PT   Novel antisense compound which is targeted to nucleic acid encoding
PT   transforming growth factor beta-3, and inhibits expression of TGF-beta 3,
PT   useful for treating a condition associated with TGF-beta 3, e.g. cancer.
XX
PS   Claim 3; Page 88; 154pp; English.
XX
CC   The present invention relates to antisense oligonucleotides (ADA66459-
CC   ADA66609), which inhibit Transforming Growth Factor (TGF) beta-3
CC   expression. The oligonucleotides are useful for inhibiting the expression
CC   of TGF-beta3 in cells or tissues, and for treating an animal having a
CC   disease condition associated with TGF-beta3, e.g. a hyperproliferative
CC   disorder such as cancers of lung, liver, colon, oesophagus, pancreas,
CC   breast, skin or haematopoietic, atherosclerosis, rheumatoid arthritis,
CC   preeclampsia and fibrosis.
XX
SQ   Sequence 20 BP; 2 A; 5 C; 4 G; 9 T; 0 U; 0 Other;

  Query Match             58.2%;  Score 12.8;  DB 10;  Length 20;
  Best Local Similarity   87.5%;  Pred. No. 1.9e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 TACAGGTAGAAAAGCC 22
              |||||| |||||| ||
Db         18 TACAGGGAGAAAATCC 3


RESULT 14
ADG89282/c
ID   ADG89282 standard; DNA; 21 BP.
XX
AC   ADG89282;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Cancer detection method related oligonucleotide #230.
XX
KW   ss; cancer; gene expression;
KW   estrogen receptor-positive invasive breast cancer.
XX
OS   Homo sapiens.
XX
PN   WO2003078662-A1.
XX
PD   25-SEP-2003.
XX
PF   12-MAR-2003; 2003WO-US007713.
XX
PR   13-MAR-2002; 2002US-0364890P.
PR   18-SEP-2002; 2002US-0412049P.
XX
PA   (GENO-) GENOMIC HEALTH INC.
XX
PI   Baker JB,  Cronin MT,  Kiefer MC,  Shak S,  Walker MG;
XX
DR   WPI; 2003-767536/72.
XX
PT   Predicting clinical outcome for a patient diagnosed with cancer comprises
PT   determining the expression level of one or more genes, and compared to
PT   the amount found in a reference cancer tissue set.
XX
PS   Disclosure; SEQ ID NO 230; 198pp; English.
XX
CC   The invention relates to a method of predicting clinical outcome for a
CC   patient diagnosed with cancer by determining the expression level of one
CC   or more genes, or their expression products, selected from p53BP2,
CC   cathepsin B, cathepsin L, Ki67/MiB1, and thymidine kinase in a cancer
CC   tissue obtained from the patient, normalized against control gene(s), and
CC   compared to the amount found in a reference cancer tissue set. The
CC   specification also discloses an array comprising polynucleotides
CC   hybridizing to the following genes: FOXMI, PRAME, Bcl2, STKI5, CEGP1, Ki-
CC   67, GSTM1, CA9, PR, BBC3, NME1, SURV, GATA3, TFRC, YB-1, DPYD, GSTM3,
CC   RPS6KB1, Sro, Chk1, ID1, EstR1, p27, CCNBI, XIAP, Chk2, CDC25B, IGFIR,
CC   AK055699, PI3KC2A, TGFB3, BAGI1, CYP3A4, EpCAM, VEGFC, pS2, hENT1, WISP1,
CC   HNF3A, NFKBp65, BRCA2, EGFR, TK1, VDR, Contig51037, pENTI, EPHXI, IFIA,
CC   CDHI, HIF1t, IGFBP3, CTSB, Her2 and DIABLO, immobilized on a solid
CC   surface. The methods are useful for predicting clinical outcome for a
CC   patient diagnosed with cancer, classifying cancer, and predicting the
CC   likelihood of long-term survival of a breast cancer patient, or a patient
CC   diagnosed with invasive breast cancer or with estrogen receptor (ER)-
CC   positive invasive breast cancer. This sequence corresponds to an
CC   oligonucleotide used in the method of the invention.
XX
SQ   Sequence 21 BP; 5 A; 6 C; 5 G; 5 T; 0 U; 0 Other;

  Query Match             58.2%;  Score 12.8;  DB 10;  Length 21;
  Best Local Similarity   87.5%;  Pred. No. 1.9e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 TACAGGTAGAAAAGCC 22
              | | ||||||||||||
Db         21 TTCTGGTAGAAAAGCC 6


RESULT 15
ADP27751/c
ID   ADP27751 standard; DNA; 21 BP.
XX
AC   ADP27751;
XX
DT   26-AUG-2004  (first entry)
XX
DE   PCR primer to amplify a human cancer prognostic marker DNA SeqID 188.
XX
KW   human; primer; PCR; prognostic marker; EGFR;
KW   epidermal growth factor receptor; cancer; gene expression profiling;
KW   microarray; head and neck cancer; colon cancer; metastatic spread;
KW   neoplastic disease; ss.
XX
OS   Homo sapiens.
XX
PN   WO2004046386-A1.
XX
PD   03-JUN-2004.
XX
PF   14-NOV-2003; 2003WO-US036777.
XX
PR   15-NOV-2002; 2002US-0427090P.
XX
PA   (GENO-) GENOMIC HEALTH INC.
PA   (VALL-) VALL HEBRON UNIV HOSPITAL.
XX
PI   Baker JB,  Cronin MT,  Shak S,  Baselga J;
XX
DR   WPI; 2004-420643/39.
XX
```

PT Prognosing a patient with EGFR-expressing colon cancer comprises
PT subjecting a sample comprising EGFR-expressing cancer cells to
PT quantitative analysis of the expression level of the RNA transcript of at
PT least one gene e.g., CD44v3.
XX
PS Claim 54; SEQ ID NO 188; 113pp; English.
XX
CC This invention relates to a novel method concerning prognostic markers
CC associated with EGFR (epidermal growth factor receptor) positive cancer.
CC Specifically, it refers to a gene expression profiling method that can
CC provide a prediction as to whether a patient is likely to respond well to
CC treatment with an EGFR inhibitor. The present invention describes the
CC quantitative analysis of the expression level of the RNA transcript of at
CC least one gene selected from the group of CD44v3, CD44v6, DR5, GR01,
CC KRT17, LAMC2 or their products thereof. It further provides a cDNA
CC microarray containing named genes that represent prognostic transcripts
CC which are useful for determining whether a patient diagnosed with an EGFR
CC -expressing head or neck cancer or colon cancer exhibits elevated or
CC decreased expression levels of these genes compared to normal. As such,
CC these methods are also useful for prognosing or predicting the likelihood
CC of cancer-attributable death or progression, including recurrence and
CC metastatic spread of a neoplastic disease, as well as drug resistance.
CC This oligonucleotide sequence is a PCR primer used to amplify a human PCR
CC amplicon DNA sequence used as a prognostic cancer marker, given in an
CC exemplification of the invention.
XX
SQ Sequence 21 BP; 5 A; 6 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 58.2%; Score 12.8; DB 12; Length 21;
Best Local Similarity 87.5%; Pred. No. 1.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 TACAGGTAGAAAAGCC 22
| | ||||||||||||
Db 21 TTCTGGTAGAAAAGCC 6

RESULT 16
ADR00153/c
ID ADR00153 standard; DNA; 21 BP.
XX
AC ADR00153;
XX
DT 21-OCT-2004 (first entry)
XX
DE COX2 probe, SEQ ID 191.
XX
KW Breast cancer; human; ss; probe; COX2.
XX
OS Homo sapiens.
XX
PN WO2004065583-A2.
XX
PD 05-AUG-2004.
XX
PF 14-JAN-2004; 2004WO-US000985.
XX
PR 15-JAN-2003; 2003US-0440861P.
XX
PA (GENO-) GENOMIC HEALTH INC.
PA (UYRU-) UNIV RUSH MEDICAL CENT.
XX
PI Cobleigh MA, Shak S, Baker JB, Cronin MT;
XX
DR WPI; 2004-593480/57.
XX
PT Predicting likelihood of long-term survival of a breast cancer patient
PT without the recurrence of breast cancer by determining the expression
PT level of prognostic RNA transcripts or their expression products in a
PT breast cancer tissue sample.
XX
PS Claim 33; SEQ ID NO 191; 125pp; English.
XX
CC The present invention relates to a method for predicting the likelihood
CC of long-term survival of a breast cancer patient without the recurrence
CC of breast cancer. The method comprises determining the expression level
CC of one or more prognostic RNA transcripts or their expression products in
CC a breast cancer tissue sample obtained from the patient. The prognostic
CC RNA transcript is the transcript of one or more genes, e.g. TP53BP2,
CC GRB7, PR, CD68, Bcl2, KRT14, IRS1, CTSL, EstR1, Chk1, IGFBP2, BAG1,
CC CEGP1, STK15, GSTM1, FHIT, RIZ1, AIB1, SURV, BBC3, IGF1R, p27, GATA3,
CC ZNF217, EGFR, CD9, MYBL2, HIF1alpha, pS2, ErbB3, TOP2B, MDM2, RAD51C,
CC KRT19, TS, Her2, KLK10, beta-Catenin, gamma-Catenin, MCM2, PI3KC2A, IGF1,
CC TBP, CCNB1, FBXO5, or DR5, where expression of one or more of GRB7, CD68,
CC CTSL, Chk1, AIB1, CCNB1, MCM2, FBXO5, Her2, STK15, SURV, EGFR, MYBL2,
CC HIF1alpha, or TS indicates a decreased likelihood of long-term survival
CC without breast cancer recurrence, and where the expression of one or more
CC of TP53BP2, PR, Bc12, KRT14, EstR1, IGFBP2, BAG1, CEGP1, KLK10, beta-
CC Catenin, gamma-Catenin, DR5, PI3KCA2, RAD51C, GSTM1, FHIT, RIZ1, BBC3,
CC TBP, p27, IRS1, IGF1R, GATA3, ZNF217, CD9, pS2, ErbB3, TOP2B, MDM2, IGF1,
CC or KRT19 indicates an increased likelihood of long-term survival without
CC breast cancer recurrence. The present sequence is a probe used to amplify
CC one such prognostic gene of the invention.
XX
SQ Sequence 21 BP; 5 A; 6 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 58.2%; Score 12.8; DB 13; Length 21;
Best Local Similarity 87.5%; Pred. No. 1.9e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 7 TACAGGTAGAAAAGCC 22
| | ||||||||||||
Db 21 TTCTGGTAGAAAAGCC 6

RESULT 17
ADQ13916/c
ID ADQ13916 standard; DNA; 20 BP.
XX
AC ADQ13916;
XX
DT 07-OCT-2004 (first entry)
XX
DE DMD region PCR primer, SEQ ID 311.
XX
KW Human; SCAIP; dystrophin; Duchenne Muscular Dystrophy; DMD;
KW Becker Muscular Dystrophy; BMD; PCR; primer; ss;
KW Single Condition Amplification/ Internal Primer.
XX
OS Homo sapiens.
XX
PN WO2004058985-A2.
XX
PD 15-JUL-2004.
XX
PF 17-DEC-2003; 2003WO-US040278.
XX
PR 17-DEC-2002; 2002US-0433774P.
XX
PA (UTAH) UNIV UTAH RES FOUND.
XX
PI Flanigan KM, Weiss RB, Dunn DM, Von Niederhausern A;
XX
DR WPI; 2004-525893/50.
XX
PT Characterizing a nucleic acid region, useful for detecting genetic
PT mutations in any large multi-exon gene e.g., those indicating
PT dystrophinopathy, comprises using a Single Condition
PT Amplification/Internal Primer (SCAIP) sequencing method.
XX
PS Example 1; Page 34; 174pp; English.
XX
CC The present invention relates to a Single Condition Amplification/
CC Internal Primer (SCAIP) sequencing method for direct sequence analysis of
CC large multi-exon genes from genomic DNA samples and identifying mutations
CC in multi-exon genes e.g. the dystrophin gene, CAPN3 gene and DYSF gene.

CC Mutations in the dystrophin gene result in both Duchenne Muscular
CC Dystrophy (DMD) and Becker Muscular Dystrophy (BMD). Mutations in the
CC CAPN3 gene, encoding calpain (calcium-activated neutral protease) result
CC in limb-girdle muscular dystrophy type 2A (LGMD2A) and mutations in the
CC DYSF gene, encoding dysferlin, result in limb-girdle muscular dystrophy
CC type 2B (LGMD2B). The method comprises bringing into contact in each of
CC the reaction chambers an amplicon from a different one of the
CC amplification reactions and one or more internal sequencing primers
CC corresponding to the amplicon and analysing the sequences of the
CC amplicons. The method allows for the rapid, accurate, and economical
CC analysis of any large multi-exon gene. The method is useful in detecting
CC genetic mutations in any large multi-exon gene. It is also useful for the
CC identification and analysis of specific individual genomic mutations
CC including deletions, point mutations, or its combinations, gene complexes
CC with multiple exons/introns spanning large genomic regions. The present
CC sequence is a PCR primer, used in the method of the invention.
XX
SQ Sequence 20 BP; 3 A; 4 C; 6 G; 7 T; 0 U; 0 Other;

Query Match 57.3%; Score 12.6; DB 12; Length 20;
Best Local Similarity 78.9%; Pred. No. 2.4e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 4 TGTTACAGGTAGAAAAGCC 22
| ||||| | ||||| |||
Db 20 TCTTACAAGCAGAAAGGCC 2

RESULT 18
ADD18145
ID ADD18145 standard; DNA; 20 BP.
XX
AC ADD18145;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human G-protein coupled receptor (GPCR) related PCR primer Seq ID44.
XX
KW G protein coupled receptor; GPCR; signal transduction pathway; G protein;
KW Alzheimer's disease; Parkinson's disease; diabetes; dwarfism;
KW colour blindness; retinal pigmentosa; asthma; depression; schizophrenia;
KW sleeplessness; hypertension; anxiety; stress; renal failure;
KW cardiovascular disorder; neural disorder; oncology disorder;
KW immune disorder; neuroprotective; gene therapy; PCR; primer; ss.
XX
OS Homo sapiens.
XX
PN WO2003016478-A2.
XX
PD 27-FEB-2003.
XX
PF 15-AUG-2002; 2002WO-US026017.
XX
PR 20-AUG-2001; 2001US-0313658P.
PR 12-SEP-2001; 2001US-0318675P.
PR 30-OCT-2001; 2001US-0340703P.
PR 26-NOV-2001; 2001US-0333417P.
PR 06-DEC-2001; 2001US-0338367P.
PR 06-FEB-2002; 2002US-0355596P.
XX
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
XX
PI Feder JN, Ramanathan CS, Gopal S, Mintier GA;
XX
DR WPI; 2003-278558/27.
XX
PT New nucleic acid, useful for manufacturing a medicament for preventing,
PT treating or ameliorating a medical condition e.g., neural disorder.
XX
PS Example 1; SEQ ID NO 44; 251pp; English.
XX
CC This invention relates to novel G protein coupled receptors (GPCRs) and
CC their encoding nucleotide sequences. Many medically significant
CC biological processes are mediated by proteins participating in signal
CC transduction pathways involving G proteins. GPCRs are one of the largest
CC receptor superfamilies known. These receptors are biologically important
CC and malfunction of these receptors results in diseases such as
CC Alzheimer's, Parkinson's, diabetes, dwarfism, colour blindness, retinal
CC pigmentosa and asthma. They are also involved in depression,
CC schizophrenia, sleeplessness, hypertension, anxiety, stress, renal
CC failure and other cardiovascular, neural, oncology and immune disorders.
CC A modulator of the GPCRs of the invention may have neuroprotective
CC activity whilst the sequences of the invention may be useful for gene
CC therapy. The invention may also be useful for manufacturing a medicament
CC for preventing, treating or ameliorating a medical condition. The present
CC sequence is that of a PCR primer which was used for amplification of a
CC region of a gene encoding a human GPCR during the exemplification of the
CC invention.
XX
SQ Sequence 20 BP; 9 A; 3 C; 7 G; 1 T; 0 U; 0 Other;

Query Match 56.4%; Score 12.4; DB 10; Length 20;
Best Local Similarity 92.9%; Pred. No. 3e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CAGGTAGAAAAGCC 22
|||| |||||||||
Db 2 CAGGAAGAAAAGCC 15

RESULT 19
ADI41032
ID ADI41032 standard; DNA; 20 BP.
XX
AC ADI41032;
XX
DT 22-APR-2004 (first entry)
XX
DE Human HGPRBMY42 gene specific antisense primer.
XX
KW Human; ss; primer; GPCR; G protein-coupled receptor;
KW reproductive disorder; testicular disorder; vas deferens disorder;
KW spermatogenesis; infertility; XX male; epididymitis; cryptorchidism;
KW sperm transport disorder; testicular cancer; testicular germ cell tumour;
KW male hormone disorder; premature puberty; Kallman syndrome;
KW Cushing's syndrome; immune disorder; leukaemia; arthritis; asthma; AIDS;
KW rheumatoid arthritis; inflammatory bowel disease; sepsis;
KW T-cell mediated cytotoxicity; graft-versus-host disease;
KW autoimmunity disorder; systemic lupus erythematosus;
KW drug induced haemolytic anaemia; Sjogren's disease;
KW T-cell maturation disorder; B-cell maturation disorder;
KW vascular disorder; stroke; ischaemia; myocardial infarction;
KW atherosclerosis; gastrointestinal disorder; ulcer; pulmonary disorder;
KW brain disorder; endocrine disorder; cancer; gene therapy; PCR.
XX
OS Homo sapiens.
XX
PN US2004018976-A1.
XX
PD 29-JAN-2004.
XX
PF 13-MAY-2003; 2003US-00436715.
XX
PR 14-MAY-2002; 2002US-0380336P.
XX
PA (FEDE/) FEDER J N.
PA (MINT/) MINTIER G.
PA (RAMA/) RAMANATHAN C S.
XX
PI Feder JN, Mintier G, Ramanathan CS;
XX
DR WPI; 2004-122081/12.
XX
PT New human G-protein coupled receptor polypeptide and polynucleotide,
PT useful for diagnosing, preventing, treating or ameliorating a medical
PT condition, e.g. reproductive disorder, immunodeficiency disease or

```
PT   testicular cancer.
XX
PS   Example 4; SEQ ID NO 92; 290pp; English.
XX
CC   The invention relates to an isolated human G protein-coupled receptor
CC   polypeptide and its encoding polynucleotide, including the full length
CC   proteins minus the start methionine (and the region of the polynucleotide
CC   encoding this protein region). The proteins are designated HGPRBMY30-1,
CC   HGPRBMY30-2, HGPRBMY30-3, HGPRBMY41-1, HGPRBMY41-2, HGPRBMY41-3,
CC   HGPRBMY42, HGPRBMY42-1, HGPRBMY43 and HGPRBMY44. Also included are
CC   expression vectors, host cells, antibodies, preventing (treating or
CC   ameliorating) a medical condition comprising administering to a mammalian
CC   subject the polypeptide or its modulator and diagnosing a pathological
CC   condition or a susceptibility to a pathological condition in a subject
CC   (comprising determining the presence or absence of a mutation in the
CC   polynucleotide, or the presence or amount of expression of the
CC   polypeptide in a biological sample and diagnosing a pathological
CC   condition or a susceptibility to a pathological condition based on the
CC   presence or absence of the mutation, or the presence or amount of
CC   expression of the polypeptide). The human G-protein coupled receptor
CC   polypeptide or polynucleotide can be used for diagnosing a pathological
CC   condition or a susceptibility to a pathological condition in a subject,
CC   and for preventing, treating or ameliorating a medical condition, such as
CC   a disorder related to aberrant G-protein coupled receptor activity, a
CC   disorder related to aberrant signal transduction, a reproductive disorder
CC   ; a male reproductive disorder, a testicular disorder, a vas deferens
CC   disorder, spermatogenesis, infertility, Klinefelter's syndrome, XX male,
CC   epididymitis, genital warts, germinal cell aplasia, cryptorchidism,
CC   varicocele, immotile cilia syndrome, viral orchitis, sperm transport
CC   disorders, testicular cancer, choriocarcinoma, non-seminoma, seminoma,
CC   testicular germ cell tumours, male hormone disorders, premature puberty,
CC   incomplete puberty, Kallman syndrome, Cushing's syndrome, an immune
CC   disorder, a proliferative immune disorder, leukaemia, arthritis, asthma,
CC   immunodeficiency diseases such as AIDS, rheumatoid arthritis,
CC   granulomatous disease, inflammatory bowel disease, sepsis, acne,
CC   neutropenia, neutrophilia, psoriasis, hypersensitivities, such as T-cell
CC   mediated cytotoxicity, immune reactions to transplanted organs and
CC   tissues, such as host-versus-graft and graft-versus-host diseases, or
CC   autoimmunity disorders, such as autoimmune infertility, demyelination,
CC   systemic lupus erythematosus, drug induced haemolytic anaemia, Sjogren's
CC   disease, scleroderma, T-cell maturation disorders, B-cell maturation
CC   disorders, vascular disorders, stroke, ischaemia, myocardial infarction,
CC   atherosclerosis, embolisms, thrombosis, gastrointestinal disorders,
CC   irritable bowel syndrome, ulcers, pulmonary disorders, brain disorders,
CC   endocrine disorders, or ovarian, stomach, colon or kidney cancer or its
CC   related proliferative condition (many other diseases and disorders are
CC   listed in the specification). The antibodies may be used to purify,
CC   detect and target the G-protein coupled receptor polypeptides. The
CC   polynucleotides are also useful in gene therapy. The present sequence is
CC   a gene specific PCR primer for a nucleic acid encoding a novel GPCR of
CC   the invention.
XX
SQ   Sequence 20 BP; 9 A; 3 C; 7 G; 1 T; 0 U; 0 Other;

  Query Match             56.4%;  Score 12.4;  DB 12;  Length 20;
  Best Local Similarity   92.9%;  Pred. No. 3e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 CAGGTAGAAAAGCC 22
              |||| |||||||||
Db          2 CAGGAAGAAAAGCC 15


RESULT 20
ABT16558/c
ID   ABT16558 standard; DNA; 21 BP.
XX
AC   ABT16558;
XX
DT   03-APR-2003  (first entry)
XX
DE   Ethylene insensitivity related PCR primer SEQ ID No 32.
XX
KW   Mutant; transformed plant; ethylene-response DNA-binding factor; edf1;
KW   edf2; edf3; edf4; fruit; transgenic plant; floral industry;
KW   fruit processing industry; floral senescence; flower longevity;
KW   decreased floral initiation; post-harvest; transportation; PCR; primer;
KW   ss.
XX
OS   Unidentified.
XX
PN   WO200289555-A2.
XX
PD   14-NOV-2002.
XX
PF   08-MAY-2002; 2002WO-US014592.
XX
PR   08-MAY-2001; 2001US-0289364P.
PR   08-MAY-2001; 2001US-0289835P.
XX
PA   (SALK ) SALK INST BIOLOGICAL STUDIES.
XX
PI   Stepanova AN,  Ecker JR;
XX
DR   WPI; 2003-120491/11.
XX
PT   Novel mutant or transformed plant comprising mutated forms of edf1, edf2,
PT   edf3 and edf4 genes, and having decreased ethylene sensitivity, such that
PT   its fruit ripens more slowly than wild-type version of the plant.
XX
PS   Disclosure; Page 35; 85pp; English.
XX
CC   The invention relates to a mutant or transformed plant comprising mutated
CC   forms of ethylene-response DNA-binding factors (edf)1, edf2, edf3 and
CC   edf4 genes such that the plant exhibits a decreased response to ethylene,
CC   and comprises fruit which ripens more slowly than a wild-type version of
CC   the plant. The transgenic plants having reduced sensitivity to ethylene
CC   are useful for floral industry and fruit processing industries. Since
CC   ethylene is involved in floral senescence, the modified plants have
CC   longer flower longevity. The modified plants e.g. lettuce, spinach, other
CC   leafy vegetables provide higher yields due to decreased floral
CC   initiation, since the transformed plants do not bolt or flower easily.
CC   The plants provide fruits which ripens more slowly than the wild-type
CC   version of the plant, and thus are advantageous in post-harvest and
CC   transportation conditions. This polynucleotide sequence represents a PCR
CC   primer relating to the ethylene sensitivity modulation process of the
CC   invention
XX
SQ   Sequence 21 BP; 6 A; 4 C; 4 G; 7 T; 0 U; 0 Other;

  Query Match             56.4%;  Score 12.4;  DB 10;  Length 21;
  Best Local Similarity   92.9%;  Pred. No. 3e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCATGTTACAGGTA 14
              |||||||||| |||
Db         18 GCATGTTACACGTA 5


RESULT 21
AAQ61732
ID   AAQ61732 standard; cDNA; 18 BP.
XX
AC   AAQ61732;
XX
DT   25-MAR-2003  (revised)
DT   21-OCT-1994  (first entry)
XX
DE   HEV strain BUR-121 primer R133.
XX
KW   Hepatitis E virus; HEV; strain SAR-55; open reading frame; ORF; PCR;
KW   antibody; detection; diagnosis; primates; stool suspension; amplify;
KW   polymerase chain reaction; primer; burma; strain BUR-121; ss.
XX
OS   Synthetic.
XX
```

PN WO9406913-A2.
XX
PD 31-MAR-1994.
XX
PF 17-SEP-1993; 93WO-US008849.
XX
PR 18-SEP-1992; 92US-00947263.
XX
PA (USSH) US SEC DEPT HEALTH.
XX
PI Tsarev SA, Emerson SU, Purcell RH;
XX
DR WPI; 1994-118462/14.
XX
PT Purified hepatitis E strain SAR-55 virus - used to develop prods. for use
PT in detection, diagnosis, vaccines and therapy of hepatitis E virus
PT infection.
XX
PS Example 1; Page 39; 114pp; English.
XX
CC The sequences given in AAQ45198-200 and AAQ61687-777 are primers which
CC were used in the isolation and amplification of the genomic sequence of
CC the hepatitis E virus (HEV) strain SAR-55. These primers were based on
CC sequences derived from the SAR-55 strain and a strain from Burma (BUR-
CC 121). The amplified sequence contains three open reading frames (ORFs).
CC The proteins encoded by this sequence can be used to stimulate the
CC production of protective antibodies upon injection into a mammal that
CC would serve to protect the mammal upon challenge with wild type HEV. The
CC proteins can be used for detection and diagnosis of HEV infection. This
CC cDNA was isolated from primates innoculated with stool suspensions
CC obtained from hepatitis E patients. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 18 BP; 8 A; 5 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 55.5%; Score 12.2; DB 2; Length 18;
Best Local Similarity 82.4%; Pred. No. 3.7e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GTTACAGGTAGAAAAGC 21
||||||| |||||| |
Db 2 GTTACAGCCAGAAAACC 18

RESULT 22
AAT27443
ID AAT27443 standard; DNA; 18 BP.
XX
AC AAT27443;
XX
DT 27-NOV-1996 (first entry)
XX
DE HEV strain Burma-121 derived reverse primer 133 (ORF-1).
XX
KW Hepatitis E virus; HEV; SAR-55 strain; enteric transmission;
KW structural region; antigen; detection; antibody; vaccine; immunisation;
KW infection; primer; Burma-121; polymerase chain reaction; PCR; ss.
XX
OS Synthetic.
XX
PN WO9610580-A2.
XX
PD 11-APR-1996.
XX
PF 03-OCT-1995; 95WO-US013102.
XX
PR 03-OCT-1994; 94US-00316765.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Tsarev SA, Emerson SU, Purcell RH;
XX
DR WPI; 1996-209320/21.
XX
PT Isolated and purified hepatitis E virus strain SAR-55 DNA - encodes
PT antigenic protein useful in diagnosis, prophylaxis and treatment of
PT hepatitis E virus infection.
XX
PS Example 1; Page 42; 121pp; English.
XX
CC The present sequence is a hepatitis E virus (HEV) strain Burma-121
CC derived primer, used in the isolation of the HEV strain SAR-55 cDNA. The
CC HEV strain SAR-55 was implicated in an enterically transmitted non-A, non
CC -B hepatitis in Pakistan. The protein encoded by the structural region of
CC the virus (i.e. ORF-2), which is capable of forming HEV like particles,
CC is useful for the detection of HEV antibodies (pref. IgG or IgM) in
CC blood, plasma, sera, cerebrospinal fluid, tissue, urine or pleural fluid.
CC The protein, and anti-HEV antibodies generated using the protein, can
CC also be used in vaccines for immunising an animal against HEV infection.
CC The protein is identified as a band of greater than 50 kD following SDS-
CC PAGE of cell lysates of insect cells infected with a HEV ORF-2 contg.
CC baculovirus, i.e. the claimed recombinant expression vectors pPIC9-1779,
CC -1780 and -1781
XX
SQ Sequence 18 BP; 8 A; 5 C; 3 G; 2 T; 0 U; 0 Other;

Query Match 55.5%; Score 12.2; DB 2; Length 18;
Best Local Similarity 82.4%; Pred. No. 3.7e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GTTACAGGTAGAAAAGC 21
||||||| |||||| |
Db 2 GTTACAGCCAGAAAACC 18

RESULT 23
AAV71653
ID AAV71653 standard; DNA; 18 BP.
XX
AC AAV71653;
XX
DT 02-FEB-1999 (first entry)
XX
DE HEV ORF proteins encoding DNA amplifying primer R 133 B.
XX
KW Hepatitis E virus; HEV; SAR-55; diagnostic agent; vaccine; antibody;
KW passive immunisation; open reading frame; ORF; PCR primer; ss.
XX
OS Synthetic.
OS Hepatitis E virus.
XX
PN WO9846761-A1.
XX
PD 22-OCT-1998.
XX
PF 09-APR-1998; 98WO-US007418.
XX
PR 11-APR-1997; 97US-00840316.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Emerson SU, Purcell RH, Tsarev SA, Robinson RA;
XX
DR WPI; 1998-568733/48.
XX
PT New hepatitis E virus DNA from Pakistani strain SAR-55 - used for, e.g.
PT developing products for diagnosis of, and vaccination against hepatitis E
PT virus infection.
XX
PS Example 1; Page 44; 204pp; English.
XX
CC Sequences AAV71605 to AAV71698 represent primers used for PCR
CC amplification of the hepatitis E virus (HEV) DNA SAR-55 encoding the open
CC reading frame (ORF) proteins ORF-1, ORF-2 and ORF-3. A host organism
CC transformed or transfected with a recombinant expression vector
CC containing the SAR-55 nucleic acid can be used to produce the HEV

```
CC   proteins, especially ORF-2 protein. The recombinant HEV proteins can be
CC   used as diagnostic agents and as vaccines for use against HEV infection.
CC   The detection of antibodies specific for HEV can be used for the
CC   diagnosis of infection and diseases caused by HEV, and for monitoring the
CC   progression of such disease. Such methods are also useful for monitoring
CC   the efficacy of therapeutic agents during the course of treatment of HEV
CC   infection and disease in a mammal. The antibodies can be used for
CC   detection or for passive immunisation of mammals
XX
SQ   Sequence 18 BP; 8 A; 5 C; 3 G; 2 T; 0 U; 0 Other;

  Query Match             55.5%;  Score 12.2;  DB 2;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 3.7e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 GTTACAGGTAGAAAAGC 21
              |||||||  |||||| |
Db          2 GTTACAGCCAGAAAACC 18


RESULT 24
AAZ70423
ID   AAZ70423 standard; DNA; 18 BP.
XX
AC   AAZ70423;
XX
DT   10-SEP-2001  (first entry)
XX
DE   Human biallelic marker upstream amplification primer SEQ ID NO:4779.
XX
KW   Human genome; biallelic marker; high density disequilibrium map;
KW   genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW   haplotyping; hybridisation; identification; characterisation;
KW   amplification; single nucleotide polymorphism; SNP; PCR primer;
KW   diagnosis; ss.
XX
OS   Homo sapiens.
XX
PN   WO9954500-A2.
XX
PD   28-OCT-1999.
XX
PF   21-APR-1999;   99WO-IB000822.
XX
PR   21-APR-1998;   98US-0082614P.
PR   23-NOV-1998;   98US-0109732P.
XX
PA   (GEST ) GENSET.
XX
PI   Cohen D,  Blumenfeld M,  Chumakov I;
XX
DR   WPI; 2000-013267/01.
XX
PT   Novel biallelic markers used to construct a high density disequilibrium
PT   map of the human genome.
XX
PS   Claim 8; Page 1250; 2745pp; English.
XX
CC   AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC   invention, which contain a polymorphic base at position 24 of their
CC   nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC   primers for the biallelic markers. The biallelic markers of the invention
CC   have a variety of uses: they can be used for high density mapping of the
CC   human genome, and in complex association studies and haplotyping studies
CC   which are useful in determining the genetic basis for disease states.
CC   Compositions and methods of the invention can also be useful for the
CC   identification of the targets for the development of pharmaceutical
CC   agents and diagnostic methods, as well as the characterisation of the
CC   differential efficacious responses to and side effects from
CC   pharmaceutical agents acting on a disease as well as other treatment.
CC   N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC   3367, are not actually given a sequence in the Sequence Listing from the
CC   present invention
XX
SQ   Sequence 18 BP; 6 A; 0 C; 9 G; 3 T; 0 U; 0 Other;

  Query Match             55.5%;  Score 12.2;  DB 3;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 3.7e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 TGTTACAGGTAGAAAAG 20
              ||| | ||||||| |||
Db          1 TGTGAGAGGTAGAGAAG 17


RESULT 25
ABN89231/c
ID   ABN89231 standard; DNA; 20 BP.
XX
AC   ABN89231;
XX
DT   29-AUG-2002  (first entry)
XX
DE   Human Talin antisense phosphorothioate oligonucleotide SEQ ID NO:44.
XX
KW   Human; Talin; antimicrobial; antiinflammatory; cytostatic; inhibitor;
KW   antisense gene therapy; infection; inflammation; Talin inhibitor; tumour;
KW   antisense oligonucleotide; phosphorothioate; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "phosphorothioate backbone"
FT   modified_base   1. .5
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
PN   US6372492-B1.
XX
PD   16-APR-2002.
XX
PF   30-OCT-2000; 2000US-00702251.
XX
PR   30-OCT-2000; 2000US-00702251.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Bennett CF,  Cowsert LM;
XX
DR   WPI; 2002-470102/50.
XX
PT   New antisense compound useful for inhibiting expression of Talin and for
PT   preventing or delaying infection, inflammation or tumor formation.
XX
PS   Example 15; Col 41; 46pp; English.
XX
CC   The present invention describes an antisense compound (I), 16 to 30 bases
CC   in length targeted to specific base regions of a nucleic acid encoding
CC   human Talin. Also described: (a) an antisense compound up to 30 bases in
CC   length which inhibits the expression of human Talin; (b) a composition
CC   (II) comprising (I) or (a); and (c) inhibiting the expression of human
CC   Talin in human cells or tissues comprising contacting the cells or
CC   tissues in vitro with (I) or (a). (I) has antimicrobial, antiinflammatory
CC   and cytostatic activities, and can be used in antisense gene therapy and
CC   as a Talin expression inhibitor. (I) can be used: to inhibit the
CC   expression of human Talin in human cells or tissues; to prevent or delay
CC   infection, inflammation or tumour formation; and in diagnostics,
CC   therapeutics, prophylaxis, and in research reagents and kits. The present
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CC   sequence represents a human Talin antisense chimeric phosphorothioate
CC   oligonucleotide, having 2'-methoxyethyl (2'-MOE) wings of 5 nucleotides
CC   at the 5' and 3' ends and a 10 nucleotide deoxy gap in the middle, which
CC   is used in an example from the present invention
XX
SQ   Sequence 20 BP; 3 A; 8 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             55.5%;  Score 12.2;  DB 6;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 3.8e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 TGTTACAGGTAGAAAAG 20
              |||| |||| || ||||
Db         19 TGTTGCAGGCAGCAAAG 3


RESULT 26
ADG90494/c
ID   ADG90494 standard; DNA; 20 BP.
XX
AC   ADG90494;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Human talin phosphorothioate antisense oligonucleotide, SEQ ID NO:44.
XX
KW   Human; talin; cellular adhesion; muscle strength; cardiac function;
KW   cardiomyocyte; platelet; prostate; androgen downregulation;
KW   prostate cancer; talin-related disorder;
KW   cellular adhesion-related disorder; expression inhibition;
KW   antisense therapy; phosphorothioate; antisense oligonucleotide; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag= a
FT                   /mod_base
FT                   /note= "This oligonucleotide has a phosphorothioate
FT                   backbone and 2-'methyoxyethyl (2'-MOE) wings at the 5'
FT                   and 3' ends, which are 5 nucleotides in length. Also all
FT                   cytosine nucleotides are 5-methylcytosines"
XX
PN   WO200268446-A1.
XX
PD   06-SEP-2002.
XX
PF   30-OCT-2001; 2001WO-US048435.
XX
PR   22-FEB-2001; 2001US-00791942.
XX
PA   (ISIS-) ISIS PHARM INC.
PA   (BOEH ) BOEHRINGER INGELHEIM PHARM INC.
XX
PI   Bennett CF,  Rothlein R,  Kishimoto TK,  Cowsert LM;
XX
DR   WPI; 2002-691651/74.
XX
PT   New antisense oligonucleotides targeted to nucleic acid molecules
PT   encoding human Talin, useful for inhibiting the expression of human Talin
PT   and for treating a human having a disease or condition associated with
PT   Talin.
XX
PS   Example 15; SEQ ID NO 44; 114pp; English.
XX
CC   Sequences ADG90460-ADG90539 represent phosphorothioate targeted to the
CC   human talin gene, which inhibit its expression. The antisense were
CC   designed to target different regions of human talin RNA, and were
CC   analysed for their effect on talin expression by quantitative real-time
CC   PCR. Talin is a cytoplasmic protein which links cytoskeletal proteins
CC   such as actin, myosin and vinculin to integrins, thereby linking the
CC   extracellular matrix to other cells. It is thought to be involved in the
CC   regulation of cellular adhesion and cell morphology. Talin is highly
CC   expressed in platelets, and may play a role in platelet adhesion as its
CC   subcellular distribution differs between resting non-adhesive platelets
CC   and activated adhesive platelets. It could also play a major role in
CC   determining muscle strength and cardiac function as it has been found to
CC   participate in the transmission of contractile force to the extracellular
CC   matrix in cardiomyocytes, and exhibits mechanical loading-dependent
CC   expression at myotendinous junctions. The expression of talin is
CC   downregulated by androgens in prostate tissues, a phenomenon known to
CC   contribute to the development of prostate cancer. The oligonucleotides of
CC   the invention are useful for diagnosis, prevention and treatment of talin
CC   -related disorders, such as those related to cellular adhesion. The
CC   present sequence represents a human c-Ha-ras phosphorothioate antisense
CC   oligonucleotide used as a positive control in determining optimal
CC   oligonucleotide concentration for a particular cell line.
XX
SQ   Sequence 20 BP; 3 A; 8 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             55.5%;  Score 12.2;  DB 6;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 3.8e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 TGTTACAGGTAGAAAAG 20
              |||| |||| || ||||
Db         19 TGTTGCAGGCAGCAAAG 3


RESULT 27
ADC65754
ID   ADC65754 standard; DNA; 20 BP.
XX
AC   ADC65754;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human TGF-beta receptor II targeted antisense oligonucleotide #31.
XX
KW   human; antisense oligonucleotide;
KW   transforming growth factor beta receptor II; TGF-beta receptor II;
KW   hyperproliferative disorder; breast cancer; autoimmune disorder;
KW   rheumatoid arthritis; 2'-O-methoxyethyl gapmer;
KW   phosphorothioate backbone; ss.
XX
OS   Homo sapiens.
XX
PN   WO2003000656-A2.
XX
PD   03-JAN-2003.
XX
PF   19-JUN-2002; 2002WO-US019665.
XX
PR   21-JUN-2001; 2001US-00888361.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Murray SF,  Wyatt JR;
XX
DR   WPI; 2003-175279/17.
XX
PT   New compound having a sequence targeted to a nucleic acid encoding
PT   Transforming growth factor beta-receptor II, useful for preparing a
PT   composition for treating hyperproliferative disorder e.g., lung, liver,
PT   colon or gastric cancer.
XX
PS   Claim 3; SEQ ID NO 50; 141pp; English.
XX
CC   The invention comprises antisense oligonucleotides that are targeted to
CC   the nucleic acid encoding transforming growth factor beta (TGF-beta)
CC   receptor II. The antisense oligonucleotides of the invention are useful
CC   for treating: hyperproliferative disorders (e.g. breast cancer), or an
CC   autoimmune disorder (e.g. rheumatoid arthritis). The present DNA sequence
CC   represents a 2'-O-methoxyethyl gapmer oligonucleotide with a
CC   phosphorothioate backbone that is targeted to human TGF-beta receptor II.
XX
```

```
SQ   Sequence 20 BP; 7 A; 4 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             55.5%;  Score 12.2;  DB 10;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 3.8e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 GTTACAGGTAGAAAAGC 21
              || |||||| ||||| |
Db          1 GTCACAGGTGGAAAATC 17


RESULT 28
ADF90932
ID   ADF90932 standard; DNA; 20 BP.
XX
AC   ADF90932;
XX
DT   26-FEB-2004  (first entry)
XX
DE   Microorganism detection PCR primer, SEQ ID 15.
XX
KW   Detection; microorganism; PCR; primer; bacterium; fungus; protozoan;
KW   virus; diarrhoea; food poisoning; ss.
XX
OS   Clostridium botulinum.
XX
PN   JP2003164282-A.
XX
PD   10-JUN-2003.
XX
PF   29-NOV-2001; 2001JP-00365153.
XX
PR   29-NOV-2001; 2001JP-00365153.
XX
PA   (RAKA-) RAKAN KK.
PA   (GIFU-) GIFU DAIGAKUCHO.
XX
DR   WPI; 2003-793230/75.
XX
PT   Rapid, sensitive detection of specific or unspecified microbes causing
PT   diarrhea and food poisoning, using primers which target universal and
PT   specific genes, and amplifying by PCR under heat cycle conditions
PT   suitable for many detections.
XX
PS   Claim 1; SEQ ID NO 15; 69pp; Japanese.
XX
CC   The present invention relates to a method for detecting microorganisms
CC   using primers (ADF90918-ADF91145). The method is used for detecting
CC   microorganisms (bacteria, fungi, protozoa, viruses) which cause diarrhoea
CC   symptoms, and pathogenic microbe of food poisoning. The method can be
CC   used to detect unspecified microbes, or specific pathogens, or for the
CC   simultaneous detection of many kinds of microorganism.
XX
SQ   Sequence 20 BP; 9 A; 2 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             55.5%;  Score 12.2;  DB 10;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 3.8e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 GTTACAGGTAGAAAAGC 21
              |||| || ||||||| |
Db          2 GTTAGAGCTAGAAAAAC 18


RESULT 29
ABZ86479/c
ID   ABZ86479 standard; DNA; 20 BP.
XX
AC   ABZ86479;
XX
DT   17-OCT-2003  (first entry)
XX
DE   Human oligonucleotide sequence.
XX
KW   Human; antisense; lung dysfunction; nasal airway dysfunction;
KW   antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW   antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW   antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW   adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW   lung inflammation; respiratory disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200285308-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013135.
XX
PR   24-APR-2001; 2001US-0286137P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-229219/22.
XX
PT   Pharmaceutical composition for treating ailments associated with impaired
PT   respiration, has oligo(s) antisense to specific gene(s) or its
PT   corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT   ubiquinone.
XX
PS   Claim 15; SEQ ID NO 1721; 872pp; English.
XX
CC   The invention relates to a novel pharmaceutical composition, which has a
CC   first active agent comprising an oligonucleotide antisense to the
CC   initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC   5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC   junctions of genes encoding a polypeptide associated with lung and/or
CC   nasal airway dysfunction and a second active agent comprising an
CC   antiinflammatory steroid and ubiquinone. A composition of the invention
CC   has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC   immunosuppressive, and cytostatic activity. The composition may have a
CC   use in antisense gene therapy. The composition is useful for treating or
CC   preventing a respiratory, lung or malignant disease or condition, also
CC   for enhancing the prophylactic or therapeutic respiratory effect of an
CC   antiinflammatory steroid in a subject, for reducing or depleting levels
CC   of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC   receptor, producing bronchodilation, increasing levels of ubiquinone or
CC   lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC   lung inflammation, lung allergies, or a respiratory disease or condition.
CC   Note: The sequence data for this patent is not represented in the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 20 BP; 8 A; 4 C; 2 G; 6 T; 0 U; 0 Other;

  Query Match             55.5%;  Score 12.2;  DB 10;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 3.8e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 TGTTACAGGTAGAAAAG 20
              | ||||| |||| ||||
Db         18 TTTTACATGTAGCAAAG 2


RESULT 30
ABD22709/c
ID   ABD22709 standard; DNA; 20 BP.
XX
AC   ABD22709;
XX
DT   29-JUL-2004  (first entry)
XX
DE   Human myosin X-derived oligonucleotide SEQ ID 1721.
```

```
XX
KW   Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW   respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW   surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW   analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW   beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW   respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW   emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;
KW   pulmonary transplantation rejection; ss; primer.
XX
OS   Homo sapiens.
XX
PN   WO200285309-A2.
XX
PD   31-OCT-2002.
XX
PF   23-APR-2002; 2002WO-US013143.
XX
PR   24-APR-2001; 2001US-0286036P.
XX
PA   (EPIG-) EPIGENESIS PHARM INC.
XX
PI   Nyce JW,  Li Y,  Sandrasagra A,  Katz E,  Pabalan J,  Aguilar D;
PI   Miller S,  Tang L,  Shahabuddin S;
XX
DR   WPI; 2003-093058/08.
XX
PT   Pharmaceutical composition for treating asthma, has antisense
PT   oligonucleotide containing less percentage of adenosine, targeted to
PT   nucleic acids associated with lung airway or lung dysfunction, and
PT   bronchodilating agent.
XX
PS   Claim 15; SEQ ID NO 1721; 763pp; English.
XX
CC   This invention describes a novel composition (a) a first active agent,
CC   comprising oligonucleotides, effective for alleviating
CC   bronchoconstriction, respiratory tract inflammation, allergies and
CC   reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC   surfactant depletion or hyposecretion, when administered to a mammal. The
CC   oligonucleotides are derived from a gene encoding or regulating
CC   expression of a target polypeptide associated with lung airway or lung
CC   dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC   The invention also describes a kit, that comprises: (a) a delivery
CC   device, in separate containers, (b) the oligonucleotides, (c)
CC   instructions for adding a carrier and for use of the kit. The composition
CC   of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC   analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC   beta-adrenergic agonist. The composition is useful for preventing or
CC   treating a respiratory, lung or malignant disease. The administered
CC   composition comprises oligo and is administered to reduce the production
CC   or availability, or to increase the degradation of the target mRNA or to
CC   reduce the amount of target polypeptide present in the lungs. The
CC   pulmonary obstruction, and/or bronchoconstriction and/or lung
CC   inflammation, allergies and/or surfactant hypoproduction are associated
CC   with a disease or condition such as pulmonary vasoconstriction,
CC   inflammation, allergies, asthma, impeded respiration, respiratory
CC   distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC   hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC   transplantation rejection, pulmonary infections, bronchitis or cancer.
CC   The reduced adenosine content of the anti-sense oligos corresponding to
CC   thymidines present in the target RNA serves to prevent the breakdown of
CC   the oligonucleotides into products that free adenosine into the system
CC   e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC   prevent any unwanted effects due to it
XX
SQ   Sequence 20 BP; 8 A; 4 C; 2 G; 6 T; 0 U; 0 Other;

  Query Match             55.5%;  Score 12.2;  DB 11;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 3.8e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 TGTTACAGGTAGAAAAG 20
              | ||||| |||| ||||
```

```
Db         18 TTTTACATGTAGCAAAG 2


RESULT 31
ADP85699/c
ID   ADP85699 standard; DNA; 20 BP.
XX
AC   ADP85699;
XX
DT   26-AUG-2004  (first entry)
XX
DE   Human Talin antisense oligonucleotide, ISIS #109143.
XX
KW   Antisense; Talin; muscular disorder; haematologic disorder;
KW   cardiac disorder; hyperproliferative disorder; cancer; human;
KW   phosphorothioate; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone where all cytidine
FT                   residues are 5-methylcytidines"
FT   modified_base   1. .5
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl (2'-MOE) nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-methoxyethyl (2'-MOE) nucleotides"
XX
PN   US2004110705-A1.
XX
PD   10-JUN-2004.
XX
PF   11-SEP-2003; 2003US-00415463.
XX
PR   30-OCT-2000; 2000US-00702251.
PR   30-OCT-2001; 2001WO-US047585.
XX
PA   (BENN/) BENNETT C F.
PA   (COWS/) COWSERT L M.
XX
PI   Bennett CF,  Cowsert LM;
XX
DR   WPI; 2004-440384/41.
XX
PT   New compounds, particularly antisense oligonucleotides targeted to a
PT   nucleic acid encoding talin, useful for treating muscular, cardiac,
PT   hematologic, or hyperproliferative disorders.
XX
PS   Example 15; SEQ ID NO 44; 48pp; English.
XX
CC   The invention relates to novel antisense compounds targeted to a nucleic
CC   acid molecule encoding human Talin to and inhibit its expression. The
CC   invention is useful for treating a disease or condition associated with
CC   Talin such as a disease or condition e.g. muscular, haematologic, cardiac
CC   or hyperproliferative disorder such as cancer. The present sequence is an
CC   antisense oilgonucleotide targeted to human Talin DNA.
XX
SQ   Sequence 20 BP; 3 A; 8 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             55.5%;  Score 12.2;  DB 12;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 3.8e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 TGTTACAGGTAGAAAAG 20
              |||| |||| || ||||
Db         19 TGTTGCAGGCAGCAAAG 3
```

RESULT 32
AAC73052
ID AAC73052 standard; DNA; 21 BP.
XX
AC AAC73052;
XX
DT 09-FEB-2001 (first entry)
XX
DE Single nucleotide polymorphism PCR primer #1921.
XX
KW Single nucleotide polymorphism; SNP; human; genetic disease;
KW disease susceptibility; cardiovascular system; endocrine system;
KW neurological system; forensic testing; paternity testing; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200058519-A2.
XX
PD 05-OCT-2000.
XX
PF 30-MAR-2000; 2000WO-US008440.
XX
PR 31-MAR-1999; 99US-0127248P.
XX
PA (WHED) WHITEHEAD INST BIOMEDICAL RES.
PA (AFFY-) AFFYMETRIX INC.
XX
PI Altshuler D, Cargill M, Daley GQ, Ireland JS, Lander ES;
PI Lipshutz RJ, Patil N, Sklar P;
XX
DR WPI; 2000-611722/58.
XX
PT Nucleic acid selected from one of 106 genes comprising single nucleotide
PT polymorphisms, allele-specific oligonucleotides to the genes are useful
PT for phenotypic correlations, forensics, paternity testing, medicine and
PT genetic analysis.
XX
PS Claim 8; Fig 5; 214pp; English.
XX
CC The present invention is concerned with a number of human single
CC nucleotide polymorphisms (SNPs) which the inventors identified in human
CC genes. These SNPs can be used in disease diagnosis and prediction of an
CC individual's susceptibility to disease, in forensic and paternity testing
CC and in genetic mapping. In particular, the SNPs of the invention can be
CC used to diagnose susceptibility to diseases of the cardiovascular,
CC endocrine and neurological systems, such as coronary artery disease,
CC schizophrenia, cancer, autoimmune diseases, Alzheimer's and Parkinson's
CC diseases
XX
SQ Sequence 21 BP; 10 A; 3 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 55.5%; Score 12.2; DB 3; Length 21;
Best Local Similarity 82.4%; Pred. No. 3.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 TTACAGGTAGAAAAGCC 22
|| ||| |||||||||
Db 2 TTCTAGGGAGAAAAGCC 18

RESULT 33
ABK41026/c
ID ABK41026 standard; DNA; 21 BP.
XX
AC ABK41026;
XX
DT 21-MAY-2002 (first entry)
XX
DE Human obesity-associated biallelic marker upstream PCR primer #103.
XX
KW Human; obesity associated-biallelic marker; chromosome 10; obesity; ss;
KW drug response; hyperuricaemia; digestive pathology; hypertension; cancer;
KW hepatic function disorder; cardiovascular disease; hyperlipidaemia; PCR;
KW insulin disorder; atheromatous disease; cardiac insufficiency; primer.
XX
OS Homo sapiens.
XX
PN WO200206525-A2.
XX
PD 24-JAN-2002.
XX
PF 28-JUN-2001; 2001WO-IB001477.
XX
PR 18-JUL-2000; 2000US-0219704P.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I, Abderrahim H, Bihain B;
XX
DR WPI; 2002-155043/20.
XX
PT Set of novel map-related biallelic markers, preferably located on obesity
PT disorder-associated chromosomal regions on chromosomes 3, 10 and 19,
PT useful, for e.g. detecting statistical correlations between marker allele
PT and a phenotype.
XX
PS Example 2; Page 248; 311pp; English.
XX
CC The invention relates to a set of novel map-related biallelic markers,
CC preferably located on obesity disorder-associated chromosomal regions on
CC chromosomes 3, 10 and 19. The markers are useful for genotyping or
CC estimating the frequency of an allele in a population, for detecting an
CC association between a genotype or haplotype and a phenotype, e.g. a
CC disease involving drug responses, obesity or disorders related to
CC obesity, such as hyperuricaemia, digestive pathology, hepatic function
CC disorders, cancer, cardiovascular disease, hypertension, hyperlipidaemia,
CC insulin disorders, atheromatous disease and cardiac insufficiency. The
CC markers are useful for detecting a statistical correlation between a
CC biallelic marker allele and a phenotype and/or between a biallelic marker
CC haplotype and a phenotype. This sequence represents a PCR primer used to
CC amplify a human obesity-associated biallelic marker
XX
SQ Sequence 21 BP; 4 A; 4 C; 3 G; 10 T; 0 U; 0 Other;

Query Match 55.5%; Score 12.2; DB 6; Length 21;
Best Local Similarity 82.4%; Pred. No. 3.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GTTACAGGTAGAAAAGC 21
||| ||| || ||||||
Db 19 GTTTCAGATAAAAAAGC 3

RESULT 34
ADH56236
ID ADH56236 standard; DNA; 22 BP.
XX
AC ADH56236;
XX
DT 25-MAR-2004 (first entry)
XX
DE Yeast YFL014W (HSP12) PCR primer HSP12-F SEQ ID NO:1.
XX
KW cold-inducible promoter activity; promoter; non-translational region;
KW Saccharomyces cerevisiae; yeast; vector; expression system;
KW RNA production regulation; molecular mechanism;
KW low-temperature inducibility; PCR; primer; ss.
XX
OS Synthetic.
OS Saccharomyces cerevisiae.
XX
PN WO2004003197-A1.
XX
PD 08-JAN-2004.

XX
PF 13-MAY-2003; 2003WO-JP005956.
XX
PR 28-JUN-2002; 2002JP-00191383.
XX
PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX
PI Sahara T, Ohgiya S, Goda T, Kawasaki K;
XX
DR WPI; 2004-083056/08.
XX
PT Yeast-originated promoters with cold-inducible activity for constructing
PT vectors and expression systems to produce difficult-to-obtain proteins
PT and for regulating RNA production.
XX
PS Example 2; SEQ ID NO 1; 106pp; Japanese.
XX
CC The present invention describes a DNA fragment with a cold-inducible
CC promoter activity which occurs in the non-translational region in the 5'-
CC upstream side of a gene selected from the 259 specified Saccharomyces
CC cerevisiae genes given in the specification (G) e.g. YAL014C and YPR200C.
CC Also described: (1) a similar DNA fragment containing: (a) a DNA derived
CC from any of the specified DNA fragments (G) but with some bases deleted,
CC substituted or added; or (b) a DNA hybridisable with a DNA fragment
CC containing a base sequence complementary to any of the specified DNA
CC fragments (G); (2) a similar DNA fragment containing a cis sequence of
CC DNA sequence A: GCTCATCG, or a DNA sequence of B: GAGATGAG; (3) a DNA
CC fragment with cold-inducible promoter activity containing: (a) a DNA
CC derived from the DNA fragment in (2) but with some bases deleted,
CC substituted or added; or (b) a DNA hybridisable with a DNA fragment
CC containing a base sequence complementary to the DNA fragment in (2); (4)
CC an expression vector containing any of the DNA fragments; (5) a
CC transformant which is transformed with any of the expression vector; (6)
CC producing a protein by culturing the transformant at a low temperature;
CC and (7) controlling RNA production by culturing the transformant at a low
CC temperature. The promoters are applicable in constructing vectors and
CC expression systems to produce difficult-to-obtain proteins and for
CC regulating RNA production as well as in studying the molecular mechanism
CC of low-temperature inducibility. The present sequence represents a PCR
CC primer which is used in an example from the present invention.
XX
SQ Sequence 22 BP; 8 A; 3 C; 7 G; 4 T; 0 U; 0 Other;

Query Match 55.5%; Score 12.2; DB 12; Length 22;
Best Local Similarity 82.4%; Pred. No. 3.8e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TGTTACAGGTAGAAAAG 20
|| |||||||||||
Db 6 TGACGCAGGTAGAAAAG 22

RESULT 35
AAZ75337/c
ID AAZ75337 standard; DNA; 20 BP.
XX
AC AAZ75337;
XX
DT 10-SEP-2001 (first entry)
XX
DE Human biallelic marker downstream amplification primer SEQ ID NO:9693.
XX
KW Human genome; biallelic marker; high density disequilibrium map;
KW genomic map; haplotype; phenotype; polymorphic base; genotyping;
KW haplotyping; hybridisation; identification; characterisation;
KW amplification; single nucleotide polymorphism; SNP; PCR primer;
KW diagnosis; ss.
XX
OS Homo sapiens.
XX
PN WO9954500-A2.
XX
PD 28-OCT-1999.
XX
PF 21-APR-1999; 99WO-IB000822.
XX
PR 21-APR-1998; 98US-0082614P.
PR 23-NOV-1998; 98US-0109732P.
XX
PA (GEST) GENSET.
XX
PI Cohen D, Blumenfeld M, Chumakov I;
XX
DR WPI; 2000-013267/01.
XX
PT Novel biallelic markers used to construct a high density disequilibrium
PT map of the human genome.
XX
PS Claim 8; Page 2297; 2745pp; English.
XX
CC AAZ65654 to AAZ69578 represent human biallelic markers from the present
CC invention, which contain a polymorphic base at position 24 of their
CC nucleotide sequences. AAZ69579 to AAZ77440 represent amplification
CC primers for the biallelic markers. The biallelic markers of the invention
CC have a variety of uses: they can be used for high density mapping of the
CC human genome, and in complex association studies and haplotyping studies
CC which are useful in determining the genetic basis for disease states.
CC Compositions and methods of the invention can also be useful for the
CC identification of the targets for the development of pharmaceutical
CC agents and diagnostic methods, as well as the characterisation of the
CC differential efficacious responses to and side effects from
CC pharmaceutical agents acting on a disease as well as other treatment.
CC N.B. The SEQ ID NOs 2852, 2913, 2974, 3035, 3096, 3157, 3227, 3297 and
CC 3367, are not actually given a sequence in the Sequence Listing from the
CC present invention
XX
SQ Sequence 20 BP; 6 A; 6 C; 1 G; 7 T; 0 U; 0 Other;

Query Match 54.5%; Score 12; DB 3; Length 20;
Best Local Similarity 75.0%; Pred. No. 4.7e+04;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GCATGTTACAGGTAGAAAAG 20
| |||| ||||| |||||
Db 20 GTATGTCTGAGGTATAAAAG 1

RESULT 36
ABK87660/c
ID ABK87660 standard; DNA; 20 BP.
XX
AC ABK87660;
XX
DT 24-SEP-2002 (first entry)
XX
DE Synthetic oligo #15, for selective randomisation of zinc finger protein.
XX
KW Selectively randomised synthetic oligonucleotide; NNN randomisation;
KW resin-splitting; zinc finger; ss.
XX
OS Synthetic.
XX
PN WO200222634-A1.
XX
PD 21-MAR-2002.
XX
PF 12-SEP-2001; 2001WO-GB004084.
XX
PR 12-SEP-2000; 2000GB-00022330.
XX
PA (SANG-) SANGAMO BIOSCIENCES INC.
XX
PI Choo Y, Isalan M;
XX
DR WPI; 2002-507792/54.
XX

```
PT   Making selectively randomized synthetic oligonucleotide by utilizing
PT   phosphoramidite dinucleotide and mononucleotide synthesis strategy, where
PT   a deprotecting step is performed after each coupling step.
XX
PS   Example 3; Fig 1B; 42pp; English.
XX
CC   The present invention relates to a new method of making selectively
CC   randomised synthetic oligonucleotides. The method involves deprotecting
CC   starting material at 3' position, which is coupled to support in nucleic
CC   acid synthesiser, coupling dinucleotide phosphoramidite to 3' position,
CC   deprotecting the new 3' position of extended oligonucleotide, coupling
CC   mononucleotide phosphoramidite to the 3' position and repeating coupling
CC   steps until desired length oligonucleotide is obtained. The method of the
CC   invention is useful for making selectively randomised synthetic
CC   oligonucleotides. Unlike prior art techniques, the method provides
CC   randomised oligonucleotides without the problems of NNN randomisation,
CC   without having to resort to complicated resin-splitting procedures or the
CC   use of low coupling efficiency trinucleotide phosphoramidites. The
CC   present nucleic acid sequence represents one of a collection (ABK87646-
CC   ABK87669 and ABK87671-ABK87676) of synthetic oligonucleotides that were
CC   used in the invention for selective randomisation of zinc finger protein
XX
SQ   Sequence 20 BP; 1 A; 6 C; 3 G; 6 T; 0 U; 4 Other;

  Query Match             54.5%;  Score 12;  DB 6;  Length 20;
  Best Local Similarity   66.7%;  Pred. No. 4.7e+04;
  Matches   12;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 TGTTACAGGTAGAAAAGC 21
              ||:   ||::||||||||
Db         19 TGKCCGAGKYAGAAAAGC 2


RESULT 37
ADJ17616/c
ID   ADJ17616 standard; DNA; 20 BP.
XX
AC   ADJ17616;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Antisense DNA oligo used to modulate human LRH1 expression SeqID 2166.
XX
KW   human; ss; liver related homologue-1; LRH1; NR5A2; antisense;
KW   phosphorothioate; 2' MOE; breast cancer; dyslipidaemia; atherosclerosis;
KW   low HDL; high density lipoprotein; high LDL; hypercholesterolaemia;
KW   gall stone; triglyceridaemia; obesity; hepatitis;
KW   hepatocellular carcinoma; aromatase; cytostatic; antilipaemic;
KW   antiarteriosclerotic; anorectic; hepatotropic; litholytic;
KW   antiinflammatory; virucidal.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /label= OTHER= phosphorothioate backbone
FT   modified_base   1. .5
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= 2' methoxyethyl (2' MOE) nucleotides. All
FT                   cytidine nucleobases are 5-methylcytidine."
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "OTHER= 2' methoxyethyl (2' MOE) nucleotides. All
FT                   cytidine nucleobases are 5-methylcytidine."
XX
PN   WO2004003201-A2.
XX
PD   08-JAN-2004.
XX
PF   01-JUL-2003; 2003WO-US020865.
XX
PR   01-JUL-2002; 2002US-0392813P.
XX
PA   (PHAA ) PHARMACIA CORP.
XX
PI   Kane CD;
XX
DR   WPI; 2004-083058/08.
XX
PT   New antisense oligonucleotides targeted to a nucleic acid encoding liver
PT   related homologue-1 (LRH1), useful for treating breast cancer,
PT   dyslipidemia, atherosclerosis, hypercholesterolemia, or hepatitis.
XX
PS   Example 15; SEQ ID NO 2166; 909pp; English.
XX
CC   This invention relates to novel antisense compounds useful for modulating
CC   the expression of liver related homologue-1 (LRH1) and splice variants
CC   thereof. Specifically, it refers to compositions 8-30 nucleobases in
CC   length that target a portion of an active site on the nucleic acid
CC   molecule encoding LRH1 (also known as NR5A2). LRH1 is a monomeric orphan
CC   nuclear receptor protein that functions as a tissue specific
CC   transcription factor. The present invention describes antisense
CC   oligonucleotides that comprise at least one modified internucleoside
CC   linkage, a phosphorothioate linkage; at least one modified sugar moiety,
CC   a 2'-O-methoxyethyl (2' MOE) and at least one modified nucleobase, a 5-
CC   methylcytidine. These antisense compounds are useful for treating or
CC   diagnosing a disease associated with LRH1, such as breast cancer,
CC   dyslipidaemia, atherosclerosis, low HDL (high density lipoprotein), high
CC   LDL (low density lipoprotein), hypercholesterolaemia, gall stones,
CC   triglyceridaemia, obesity, hepatitis B virus-mediated acute or chronic
CC   hepatitis, as well as hepatocellular carcinoma or a condition associated
CC   with aromatase activity. Accordingly, these compositions exhibit
CC   cytostatic, antilipaemic, antiarteriosclerotic, anorectic, hepatotropic,
CC   litholytic, antiinflammatory and virucidal activities. This
CC   oligonucleotide sequence is an antisense DNA oligo used to modulate the
CC   expression of the human LRH1 protein of the invention.
XX
SQ   Sequence 20 BP; 4 A; 5 C; 4 G; 7 T; 0 U; 0 Other;

  Query Match             54.5%;  Score 12;  DB 12;  Length 20;
  Best Local Similarity   75.0%;  Pred. No. 4.7e+04;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 ATGTTACAGGTAGAAAAGCC 22
              |||  |||||||  |||| |
Db         20 ATGCCACAGGTATGAAAGTC 1


RESULT 38
ADL01087
ID   ADL01087 standard; DNA; 20 BP.
XX
AC   ADL01087;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Human VEGF co-regulated chemokine-1 DNA antisense oligonucleotide #620.
XX
KW   Human; VEGF co-regulated chemokine-1; VCC-1;
KW   vascular endothelial growth factor; ss; antisense compound;
KW   phosphorothioate linkage; 2'-O-methoxyethyl sugar moiety;
KW   5-methylcytosine; antisense oligonucleotide; diabetes;
KW   immunological disorder; cardiovascular disorder; neurological disorder;
KW   ischaemia; reperfusion injury; cancer; angiogenic disorder; haemangioma;
KW   tumour angiogenesis; rheumatoid arthritis; atherosclerosis; psoriasis;
KW   fibrosis; myocardial infarction; wound healing; bone fracture;
KW   cartilage damage; tissue regeneration; organ regeneration;
KW   periodontal disease; gut regeneration; atrial fibrillation.
XX
OS   Homo sapiens.
XX
```

PN WO2004016224-A2.
XX
PD 26-FEB-2004.
XX
PF 19-AUG-2003; 2003WO-US025891.
XX
PR 19-AUG-2002; 2002US-0404484P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Weinstein EJ;
XX
DR WPI; 2004-192065/18.
XX
PT New antisense compounds targeted to a nucleic acid molecule encoding
PT vascular endothelial growth factor co-regulated chemokine-1 (VCC-1),
PT useful for treating VCC-1-associated disorders, e.g. diabetes or a
PT neurologic disorder.
XX
PS Claim 4; SEQ ID NO 620; 336pp; English.
XX
CC The invention relates to an antisense compound targeted to a nucleic acid
CC molecule encoding human vascular endothelial growth factor (VEGF) co-
CC regulated chemokine-1 (VCC-1), and which specifically hybridises with and
CC inhibits the expression of VCC-1. The invention also relates to a
CC composition comprising the antisense compound, a method of inhibiting the
CC expression of VCC-1 in cells or tissues comprising contacting the cells
CC or tissues with the antisense compound and a method of treating a human
CC having a disease or condition associated with VCC-1 comprising
CC administering the antisense compound to an animal to inhibit expression
CC of VCC-1. The antisense oligonucleotide comprises at least one modified
CC internucleoside linkage, preferably a phosphorothioate linkage. It also
CC comprises at least one modified sugar moiety, preferably a 2'-O-
CC methoxyethyl sugar moiety, and at least one modified nucleobase,
CC specifically a 5-methylcytosine. The antisense oligonucleotide preferably
CC is a chimeric oligonucleotide. The antisense compound is useful for
CC treating a disease or condition associated with VCC-1, such as diabetes,
CC an immunological disorder, a cardiovascular disorder, a neurological
CC disorder, ischaemia, reperfusion injury, cancer or an angiogenic
CC disorder, e.g. haemangioma, tumour angiogenesis, rheumatoid arthritis,
CC atherosclerosis, psoriasis or fibrosis after myocardial infarction. VCC-1
CC antisense oligonucleotides may also be used for wound healing, for
CC healing of bone fractures and cartilage damage, for regeneration of
CC tissues or organs, for treating periodontal diseases, for gut protection
CC or regeneration, for treatment of lung or liver fibrosis or for
CC management of atrial fibrillation. This sequence represents an antisense
CC oligonucleotide targeted to DNA encoding the human VCC-1 polypeptide of
CC the invention.
XX
SQ Sequence 20 BP; 6 A; 4 C; 3 G; 7 T; 0 U; 0 Other;

```
  Query Match             54.5%;  Score 12;  DB 12;  Length 20;
  Best Local Similarity   75.0%;  Pred. No. 4.7e+04;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 ATGTTACAGGTAGAAAAGCC 22
              || || ||||||   |||||
Db          1 ATCTTTCAGGTAATTAAGCC 20
```

RESULT 39
AAH62090/c
ID AAH62090 standard; DNA; 21 BP.
XX
AC AAH62090;
XX
DT 10-SEP-2001 (first entry)
XX
DE VEGF hammerhead ribozyme recognition site SEQ ID NO:4514.
XX
KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW recognition site; target; ribozyme binding site; eye disease; vulnerary;
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW sickle cell retinopathy; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200130362-A2.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-US029500.
XX
PR 26-OCT-1999; 99US-0161532P.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Robbins JM, Tritz R;
XX
DR WPI; 2001-300427/31.
XX
PT Treating proliferative skin or eye diseases and scarring, using ribozymes
PT that cleave RNA encoding cytokines involved in inflammation, matrix
PT metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
PS Example 1; Page 26; 408pp; English.
XX
CC The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC ophthalmological, vulnerary, keratolytic and virucide activities, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative skin
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 21 BP; 3 A; 9 C; 3 G; 6 T; 0 U; 0 Other;

```
  Query Match             54.5%;  Score 12;  DB 5;  Length 21;
  Best Local Similarity   75.0%;  Pred. No. 4.8e+04;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 CATGTTACAGGTAGAAAAGC 21
              |||| |  |||||||  |||
Db         21 CATGGTGGAGGTAGAGCAGC 2
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RESULT 40
ADO16516
ID ADO16516 standard; DNA; 22 BP.
XX
AC ADO16516;
XX
DT 29-JUL-2004 (first entry)
XX
DE 4 synthesis-period of neuroblastoma related primer, SEQ ID 778.
XX
KW Human; 4 synthesis-period; neuroblastoma; stage 4S; primer; ss.

XX
OS Synthetic.
XX
PN WO2004039975-A1.
XX
PD 13-MAY-2004.
XX
PF 30-OCT-2003; 2003WO-JP013932.
XX
PR 30-OCT-2002; 2002JP-00316586.
XX
PA (HISM) HISAMITSU PHARM CO LTD.
PA (CHIB-) CHIBA PREFECTURE.
XX
PI Nakagawara A, Ohira M;
XX
DR WPI; 2004-390323/36.
XX
PT Novel nucleic acid obtained from 4 synthesis-period of neuroblastoma
PT cells useful for prognosing and determining progress stage of
PT neuroblastomas.
XX
PS Claim 8; SEQ ID NO 778; 455pp; Japanese.
XX
CC The present invention relates to human nucleic acid sequences (I;
CC ADO15739-ADO15912) obtained from 4 synthesis-period (stage 4S) of
CC neuroblastoma cell. (I) is useful for prognosing and determining the
CC progress stage of 4 synthesis-period of neuroblastoma. The present
CC sequence is a primer, used to illustrate the invention.
XX
SQ Sequence 22 BP; 10 A; 6 C; 4 G; 2 T; 0 U; 0 Other;

Query Match 54.5%; Score 12; DB 12; Length 22;
Best Local Similarity 100.0%; Pred. No. 4.8e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TACAGGTAGAAA 18
||||||||||||
Db 1 TACAGGTAGAAA 12

Search completed: August 12, 2005, 08:58:58
Job time : 245 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 12, 2005, 08:29:02 ; Search time 95 Seconds
(without alignments)
378.927 Million cell updates/sec

Title: US-09-743-825-7
Perfect score: 22
Sequence: 1 gcatgttacaggtagaaaagcc 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 487750

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
c	1	15.2	69.1	20	4	US-09-198-452A-5333	Sequence 5333, Ap
	2	13.2	60.0	21	4	US-09-689-065B-50	Sequence 50, Appl
c	3	12.8	58.2	19	3	US-09-564-805-157	Sequence 157, App
	4	12.2	55.5	18	3	US-08-840-316-53	Sequence 53, Appl
	5	12.2	55.5	18	3	US-08-809-523-53	Sequence 53, Appl
	6	12.2	55.5	18	3	US-08-471-971-53	Sequence 53, Appl
	7	12.2	55.5	18	3	US-09-402-776-53	Sequence 53, Appl
	8	12.2	55.5	18	4	US-09-422-978-4779	Sequence 4779, Ap
	9	12.2	55.5	18	4	US-08-470-246-53	Sequence 53, Appl
	10	12.2	55.5	18	4	US-08-316-765-53	Sequence 53, Appl
	11	12.2	55.5	18	4	US-09-724-475-53	Sequence 53, Appl
	12	12.2	55.5	18	5	PCT-US93-08849A-53	Sequence 53, Appl
	13	12.2	55.5	18	5	PCT-US93-08849-53	Sequence 53, Appl
c	14	12.2	55.5	20	3	US-09-702-251-44	Sequence 44, Appl
	15	12	54.5	20	3	US-08-765-340-23	Sequence 23, Appl
c	16	12	54.5	20	4	US-09-422-978-9693	Sequence 9693, Ap
c	17	12	54.5	21	4	US-09-696-791-4514	Sequence 4514, Ap
	18	11.8	53.6	19	4	US-09-422-978-6072	Sequence 6072, Ap
c	19	11.8	53.6	20	1	US-08-477-270-27	Sequence 27, Appl
	20	11.8	53.6	20	3	US-09-487-445-98	Sequence 98, Appl
c	21	11.6	52.7	19	3	US-09-648-520E-29	Sequence 29, Appl
	22	11.6	52.7	19	4	US-09-422-978-4544	Sequence 4544, Ap
	23	11.4	51.8	17	3	US-08-985-162-702	Sequence 702, App
	24	11.4	51.8	17	3	US-08-985-162-703	Sequence 703, App
	25	11.4	51.8	17	3	US-08-985-162-704	Sequence 704, App
	26	11.4	51.8	17	3	US-08-985-162-705	Sequence 705, App
	27	11.4	51.8	17	3	US-08-584-040-1534	Sequence 1534, Ap
	28	11.4	51.8	17	4	US-09-371-772B-79	Sequence 79, Appl
	29	11.4	51.8	17	4	US-09-371-772B-4284	Sequence 4284, Ap
	30	11.4	51.8	17	4	US-09-401-063-702	Sequence 702, App
	31	11.4	51.8	17	4	US-09-401-063-703	Sequence 703, App
	32	11.4	51.8	17	4	US-09-401-063-704	Sequence 704, App
	33	11.4	51.8	17	4	US-09-401-063-705	Sequence 705, App
	34	11.4	51.8	17	4	US-09-685-664B-79	Sequence 79, Appl
	35	11.4	51.8	18	3	US-08-981-988A-27	Sequence 27, Appl
	36	11.4	51.8	19	3	US-09-531-000-7	Sequence 7, Appli
	37	11.4	51.8	19	3	US-09-531-000-34	Sequence 34, Appl
	38	11.4	51.8	19	3	US-09-531-000-38	Sequence 38, Appl
	39	11.4	51.8	19	4	US-09-422-978-6684	Sequence 6684, Ap
c	40	11.4	51.8	20	3	US-08-882-046-89	Sequence 89, Appl
	41	11.4	51.8	20	3	US-09-716-161A-85	Sequence 85, Appl
c	42	11.4	51.8	20	4	US-09-198-452A-3425	Sequence 3425, Ap
	43	11.4	51.8	20	4	US-09-843-376-44	Sequence 44, Appl
	44	11.4	51.8	20	4	US-09-555-554-13	Sequence 13, Appl
	45	11.4	51.8	20	4	US-09-112-580-230	Sequence 230, App
c	46	11.4	51.8	20	4	US-09-566-047-89	Sequence 89, Appl
c	47	11.4	51.8	20	4	US-09-953-318-28	Sequence 28, Appl
c	48	11.4	51.8	21	3	US-08-936-107A-26	Sequence 26, Appl
c	49	11.4	51.8	21	4	US-09-422-978-6627	Sequence 6627, Ap
c	50	11.4	51.8	22	4	US-09-548-130-9	Sequence 9, Appli
c	51	11.4	51.8	22	4	US-10-119-466-6	Sequence 6, Appli
c	52	11.2	50.9	18	1	US-08-434-255-20	Sequence 20, Appl
c	53	11.2	50.9	18	1	US-08-459-967-20	Sequence 20, Appl
c	54	11.2	50.9	18	1	US-08-460-327-20	Sequence 20, Appl
c	55	11.2	50.9	18	1	US-08-459-871-20	Sequence 20, Appl
	56	11.2	50.9	20	1	US-08-240-012-9	Sequence 9, Appli
	57	11.2	50.9	20	3	US-08-896-162A-9	Sequence 9, Appli
	58	11.2	50.9	20	4	US-08-983-605-261	Sequence 261, App
c	59	11.2	50.9	20	4	US-09-269-446D-107	Sequence 107, App
	60	11.2	50.9	21	4	US-09-422-978-11567	Sequence 11567, A
	61	11.2	50.9	22	1	US-08-446-918A-9	Sequence 9, Appli
	62	11.2	50.9	22	2	US-08-580-806-9	Sequence 9, Appli
	63	11.2	50.9	22	3	US-08-188-275A-11	Sequence 11, Appl
c	64	11	50.0	19	1	US-07-768-437-14	Sequence 14, Appl
c	65	11	50.0	19	1	US-07-768-437-15	Sequence 15, Appl
c	66	11	50.0	20	3	US-09-513-729B-26	Sequence 26, Appl
	67	11	50.0	20	3	US-09-382-616A-38	Sequence 38, Appl
	68	11	50.0	20	3	US-09-484-617-80	Sequence 80, Appl
c	69	11	50.0	20	3	US-09-563-826-7	Sequence 7, Appli
	70	11	50.0	20	3	US-09-580-189-3	Sequence 3, Appli
c	71	11	50.0	20	4	US-09-305-856B-23	Sequence 23, Appl
	72	11	50.0	20	4	US-09-728-466-38	Sequence 38, Appl
c	73	11	50.0	20	4	US-09-533-149-7	Sequence 7, Appli
	74	11	50.0	21	1	US-08-136-741-5	Sequence 5, Appli
	75	11	50.0	21	3	US-08-840-316-12	Sequence 12, Appl
	76	11	50.0	21	3	US-08-809-523-12	Sequence 12, Appl
	77	11	50.0	21	3	US-08-471-971-12	Sequence 12, Appl
	78	11	50.0	21	3	US-09-402-776-12	Sequence 12, Appl
c	79	11	50.0	21	4	US-09-422-978-10032	Sequence 10032, A
	80	11	50.0	21	4	US-08-470-246-12	Sequence 12, Appl
	81	11	50.0	21	4	US-08-316-765-12	Sequence 12, Appl
	82	11	50.0	21	4	US-09-724-475-12	Sequence 12, Appl
	83	11	50.0	21	5	PCT-US93-08849A-12	Sequence 12, Appl
	84	11	50.0	21	5	PCT-US93-08849-12	Sequence 12, Appl
c	85	11	50.0	22	3	US-08-545-196B-30	Sequence 30, Appl
c	86	10.8	49.1	20	1	US-08-249-386A-12	Sequence 12, Appl
c	87	10.8	49.1	20	3	US-09-844-634-160	Sequence 160, App
c	88	10.8	49.1	20	4	US-09-422-978-6306	Sequence 6306, Ap
	89	10.8	49.1	20	4	US-09-975-327A-12	Sequence 12, Appl
c	90	10.8	49.1	20	4	US-10-027-983-91	Sequence 91, Appl
c	91	10.8	49.1	20	4	US-10-029-517-85	Sequence 85, Appl
c	92	10.8	49.1	20	4	US-10-215-448-78	Sequence 78, Appl
c	93	10.8	49.1	20	5	PCT-US95-06160-12	Sequence 12, Appl
c	94	10.8	49.1	22	1	US-08-394-210-5	Sequence 5, Appli
c	95	10.6	48.2	18	3	US-09-106-038A-50	Sequence 50, Appl
	96	10.6	48.2	18	3	US-09-338-907-414	Sequence 414, App
	97	10.6	48.2	18	3	US-09-218-207-414	Sequence 414, App
	98	10.6	48.2	18	4	US-09-422-978-8311	Sequence 8311, Ap
	99	10.6	48.2	19	4	US-09-422-978-9517	Sequence 9517, Ap
c	100	10.6	48.2	19	4	US-09-696-791-1775	Sequence 1775, Ap

ALIGNMENTS

```
RESULT 1
US-09-198-452A-5333/c
; Sequence 5333, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, preve
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/09/198,452A
;  CURRENT FILING DATE:  1998-11-24
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 5333
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: Chlamydia pneumoniae
US-09-198-452A-5333

  Query Match             69.1%;  Score 15.2;  DB 4;  Length 20;
  Best Local Similarity   85.0%;  Pred. No. 3.2e+02;
  Matches   17;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCATGTTACAGGTAGAAAAG 20
              || |||| ||| ||||||||
Db         20 GCCTGTTCCAGATAGAAAAG 1


RESULT 2
US-09-689-065B-50
; Sequence 50, Application US/09689065B
; Patent No. 6605696
; GENERAL INFORMATION:
;  APPLICANT: Pfizer Products, Inc.
;  TITLE OF INVENTION: LAWSONIA INTRACELLULARIS PROTEINS AND RELATED METHODS AND
;  TITLE OF INVENTION:  MATERIALS
;  FILE REFERENCE: 3153.00187/PC10589A
;  CURRENT APPLICATION NUMBER: US/09/689,065B
;  CURRENT FILING DATE:  2000-10-12
;  PRIOR APPLICATION NUMBER: US Prov. 60/160,922
;  PRIOR FILING DATE: 1999-10-22
;  PRIOR APPLICATION NUMBER: US Prov. 60/163,858
;  PRIOR FILING DATE: 1999-11-05
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50
;    LENGTH: 21
;    TYPE: DNA
;    ORGANISM: Lawsonia intracellularis
US-09-689-065B-50

  Query Match             60.0%;  Score 13.2;  DB 4;  Length 21;
  Best Local Similarity   83.3%;  Pred. No. 3.1e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 TGTTACAGGTAGAAAAGC 21
              || |||||  ||||||||
Db          2 TGGTACAGCAAGAAAAGC 19


RESULT 3
US-09-564-805-157/c
; Sequence 157, Application US/09564805
; Patent No. 6333403
; GENERAL INFORMATION:
;  APPLICANT:  Tavtigian, Sean V.
;  APPLICANT:  Teng, David H.F.
;  APPLICANT:  Simard, Jacques
;  APPLICANT:  Rommens, Johanna M.
;  APPLICANT:  Myriad Genetics, Inc.
;  TITLE OF INVENTION:  Chromosome 17p-Linked Prostate Cancer Susceptibility
;  TITLE OF INVENTION:  Gene and a Paralog and Orthologous Genes
;  FILE REFERENCE:  2318-258
;  CURRENT APPLICATION NUMBER: US/09/564,805
;  CURRENT FILING DATE:  2000-05-05
;  PRIOR APPLICATION NUMBER:  US 60/107,468
;  PRIOR FILING DATE:  1998-11-06
;  PRIOR APPLICATION NUMBER:  09/434,382
;  PRIOR FILING DATE:  1999-11-05
;  NUMBER OF SEQ ID NOS:  240
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 157
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-564-805-157

  Query Match             58.2%;  Score 12.8;  DB 3;  Length 19;
  Best Local Similarity   87.5%;  Pred. No. 4.8e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 ATGTTACAGGTAGAAA 18
              |||| ||||| |||||
Db         19 ATGTCACAGGCAGAAA 4


RESULT 4
US-08-840-316-53
; Sequence 53, Application US/08840316
; Patent No. 6054567
;  GENERAL INFORMATION:
;    APPLICANT:  Emerson, Suzanne U., Purcell, Robert H.,
;    APPLICANT:  Tsarev, Sergei. A., and Robinson, Robin A.
;    TITLE OF INVENTION:  Recombinant Proteins Of
;    TITLE OF INVENTION:  A Pakistani Strain Of Hepatitis E And Their
;    TITLE OF INVENTION:  Use In Diagnostic Methods And Vaccines
;    NUMBER OF SEQUENCES:  111
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORGAN & FINNEGAN
;      STREET:  345 PARK AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10154
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WORDPERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/840,316
;      FILING DATE:  11-APR-1997
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Richard W. Bork
;      REGISTRATION NUMBER:  36,459
;      REFERENCE/DOCKET NUMBER:  2026-4255
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 758-4800
;      TELEFAX:  (212) 751-6849
;  INFORMATION FOR SEQ ID NO:  53:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-840-316-53
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  Query Match             55.5%;  Score 12.2;  DB 3;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 9.3e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 GTTACAGGTAGAAAAGC 21
              |||||||  |||||| |
Db          2 GTTACAGCCAGAAAACC 18


RESULT 5
US-08-809-523-53
; Sequence 53, Application US/08809523
; Patent No. 6207416
;  GENERAL INFORMATION:
;    APPLICANT:  Tsarev, Sergei. A., Emerson,
;    APPLICANT:  Suzanne U., Purcell, Robert H.
;    TITLE OF INVENTION:  Recombinant Proteins Of
;    TITLE OF INVENTION:  A Pakistani Strain Of Hepatitis E And Their
;    TITLE OF INVENTION:  Use In Diagnostic Methods And Vaccines
;    NUMBER OF SEQUENCES:  107
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORGAN & FINNEGAN, L.L.P.
;      STREET:  345 PARK AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10154
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WORDPERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/809,523
;      FILING DATE:  28-MAY-1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/13102
;      FILING DATE:  03-OCT-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US08/316,765
;      FILING DATE:  03-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/947,263
;      FILING DATE:  18-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Richard W. Bork
;      REGISTRATION NUMBER:  36,459
;      REFERENCE/DOCKET NUMBER:  2026-4032US4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 758-4800
;      TELEFAX:  (212) 751-6849
;  INFORMATION FOR SEQ ID NO:  53:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-809-523-53

  Query Match             55.5%;  Score 12.2;  DB 3;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 9.3e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 GTTACAGGTAGAAAAGC 21
              |||||||  |||||| |
Db          2 GTTACAGCCAGAAAACC 18


RESULT 6
US-08-471-971-53
; Sequence 53, Application US/08471971
; Patent No. 6287759
;  GENERAL INFORMATION:
;    APPLICANT:  Tsarev, Sergei. A., Emerson,
;    APPLICANT:  Suzanne U., Purcell, Robert H.
;    TITLE OF INVENTION:  Recombinant Proteins Of
;    TITLE OF INVENTION:  A Pakistani Strain Of Hepatitis E And Their
;    TITLE OF INVENTION:  Use In Diagnostic Methods And Vaccines
;    NUMBER OF SEQUENCES:  107
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORGAN & FINNEGAN
;      STREET:  345 PARK AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10154
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WORDPERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/471,971
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US08/316,765
;      FILING DATE:  03-OCT-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US07/947,263
;      FILING DATE:  18-SEP-1992
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Richard W. Bork
;      REGISTRATION NUMBER:  36,459
;      REFERENCE/DOCKET NUMBER:  2026-4032US2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 758-4800
;      TELEFAX:  (212) 751-6849
;  INFORMATION FOR SEQ ID NO:  53:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-471-971-53

  Query Match             55.5%;  Score 12.2;  DB 3;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 9.3e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 GTTACAGGTAGAAAAGC 21
              |||||||  |||||| |
Db          2 GTTACAGCCAGAAAACC 18


RESULT 7
US-09-402-776-53
; Sequence 53, Application US/09402776
; Patent No. 6458562
;  GENERAL INFORMATION:
;    APPLICANT:  Emerson, Suzanne U., Purcell, Robert H.,
;    APPLICANT:  Tsarev, Sergei. A., and Robinson, Robin A.
;    TITLE OF INVENTION:  Recombinant Proteins Of
;    TITLE OF INVENTION:  A Pakistani Strain Of Hepatitis E And Their
;    TITLE OF INVENTION:  Use In Diagnostic Methods And Vaccines
;    NUMBER OF SEQUENCES:  111
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORGAN & FINNEGAN
;      STREET:  345 PARK AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10154
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;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WORDPERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/402,776
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/840,316
;      FILING DATE:  11-APR-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Richard W. Bork
;      REGISTRATION NUMBER:  36,459
;      REFERENCE/DOCKET NUMBER:  2026-4255
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 758-4800
;      TELEFAX:  (212) 751-6849
;  INFORMATION FOR SEQ ID NO:  53:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-402-776-53

  Query Match             55.5%;  Score 12.2;  DB 3;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 9.3e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 GTTACAGGTAGAAAAGC 21
              |||||||  |||||| |
Db          2 GTTACAGCCAGAAAACC 18


RESULT 8
US-09-422-978-4779
; Sequence 4779, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT: Blumenfeld, Marta
;  APPLICANT: Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/09/422,978
;  CURRENT FILING DATE: 1999-10-20
;  EARLIER APPLICATION NUMBER: US 09/298,850
;  EARLIER FILING DATE: 1999-04-21
;  EARLIER APPLICATION NUMBER: US 60/109,732
;  EARLIER FILING DATE: 1998-11-23
;  EARLIER APPLICATION NUMBER: US 60/082,614
;  EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4779
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..18
;   OTHER INFORMATION: upstream amplification primer 99-17762 for SEQ 845,
US-09-422-978-4779

  Query Match             55.5%;  Score 12.2;  DB 4;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 9.3e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 TGTTACAGGTAGAAAAG 20
              ||| | |||||| |||
Db          1 TGTGAGAGGTAGAGAAG 17


RESULT 9
US-08-470-246-53
; Sequence 53, Application US/08470246
; Patent No. 6696242
;  GENERAL INFORMATION:
;    APPLICANT:  Tsarev, Sergei. A., Emerson,
;    APPLICANT:  Suzanne U., Purcell, Robert H.
;    TITLE OF INVENTION:  Recombinant Proteins Of
;    TITLE OF INVENTION:  A Pakistani Strain Of Hepatitis E And Their
;    TITLE OF INVENTION:  Use In Diagnostic Methods And Vaccines
;    NUMBER OF SEQUENCES:  107
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORGAN & FINNEGAN
;      STREET:  345 PARK AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10154
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WORDPERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/470,246
;      FILING DATE:  06-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US08/316,765
;      FILING DATE:  03-OCT-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US07/947,263
;      FILING DATE:  18-SEP-1992
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Richard W. Bork
;      REGISTRATION NUMBER:  36,459
;      REFERENCE/DOCKET NUMBER:  2026-4032US3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 758-4800
;      TELEFAX:  (212) 751-6849
;  INFORMATION FOR SEQ ID NO:  53:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-470-246-53

  Query Match             55.5%;  Score 12.2;  DB 4;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 9.3e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 GTTACAGGTAGAAAAGC 21
              |||||||  |||||| |
Db          2 GTTACAGCCAGAAAACC 18


RESULT 10
US-08-316-765-53
; Sequence 53, Application US/08316765
; Patent No. 6706873
;  GENERAL INFORMATION:
;    APPLICANT:  Tsarev, Sergei. A., Emerson,
;    APPLICANT:  Suzanne U., Purcell, Robert H.
;    TITLE OF INVENTION:  Recombinant Proteins Of
;    TITLE OF INVENTION:  A Pakistani Strain Of Hepatitis E And Their
;    TITLE OF INVENTION:  Use In Diagnostic Methods And Vaccines
;    NUMBER OF SEQUENCES:  107
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORGAN & FINNEGAN
```

```
;      STREET:  345 PARK AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10154
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WORDPERFECT 5.1
;    CURRENT APPLICATION DATA:  08/316,765
;      APPLICATION NUMBER:  US/08/316,765
;      FILING DATE:  03-OCT-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US07/947,263
;      FILING DATE:  18-SEP-1992
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Richard W. Bork
;      REGISTRATION NUMBER:  36,459
;      REFERENCE/DOCKET NUMBER:  2026-4032US1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 758-4800
;      TELEFAX:  (212) 751-6849
;  INFORMATION FOR SEQ ID NO:  53:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-316-765-53

  Query Match             55.5%;  Score 12.2;  DB 4;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 9.3e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 GTTACAGGTAGAAAAGC 21
              |||||||  ||||||  |
Db          2 GTTACAGCCAGAAAACC 18


RESULT 11
US-09-724-475-53
; Sequence 53, Application US/09724475
; Patent No. 6787145
;   GENERAL INFORMATION:
;        APPLICANT: Tsarev, Sergei. A., Emerson,
;                   Suzanne U., Purcell, Robert H.
;        TITLE OF INVENTION: Recombinant Proteins Of
;                            A Pakistani Strain Of Hepatitis E And Their
;                            Use In Diagnostic Methods And Vaccines
;        NUMBER OF SEQUENCES: 107
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
;             STREET: 345 PARK AVENUE
;             CITY: NEW YORK
;             STATE: NEW YORK
;             COUNTRY: USA
;             ZIP: 10154
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: FLOPPY DISK
;             COMPUTER: IBM PC COMPATIBLE
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: WORDPERFECT 5.1
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/724,475
;             FILING DATE: 28-No. 6787145-2000
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/809,523
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: US08/316,765
;             FILING DATE: 03-OCT-1994
;             APPLICATION NUMBER: 07/947,263
;             FILING DATE: 18-SEP-1992
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Richard W. Bork
;             REGISTRATION NUMBER: 36,459
;             REFERENCE/DOCKET NUMBER: 2026-4032US4
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 758-4800
;             TELEFAX: (212) 751-6849
;   INFORMATION FOR SEQ ID NO: 53:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 18 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-09-724-475-53

  Query Match             55.5%;  Score 12.2;  DB 4;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 9.3e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 GTTACAGGTAGAAAAGC 21
              |||||||  ||||||  |
Db          2 GTTACAGCCAGAAAACC 18


RESULT 12
PCT-US93-08849A-53
; Sequence 53, Application PC/TUS9308849A
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Recombinant Proteins Of
;    TITLE OF INVENTION:  A Pakistani Strain Of Hepatitis E And Their
;    TITLE OF INVENTION:  Use In Diagnostic Methods And Vaccines
;    NUMBER OF SEQUENCES:  98
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORGAN & FINNEGAN
;      STREET:  345 PARK AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10154
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WORDPERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/08849A
;      FILING DATE:  17-SEP-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US07/947,263
;      FILING DATE:  18-SEP-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  William S. Feiler
;      REGISTRATION NUMBER:  26,728
;      REFERENCE/DOCKET NUMBER:  2026-4032 PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 758-4800
;      TELEFAX:  (212) 751-6849
;  INFORMATION FOR SEQ ID NO:  53:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
PCT-US93-08849A-53

  Query Match             55.5%;  Score 12.2;  DB 5;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 9.3e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;
```

```
Qy          5 GTTACAGGTAGAAAAGC 21
              ||||||| |||||| |
Db          2 GTTACAGCCAGAAAACC 18


RESULT 13
PCT-US93-08849-53
; Sequence 53, Application PC/TUS9308849
;  GENERAL INFORMATION:
;    APPLICANT:  Tsarev, Sergei A., Emerson,
;    APPLICANT:  Suzanne U., Purcell, Robert H.
;    TITLE OF INVENTION:  Recombinant Proteins Of
;    TITLE OF INVENTION:  A Pakistani Strain Of Hepatitis E And Their
;    TITLE OF INVENTION:  Use In Diagnostic Methods And Vaccines
;    NUMBER OF SEQUENCES:  98
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORGAN & FINNEGAN
;      STREET:  345 PARK AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10154
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  FLOPPY DISK
;      COMPUTER:  IBM PC COMPATIBLE
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WORDPERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/08849
;      FILING DATE:  17-SEP-1993
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/947,263
;      FILING DATE:  18-SEP-1992
;      NAME:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bork, Richard, W.
;      REGISTRATION NUMBER:  36,459
;      REFERENCE/DOCKET NUMBER:  2026-4032
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 758-4800
;      TELEFAX:  (212) 751-6849
;  INFORMATION FOR SEQ ID NO:  53:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
PCT-US93-08849-53

  Query Match             55.5%;  Score 12.2;  DB 5;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 9.3e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 GTTACAGGTAGAAAAGC 21
              ||||||| |||||| |
Db          2 GTTACAGCCAGAAAACC 18


RESULT 14
US-09-702-251-44/c
; Sequence 44, Application US/09702251
; Patent No. 6372492
; GENERAL INFORMATION:
;  APPLICANT:  C. Frank Bennett
;  APPLICANT:  Lex M. Cowsert
;  TITLE OF INVENTION:  ANTISENSE MODULATION OF TALIN EXPRESSION
;  FILE REFERENCE:  RTS-0199
;  CURRENT APPLICATION NUMBER: US/09/702,251
;  CURRENT FILING DATE:  2000-10-30
;  NUMBER OF SEQ ID NOS:  89
; SEQ ID NO 44
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-702-251-44

  Query Match             55.5%;  Score 12.2;  DB 3;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 9.5e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 TGTTACAGGTAGAAAAG 20
              |||| |||| || ||||
Db         19 TGTTGCAGGCAGCAAAG 3


RESULT 15
US-08-765-340-23
; Sequence 23, Application US/08765340
; Patent No. 6150092
;  GENERAL INFORMATION:
;    APPLICANT:  UCHIDA, K.,
;    APPLICANT:  UCHIDA, T.,
;    APPLICANT:  TANAKA, Y.,
;    APPLICANT:  MATSUDA, Y.,
;    APPLICANT:  KONDO, S.
;    TITLE OF INVENTION:  AN ANTISENSE NUCLEIC ACID
;    TITLE OF INVENTION:  COMPOUND
;    NUMBER OF SEQUENCES:  185
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  MORGAN & FINNEGAN, L.L.P.
;      STREET:  345 PARK AVENUE
;      CITY:  NEW YORK
;      STATE:  NEW YORK
;      COUNTRY:  USA
;      ZIP:  10154
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version
;      SOFTWARE:  #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/765,340
;      FILING DATE:  23-DEC-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 145146/94
;      FILING DATE:  27-JUN-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 311130/94
;      FILING DATE:  21-NOV-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SERUNIAN, LESLIE
;      REGISTRATION NUMBER:  35,353
;      REFERENCE/DOCKET NUMBER:  1452-4005
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 758-4800
;      TELEFAX:  (212) 751-6849
;  INFORMATION FOR SEQ ID NO:  23:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "synthetic DNA"
US-08-765-340-23

  Query Match             54.5%;  Score 12;  DB 3;  Length 20;
  Best Local Similarity   75.0%;  Pred. No. 1.2e+04;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GCATGTTACAGGTAGAAAAG 20
              ||||| |  ||||||| ||
```

```
Db          1 GCATGGTGGAGGTAGAGCAG 20


RESULT 16
US-09-422-978-9693/c
; Sequence 9693, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT: Blumenfeld, Marta
;  APPLICANT: Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/09/422,978
;  CURRENT FILING DATE: 1999-10-20
;  EARLIER APPLICATION NUMBER: US 09/298,850
;  EARLIER FILING DATE: 1999-04-21
;  EARLIER APPLICATION NUMBER: US 60/109,732
;  EARLIER FILING DATE: 1998-11-23
;  EARLIER APPLICATION NUMBER: US 60/082,614
;  EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 9693
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..20
;   OTHER INFORMATION: downstream amplification primer 99-669 for SEQ 1828, in complemer
US-09-422-978-9693

  Query Match           54.5%;  Score 12;  DB 4;  Length 20;
  Best Local Similarity  75.0%;  Pred. No. 1.2e+04;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GCATGTTACAGGTAGAAAAG 20
              | ||||   ||||| |||||
Db         20 GTATGTCTGAGGTATAAAAG 1


RESULT 17
US-09-696-791-4514/c
; Sequence 4514, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
;  APPLICANT:  Robbins, Joan M.
;  APPLICANT:  Tritz, Richard
;  TITLE OF INVENTION:  RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
;  TITLE OF INVENTION:  SKIN AND EYE DISEASES
;  FILE REFERENCE:  480124.407
;  CURRENT APPLICATION NUMBER: US/09/696,791
;  CURRENT FILING DATE:  2000-10-25
;  NUMBER OF SEQ ID NOS:  4523
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 4514
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Homo sapien
;   FEATURE:
;   OTHER INFORMATION: VEGF hammerhead ribozyme recognition site
US-09-696-791-4514

  Query Match           54.5%;  Score 12;  DB 4;  Length 21;
  Best Local Similarity  75.0%;  Pred. No. 1.2e+04;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 CATGTTACAGGTAGAAAAGC 21
              |||| |  |||||||  |||
Db         21 CATGGTGGAGGTAGAGCAGC 2


RESULT 18
US-09-422-978-6072
; Sequence 6072, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT: Blumenfeld, Marta
;  APPLICANT: Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/09/422,978
;  CURRENT FILING DATE: 1999-10-20
;  EARLIER APPLICATION NUMBER: US 09/298,850
;  EARLIER FILING DATE: 1999-04-21
;  EARLIER APPLICATION NUMBER: US 60/109,732
;  EARLIER FILING DATE: 1998-11-23
;  EARLIER APPLICATION NUMBER: US 60/082,614
;  EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6072
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..19
;   OTHER INFORMATION: upstream amplification primer 99-8748 for SEQ 2138,
US-09-422-978-6072

  Query Match           53.6%;  Score 11.8;  DB 4;  Length 19;
  Best Local Similarity  86.7%;  Pred. No. 1.5e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 GTTACAGGTAGAAAA 19
              |||| |||| |||||
Db          1 GTTAGAGGTTGAAAA 15


RESULT 19
US-08-477-270-27/c
; Sequence 27, Application US/08477270
; Patent No. 5629158
;  GENERAL INFORMATION:
;    APPLICANT:  UHLEN, Mathias
;    TITLE OF INVENTION:  SOLID PHASE DIAGNOSIS OF MEDICAL
;    TITLE OF INVENTION:  CONDITIONS
;    NUMBER OF SEQUENCES:  30
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/477,270
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/261,010
;      FILING DATE:
;      APPLICATION NUMBER:  US 07/781,157
;      FILING DATE:  07-NOV-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  16787/153 DFBC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
```

```
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  27:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Other nucleic acid;
;      DESCRIPTION:  Synthetic DNA oligonucleotide
;    IMMEDIATE SOURCE:
;      CLONE:  RIT 34
US-08-477-270-27

  Query Match             53.6%;  Score 11.8;  DB 1;  Length 20;
  Best Local Similarity   86.7%;  Pred. No. 1.5e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 TGTTACAGGTAGAAA 18
              || |||||| |||||
Db         19 TGGTACAGGCAGAAA 5


RESULT 20
US-09-487-445-98
; Sequence 98, Application US/09487445
; Patent No. 6258600
; GENERAL INFORMATION:
;  APPLICANT: Hong Zhang
;  APPLICANT: Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 8 EXPRESSION
;  FILE REFERENCE: RTS-0107
;  CURRENT APPLICATION NUMBER: US/09/487,445
;  CURRENT FILING DATE: 2000-01-19
;  NUMBER OF SEQ ID NOS: 176
; SEQ ID NO 98
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-487-445-98

  Query Match             53.6%;  Score 11.8;  DB 3;  Length 20;
  Best Local Similarity   86.7%;  Pred. No. 1.5e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 ACAGGTAGAAAAGCC 22
              | |||||||| ||||
Db          4 AGAGGTAGAAGAGCC 18


RESULT 21
US-09-648-520E-29/c
; Sequence 29, Application US/09648520E
; Patent No. 6432649
; GENERAL INFORMATION:
;  APPLICANT: Stich, Roger W.
;  APPLICANT:  Rikihisa, Yasuko
;  TITLE OF INVENTION: Methods for Detecting Ehrlichia Canis and Ehrlichia Chaffeensis i
;  TITLE OF INVENTION:  Vertebrate and Invertebrate Hosts
;  FILE REFERENCE: 22727/04069
;  CURRENT APPLICATION NUMBER: US/09/648,520E
;  CURRENT FILING DATE:  2000-08-25
;  NUMBER OF SEQ ID NOS: 51
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: synthetic sequence
US-09-648-520E-29

  Query Match             52.7%;  Score 11.6;  DB 3;  Length 19;
  Best Local Similarity   77.8%;  Pred. No. 1.9e+04;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 ATGTTACAGGTAGAAAAG 20
              ||  | |||||||| |||
Db         18 ATACTCCAGGTAGAGAAG 1


RESULT 22
US-09-422-978-4544
; Sequence 4544, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT: Blumenfeld, Marta
;  APPLICANT: Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/09/422,978
;  CURRENT FILING DATE: 1999-10-20
;  EARLIER APPLICATION NUMBER: US 09/298,850
;  EARLIER FILING DATE: 1999-04-21
;  EARLIER APPLICATION NUMBER: US 60/109,732
;  EARLIER FILING DATE: 1998-11-23
;  EARLIER APPLICATION NUMBER: US 60/082,614
;  EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4544
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..19
;   OTHER INFORMATION: upstream amplification primer 99-15744 for SEQ 610,
US-09-422-978-4544

  Query Match             52.7%;  Score 11.6;  DB 4;  Length 19;
  Best Local Similarity   77.8%;  Pred. No. 1.9e+04;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 TGTTACAGGTAGAAAAGC 21
              ||| | || |||||| ||
Db          2 TGTCATAGTTAGAAAGGC 19


RESULT 23
US-08-985-162-702
; Sequence 702, Application US/08985162
; Patent No. 6057156
;  GENERAL INFORMATION:
;    APPLICANT:  Akhtar, Saghir
;    APPLICANT:  Fell, Patricia
;    APPLICANT:  McSwiggen, James
;    TITLE OF INVENTION:  ENZYMATIC NUCLEIC ACID TREATMENT
;    TITLE OF INVENTION:  OF DISEASES OR CONDITIONS RELATED
;    TITLE OF INVENTION:  TO LEVELS OF EPIDERMAL GROWTH
;    TITLE OF INVENTION:  FACTOR RECEPTORS
;    NUMBER OF SEQUENCES:  1877
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
```

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;       OPERATING SYSTEM:  IBM P.C. DOS 5.0
;       SOFTWARE:  FastSEQ for Windows 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/985,162
;       FILING DATE:  04 December 1997
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  60/036,476
;       FILING DATE:  31 January 1997
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Warburg, Richard J.
;       REGISTRATION NUMBER:  32,327
;       REFERENCE/DOCKET NUMBER:  230/107
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (213) 489-1600
;       TELEFAX:  (213)  955-0440
;       TELEX:  67-3510
;   INFORMATION FOR SEQ ID NO:  702:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  17 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
US-08-985-162-702

  Query Match             51.8%;  Score 11.4;  DB 3;  Length 17;
  Best Local Similarity   61.5%;  Pred. No. 2.3e+04;
  Matches    8;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCATGTTACAGGT 13
              |||: ::|||||:
Db          5 GCAUUUUACAGGU 17


RESULT 24
US-08-985-162-703
; Sequence 703, Application US/08985162
; Patent No. 6057156
;  GENERAL INFORMATION:
;    APPLICANT:  Akhtar, Saghir
;    APPLICANT:  Fell, Patricia
;    APPLICANT:  McSwiggen, James
;    TITLE OF INVENTION:  ENZYMATIC NUCLEIC ACID TREATMENT
;    TITLE OF INVENTION:  OF DISEASES OR CONDITIONS RELATED
;    TITLE OF INVENTION:  TO LEVELS OF EPIDERMAL GROWTH
;    TITLE OF INVENTION:  FACTOR RECEPTORS
;    NUMBER OF SEQUENCES:  1877
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/985,162
;      FILING DATE:  04 December 1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/036,476
;      FILING DATE:  31 January 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  230/107
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213)  955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  703:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-985-162-703

  Query Match             51.8%;  Score 11.4;  DB 3;  Length 17;
  Best Local Similarity   61.5%;  Pred. No. 2.3e+04;
  Matches    8;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCATGTTACAGGT 13
              |||: ::|||||:
Db          4 GCAUUUUACAGGU 16


RESULT 25
US-08-985-162-704
; Sequence 704, Application US/08985162
; Patent No. 6057156
;  GENERAL INFORMATION:
;    APPLICANT:  Akhtar, Saghir
;    APPLICANT:  Fell, Patricia
;    APPLICANT:  McSwiggen, James
;    TITLE OF INVENTION:  ENZYMATIC NUCLEIC ACID TREATMENT
;    TITLE OF INVENTION:  OF DISEASES OR CONDITIONS RELATED
;    TITLE OF INVENTION:  TO LEVELS OF EPIDERMAL GROWTH
;    TITLE OF INVENTION:  FACTOR RECEPTORS
;    NUMBER OF SEQUENCES:  1877
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/985,162
;      FILING DATE:  04 December 1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/036,476
;      FILING DATE:  31 January 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  230/107
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213)  955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  704:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-985-162-704

  Query Match             51.8%;  Score 11.4;  DB 3;  Length 17;
  Best Local Similarity   61.5%;  Pred. No. 2.3e+04;
  Matches    8;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;
```

```
Qy          1 GCATGTTACAGGT 13
              |||: ::|||||:
Db          3 GCAUUUUACAGGU 15


RESULT 26
US-08-985-162-705
; Sequence 705, Application US/08985162
; Patent No. 6057156
;  GENERAL INFORMATION:
;    APPLICANT:  Akhtar, Saghir
;    APPLICANT:  Fell, Patricia
;    APPLICANT:  McSwiggen, James
;    TITLE OF INVENTION:  ENZYMATIC NUCLEIC ACID TREATMENT
;    TITLE OF INVENTION:  OF DISEASES OR CONDITIONS RELATED
;    TITLE OF INVENTION:  TO LEVELS OF EPIDERMAL GROWTH
;    TITLE OF INVENTION:  FACTOR RECEPTORS
;    NUMBER OF SEQUENCES:  1877
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/985,162
;      FILING DATE:  04 December 1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/036,476
;      FILING DATE:  31 January 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  230/107
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213)  955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  705:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-985-162-705

  Query Match             51.8%;  Score 11.4;  DB 3;  Length 17;
  Best Local Similarity   61.5%;  Pred. No. 2.3e+04;
  Matches    8;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCATGTTACAGGT 13
              |||: ::|||||:
Db          2 GCAUUUUACAGGU 14


RESULT 27
US-08-584-040-1534
; Sequence 1534, Application US/08584040
; Patent No. 6346398
;  GENERAL INFORMATION:
;    APPLICANT:  Pavco, Pamela
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Escobedo, Jaime
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES OR
;    TITLE OF INVENTION:  CONDITIONS RELATED TO LEVELS
;    TITLE OF INVENTION:  OF VASCULAR ENDOTHELIAL
;    TITLE OF INVENTION:  GROWTH FACTOR
;    NUMBER OF SEQUENCES:  8502
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/584,040
;      FILING DATE:  January 11, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,974
;      FILING DATE:  October 26, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/064
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  1534:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-584-040-1534

  Query Match             51.8%;  Score 11.4;  DB 3;  Length 17;
  Best Local Similarity   69.2%;  Pred. No. 2.3e+04;
  Matches    9;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TGTTACAGGTAGA 16
              :| :|||||:|||
Db          5 UGAUACAGGUAGA 17


RESULT 28
US-09-371-772B-79
; Sequence 79, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
```

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;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 79
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-371-772B-79

  Query Match             51.8%;  Score 11.4;  DB 4;  Length 17;
  Best Local Similarity   69.2%;  Pred. No. 2.3e+04;
  Matches    9;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TGTTACAGGTAGA 16
              :| :|||||:|||
Db          5 UGAUACAGGUAGA 17


RESULT 29
US-09-371-772B-4284
; Sequence 4284, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4284
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-371-772B-4284

  Query Match             51.8%;  Score 11.4;  DB 4;  Length 17;
  Best Local Similarity   69.2%;  Pred. No. 2.3e+04;
  Matches    9;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TGTTACAGGTAGA 16
              :| :|||||:|||
Db          3 UGAUACAGGUAGA 15


RESULT 30
US-09-401-063-702
; Sequence 702, Application US/09401063
; Patent No. 6623962
;  GENERAL INFORMATION:
;    APPLICANT:  Akhtar, Saghir
;    APPLICANT:  Fell, Patricia
;    APPLICANT:  McSwiggen, James
;    TITLE OF INVENTION:  ENZYMATIC NUCLEIC ACID TREATMENT
;    TITLE OF INVENTION:  OF DISEASES OR CONDITIONS RELATED
;    TITLE OF INVENTION:  TO LEVELS OF EPIDERMAL GROWTH
;    TITLE OF INVENTION:  FACTOR RECEPTORS
;    NUMBER OF SEQUENCES:  1877
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/401,063
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/985,162
;      FILING DATE:  04 December 1997
;      APPLICATION NUMBER:  60/036,476
;      FILING DATE:  31 January 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  230/107
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213)  955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  702:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-401-063-702

  Query Match             51.8%;  Score 11.4;  DB 4;  Length 17;
  Best Local Similarity   61.5%;  Pred. No. 2.3e+04;
  Matches    8;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCATGTTACAGGT 13
              |||: ::|||||:
Db          5 GCAUUUUACAGGU 17


RESULT 31
US-09-401-063-703
; Sequence 703, Application US/09401063
; Patent No. 6623962
;  GENERAL INFORMATION:
;    APPLICANT:  Akhtar, Saghir
;    APPLICANT:  Fell, Patricia
;    APPLICANT:  McSwiggen, James
;    TITLE OF INVENTION:  ENZYMATIC NUCLEIC ACID TREATMENT
;    TITLE OF INVENTION:  OF DISEASES OR CONDITIONS RELATED
;    TITLE OF INVENTION:  TO LEVELS OF EPIDERMAL GROWTH
;    TITLE OF INVENTION:  FACTOR RECEPTORS
;    NUMBER OF SEQUENCES:  1877
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/401,063
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/985,162
```

```
;      FILING DATE:  04 December 1997
;      APPLICATION NUMBER:  60/036,476
;      FILING DATE:  31 January 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  230/107
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213)  955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  703:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-401-063-703

  Query Match             51.8%;  Score 11.4;  DB 4;  Length 17;
  Best Local Similarity   61.5%;  Pred. No. 2.3e+04;
  Matches    8;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCATGTTACAGGT 13
              |||: ::|||||:
Db          4 GCAUUUUACAGGU 16


RESULT 32
US-09-401-063-704
; Sequence 704, Application US/09401063
; Patent No. 6623962
;  GENERAL INFORMATION:
;    APPLICANT:  Akhtar, Saghir
;    APPLICANT:  Fell, Patricia
;    APPLICANT:  McSwiggen, James
;    TITLE OF INVENTION:  ENZYMATIC NUCLEIC ACID TREATMENT
;    TITLE OF INVENTION:  OF DISEASES OR CONDITIONS RELATED
;    TITLE OF INVENTION:  TO LEVELS OF EPIDERMAL GROWTH
;    TITLE OF INVENTION:  FACTOR RECEPTORS
;    NUMBER OF SEQUENCES:  1877
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/401,063
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/985,162
;      FILING DATE:  04 December 1997
;      APPLICATION NUMBER:  60/036,476
;      FILING DATE:  31 January 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  230/107
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213)  955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  704:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-401-063-704

  Query Match             51.8%;  Score 11.4;  DB 4;  Length 17;
  Best Local Similarity   61.5%;  Pred. No. 2.3e+04;
  Matches    8;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCATGTTACAGGT 13
              |||: ::|||||:
Db          3 GCAUUUUACAGGU 15


RESULT 33
US-09-401-063-705
; Sequence 705, Application US/09401063
; Patent No. 6623962
;  GENERAL INFORMATION:
;    APPLICANT:  Akhtar, Saghir
;    APPLICANT:  Fell, Patricia
;    APPLICANT:  McSwiggen, James
;    TITLE OF INVENTION:  ENZYMATIC NUCLEIC ACID TREATMENT
;    TITLE OF INVENTION:  OF DISEASES OR CONDITIONS RELATED
;    TITLE OF INVENTION:  TO LEVELS OF EPIDERMAL GROWTH
;    TITLE OF INVENTION:  FACTOR RECEPTORS
;    NUMBER OF SEQUENCES:  1877
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/401,063
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/985,162
;      FILING DATE:  04 December 1997
;      APPLICATION NUMBER:  60/036,476
;      FILING DATE:  31 January 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  230/107
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213)  955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  705:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-401-063-705

  Query Match             51.8%;  Score 11.4;  DB 4;  Length 17;
  Best Local Similarity   61.5%;  Pred. No. 2.3e+04;
  Matches    8;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCATGTTACAGGT 13
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              |||: ::||||||:
Db          2 GCAUUUUACAGGU 14


RESULT 34
US-09-685-664B-79
; Sequence 79, Application US/09685664B
; Patent No. 6818447
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Recptor
;  FILE REFERENCE: MBHB00-876-K (400/021)
;  CURRENT APPLICATION NUMBER: US/09/685,664B
;  CURRENT FILING DATE:  2000-10-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  PRIOR APPLICATION NUMBER: US 09/371,772
;  PRIOR FILING DATE: 1999-08-10
;  NUMBER OF SEQ ID NOS: 8231
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 79
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-685-664B-79

  Query Match             51.8%;  Score 11.4;  DB 4;  Length 17;
  Best Local Similarity   69.2%;  Pred. No. 2.3e+04;
  Matches    9;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          4 TGTTACAGGTAGA 16
              :| :|||||:|||
Db          5 UGAUACAGGUAGA 17


RESULT 35
US-08-981-988A-27
; Sequence 27, Application US/08981988A
; Patent No. 6337194
;  GENERAL INFORMATION:
;    APPLICANT:  Vittal Mallya Scientific Research Foundation
;    APPLICANT:  The University of Leicester
;    TITLE OF INVENTION:  Insulin
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  VITTAL MALLYA SCIENTIFIC RESEARCH FOUNDATION
;      STREET:  K. R. ROAD
;      CITY:  BANGALORE
;      COUNTRY:  INDIA
;      ZIP:  560 004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/981,988A
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9513967.1
;      FILING DATE:  08-JUL-1995
;  INFORMATION FOR SEQ ID NO:  27:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-981-988A-27

  Query Match             51.8%;  Score 11.4;  DB 3;  Length 18;
  Best Local Similarity   92.3%;  Pred. No. 2.3e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 AGGTAGAAAAGCC 22
              ||||||| |||||
Db          3 AGGTAGACAAGCC 15


RESULT 36
US-09-531-000-7
; Sequence 7, Application US/09531000
; Patent No. 6461810
; GENERAL INFORMATION:
;  APPLICANT:  JOHNSON, Marion D.
;  APPLICANT:  FRESCO, Jacques R.
;  TITLE OF INVENTION:  TRIPLEX IN-SITU HYBRIDIZATION
;  FILE REFERENCE:  2448-103
;  CURRENT APPLICATION NUMBER: US/09/531,000
;  CURRENT FILING DATE:  2000-09-08
;  PRIOR APPLICATION NUMBER:  PCT/US98/23765
;  PRIOR FILING DATE:  1998-11-10
;  PRIOR APPLICATION NUMBER:  60/064,997
;  PRIOR FILING DATE:  1997-11-10
;  NUMBER OF SEQ ID NOS:  77
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target
;   OTHER INFORMATION: sequences
US-09-531-000-7

  Query Match             51.8%;  Score 11.4;  DB 3;  Length 19;
  Best Local Similarity   92.3%;  Pred. No. 2.3e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 ACAGGTAGAAAAG 20
              | ||||||||||||
Db          1 AAAGGTAGAAAAG 13


RESULT 37
US-09-531-000-34
; Sequence 34, Application US/09531000
; Patent No. 6461810
; GENERAL INFORMATION:
;  APPLICANT:  JOHNSON, Marion D.
;  APPLICANT:  FRESCO, Jacques R.
;  TITLE OF INVENTION:  TRIPLEX IN-SITU HYBRIDIZATION
;  FILE REFERENCE:  2448-103
;  CURRENT APPLICATION NUMBER: US/09/531,000
;  CURRENT FILING DATE:  2000-09-08
;  PRIOR APPLICATION NUMBER:  PCT/US98/23765
;  PRIOR FILING DATE:  1998-11-10
;  PRIOR APPLICATION NUMBER:  60/064,997
;  PRIOR FILING DATE:  1997-11-10
;  NUMBER OF SEQ ID NOS:  77
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 34
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target
;   OTHER INFORMATION: sequences
US-09-531-000-34
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  Query Match             51.8%;  Score 11.4;  DB 3;  Length 19;
  Best Local Similarity   92.3%;  Pred. No. 2.3e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 ACAGGTAGAAAAG 20
              | ||||||||||||
Db          1 AAAGGTAGAAAAG 13


RESULT 38
US-09-531-000-38
; Sequence 38, Application US/09531000
; Patent No. 6461810
; GENERAL INFORMATION:
;  APPLICANT:  JOHNSON, Marion D.
;  APPLICANT:  FRESCO, Jacques R.
;  TITLE OF INVENTION:  TRIPLEX IN-SITU HYBRIDIZATION
;  FILE REFERENCE:  2448-103
;  CURRENT APPLICATION NUMBER: US/09/531,000
;  CURRENT FILING DATE:  2000-09-08
;  PRIOR APPLICATION NUMBER:  PCT/US98/23765
;  PRIOR FILING DATE:  1998-11-10
;  PRIOR APPLICATION NUMBER:  60/064,997
;  PRIOR FILING DATE:  1997-11-10
;  NUMBER OF SEQ ID NOS:  77
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 38
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target
;   OTHER INFORMATION: sequences
US-09-531-000-38

  Query Match             51.8%;  Score 11.4;  DB 3;  Length 19;
  Best Local Similarity   92.3%;  Pred. No. 2.3e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 ACAGGTAGAAAAG 20
              | ||||||||||||
Db          1 AAAGGTAGAAAAG 13


RESULT 39
US-09-422-978-6684
; Sequence 6684, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT: Blumenfeld, Marta
;  APPLICANT: Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/09/422,978
;  CURRENT FILING DATE: 1999-10-20
;  EARLIER APPLICATION NUMBER: US 09/298,850
;  EARLIER FILING DATE: 1999-04-21
;  EARLIER APPLICATION NUMBER: US 60/109,732
;  EARLIER FILING DATE: 1998-11-23
;  EARLIER APPLICATION NUMBER: US 60/082,614
;  EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6684
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..19
;   OTHER INFORMATION: upstream amplification primer 99-16772 for SEQ 2750,
US-09-422-978-6684

  Query Match             51.8%;  Score 11.4;  DB 4;  Length 19;
  Best Local Similarity   92.3%;  Pred. No. 2.3e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 ACAGGTAGAAAAG 20
              ||||| |||||||
Db          6 ACAGGAAGAAAAG 18


RESULT 40
US-08-882-046-89/c
; Sequence 89, Application US/08882046
; Patent No. 6136952
;  GENERAL INFORMATION:
;    APPLICANT:  Li, Linheng
;    APPLICANT:  Hood, Leroy
;    APPLICANT:  Krantz, Ian D.
;    APPLICANT:  Spinner, Nancy B.
;    TITLE OF INVENTION:  Human Jagged Polypeptide, Encoding
;    TITLE OF INVENTION:  Nucleic Acids and Methods of Use
;    NUMBER OF SEQUENCES:  110
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Campbell & Flores LLP
;      STREET:  4370 La Jolla Village Drive, Suite 700
;      CITY:  San Diego
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  92122
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/882,046
;      FILING DATE:  25-JUN-1997
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Campbell, Cathryn A.
;      REGISTRATION NUMBER:  31,815
;      REFERENCE/DOCKET NUMBER:  P-UW 2637
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (619) 535-9001
;      TELEFAX:  (619) 535-8949
;  INFORMATION FOR SEQ ID NO:  89:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-882-046-89

  Query Match             51.8%;  Score 11.4;  DB 3;  Length 20;
  Best Local Similarity   92.3%;  Pred. No. 2.4e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          3 ATGTTACAGGTAG 15
              |||||||||||.|
Db         17 ATGTTACAGGTTG 5


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Job time : 97 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 12, 2005, 08:55:07 ; Search time 371 Seconds
(without alignments)
384.741 Million cell updates/sec

Title: US-09-743-825-7
Perfect score: 22
Sequence: 1 gcatgttacaggtagaaaagcc 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7305758 seqs, 3244068913 residues

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Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published_Applications_NA:*
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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
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21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq:*
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26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
c 1	15.2	69.1	20	17	US-10-289-762-5333	Sequence 5333, Ap
2	13.2	60.0	21	14	US-10-210-296-50	Sequence 50, Appl
3	13.2	60.0	21	17	US-10-449-462-50	Sequence 50, Appl
4	13.2	60.0	21	22	US-10-449-648-50	Sequence 50, Appl
c 5	12.8	58.2	19	10	US-09-988-626-157	Sequence 157, App
c 6	12.8	58.2	19	10	US-09-988-687-157	Sequence 157, App
c 7	12.8	58.2	19	10	US-09-988-686-157	Sequence 157, App
c 8	12.8	58.2	20	10	US-09-906-158-75	Sequence 75, Appl
c 9	12.8	58.2	20	17	US-10-388-263-524	Sequence 524, App
c 10	12.8	58.2	21	17	US-10-388-360-230	Sequence 230, App
c 11	12.8	58.2	21	20	US-10-758-307-191	Sequence 191, App
c 12	12.8	58.2	21	21	US-10-690-880-48	Sequence 48, Appl
c 13	12.8	58.2	21	21	US-10-714-195-188	Sequence 188, App
c 14	12.8	58.2	21	21	US-10-852-797-80	Sequence 80, Appl
c 15	12.6	57.3	20	21	US-10-831-901A-12579	Sequence 12579, A
c 16	12.6	57.3	20	21	US-10-831-901A-12580	Sequence 12580, A
c 17	12.4	56.4	19	22	US-10-883-218-177	Sequence 177, App
18	12.4	56.4	19	22	US-10-883-218-579	Sequence 579, App
19	12.4	56.4	20	14	US-10-219-834-44	Sequence 44, Appl
20	12.4	56.4	20	17	US-10-436-715-92	Sequence 92, Appl
21	12.2	55.5	18	17	US-10-349-143-4779	Sequence 4779, Ap
c 22	12.2	55.5	19	22	US-10-922-626-197	Sequence 197, App
23	12.2	55.5	19	22	US-10-922-626-438	Sequence 438, App
c 24	12.2	55.5	20	9	US-09-791-942-44	Sequence 44, Appl
25	12.2	55.5	20	10	US-09-888-361-50	Sequence 50, Appl
c 26	12.2	55.5	20	19	US-10-415-463-44	Sequence 44, Appl
27	12.2	55.5	20	21	US-10-889-101-72	Sequence 72, Appl
c 28	12.2	55.5	20	21	US-10-889-101-218	Sequence 218, App
29	12.2	55.5	20	22	US-10-705-715-50	Sequence 50, Appl
c 30	12.2	55.5	21	18	US-10-333-429-274	Sequence 274, App
c 31	12.2	55.5	21	20	US-10-751-736-831	Sequence 831, App
c 32	12.2	55.5	21	20	US-10-751-736-1680	Sequence 1680, Ap
33	12.2	55.5	21	20	US-10-751-736-10500	Sequence 10500, A
34	12.2	55.5	21	20	US-10-751-736-15982	Sequence 15982, A
35	12.2	55.5	21	20	US-10-751-736-15983	Sequence 15983, A
c 36	12.2	55.5	21	20	US-10-751-736-40680	Sequence 40680, A
c 37	12	54.5	20	17	US-10-349-143-9693	Sequence 9693, Ap
38	11.8	53.6	19	9	US-09-969-373-4522	Sequence 4522, Ap
39	11.8	53.6	19	9	US-09-969-373-4524	Sequence 4524, Ap
40	11.8	53.6	19	17	US-10-349-143-6072	Sequence 6072, Ap
c 41	11.8	53.6	19	22	US-10-844-072-317	Sequence 317, App
42	11.8	53.6	19	22	US-10-844-072-454	Sequence 454, App
c 43	11.8	53.6	19	22	US-10-922-340-317	Sequence 317, App
44	11.8	53.6	19	22	US-10-922-340-454	Sequence 454, App
45	11.8	53.6	20	14	US-10-181-177-98	Sequence 98, Appl
c 46	11.8	53.6	20	17	US-10-210-589-76	Sequence 76, Appl
c 47	11.8	53.6	20	19	US-10-346-268-22	Sequence 22, Appl
c 48	11.8	53.6	20	19	US-10-346-268-35	Sequence 35, Appl
49	11.8	53.6	20	19	US-10-346-268-171	Sequence 171, App
50	11.8	53.6	20	19	US-10-346-268-181	Sequence 181, App
c 51	11.8	53.6	20	21	US-10-831-901A-12793	Sequence 12793, A
c 52	11.8	53.6	20	21	US-10-831-901A-12794	Sequence 12794, A
c 53	11.8	53.6	20	21	US-10-831-901A-12795	Sequence 12795, A
c 54	11.8	53.6	20	21	US-10-831-901A-12796	Sequence 12796, A
c 55	11.8	53.6	20	21	US-10-831-901A-12797	Sequence 12797, A
c 56	11.8	53.6	20	21	US-10-831-901A-12798	Sequence 12798, A
c 57	11.8	53.6	21	19	US-10-769-612-11	Sequence 11, Appl
58	11.8	53.6	21	19	US-10-769-612-12	Sequence 12, Appl
c 59	11.8	53.6	21	20	US-10-751-736-28206	Sequence 28206, A
c 60	11.8	53.6	21	20	US-10-751-736-28209	Sequence 28209, A
c 61	11.8	53.6	21	20	US-10-751-736-33372	Sequence 33372, A
c 62	11.6	52.7	18	22	US-10-702-817-117	Sequence 117, App
63	11.6	52.7	19	17	US-10-349-143-4544	Sequence 4544, Ap
c 64	11.6	52.7	19	22	US-10-138-162-29	Sequence 29, Appl
c 65	11.6	52.7	20	17	US-10-352-179-31	Sequence 31, Appl
c 66	11.6	52.7	20	21	US-10-831-901A-12578	Sequence 12578, A
c 67	11.6	52.7	20	21	US-10-831-901A-12581	Sequence 12581, A
68	11.6	52.7	20	21	US-10-831-901A-14588	Sequence 14588, A
69	11.6	52.7	20	21	US-10-831-901A-14589	Sequence 14589, A
70	11.6	52.7	20	21	US-10-831-901A-14590	Sequence 14590, A
c 71	11.6	52.7	21	20	US-10-751-736-19851	Sequence 19851, A
72	11.6	52.7	21	20	US-10-751-736-31339	Sequence 31339, A
73	11.6	52.7	21	20	US-10-751-736-31340	Sequence 31340, A
c 74	11.6	52.7	21	20	US-10-751-736-31723	Sequence 31723, A
c 75	11.6	52.7	22	18	US-10-431-096-286	Sequence 286, App
76	11.4	51.8	13	20	US-10-257-017B-71423	Sequence 71423, A
c 77	11.4	51.8	13	20	US-10-257-017B-71424	Sequence 71424, A
78	11.4	51.8	14	10	US-09-998-027-18	Sequence 18, Appl
79	11.4	51.8	14	16	US-10-165-099-18	Sequence 18, Appl
80	11.4	51.8	17	10	US-09-848-754A-702	Sequence 702, App

81	11.4	51.8	17	10	US-09-848-754A-703	Sequence 703, App
82	11.4	51.8	17	10	US-09-848-754A-704	Sequence 704, App
83	11.4	51.8	17	10	US-09-848-754A-705	Sequence 705, App
84	11.4	51.8	17	18	US-10-138-674-79	Sequence 79, Appl
85	11.4	51.8	17	18	US-10-138-674-4284	Sequence 4284, Ap
86	11.4	51.8	17	18	US-10-138-674-7261	Sequence 7261, Ap
87	11.4	51.8	17	19	US-10-287-949A-79	Sequence 79, Appl
88	11.4	51.8	17	19	US-10-287-949A-4284	Sequence 4284, Ap
89	11.4	51.8	17	19	US-10-287-949A-7261	Sequence 7261, Ap
90	11.4	51.8	17	20	US-10-712-633-146	Sequence 146, App
91	11.4	51.8	17	20	US-10-712-633-147	Sequence 147, App
92	11.4	51.8	19	17	US-10-349-143-6684	Sequence 6684, Ap
93	11.4	51.8	19	19	US-10-665-951-36	Sequence 36, Appl
c 94	11.4	51.8	19	19	US-10-665-951-463	Sequence 463, App
95	11.4	51.8	19	21	US-10-758-155-36	Sequence 36, Appl
c 96	11.4	51.8	19	21	US-10-758-155-463	Sequence 463, App
97	11.4	51.8	19	22	US-10-831-620-36	Sequence 36, Appl
c 98	11.4	51.8	19	22	US-10-831-620-463	Sequence 463, App
99	11.4	51.8	19	22	US-10-844-076-36	Sequence 36, Appl
c 100	11.4	51.8	19	22	US-10-844-076-463	Sequence 463, App

ALIGNMENTS

RESULT 1
US-10-289-762-5333/c
; Sequence 5333, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 5333
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-5333

Query Match 69.1%; Score 15.2; DB 17; Length 20;
Best Local Similarity 85.0%; Pred. No. 1.7e+03;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          1 GCATGTTACAGGTAGAAAAG 20
              || |||| ||| ||||||||
Db         20 GCCTGTTCCAGATAGAAAAG 1
```

RESULT 2
US-10-210-296-50
; Sequence 50, Application US/10210296
; Publication No. US20030021802A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Products Inc.
; TITLE OF INVENTION: LAWSONIA INTRACELLULARIS PROTEINS, AND RELATED
; TITLE OF INVENTION: METHODS
; TITLE OF INVENTION: AND MATERIALS
; FILE REFERENCE: PC10589A
; CURRENT APPLICATION NUMBER: US/10/210,296
; CURRENT FILING DATE: 2002-08-01
; PRIOR APPLICATION NUMBER: US/09/689,065
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 50
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Lawsonia intracellularis
US-10-210-296-50

Query Match 60.0%; Score 13.2; DB 14; Length 21;
Best Local Similarity 83.3%; Pred. No. 1.7e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          4 TGTTACAGGTAGAAAAGC 21
              || |||||  ||||||||
Db          2 TGGTACAGCAAGAAAAGC 19
```

RESULT 3
US-10-449-462-50
; Sequence 50, Application US/10449462
; Publication No. US20030202983A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Products, Inc.
; TITLE OF INVENTION: LAWSONIA INTRACELLULARIS PROTEINS AND RELATED METHODS AND
; TITLE OF INVENTION: MATERIALS
; FILE REFERENCE: 3153.00187/PC10589A
; CURRENT APPLICATION NUMBER: US/10/449,462
; CURRENT FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: US/09/689,065
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: US Prov. 60/160,922
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: US Prov. 60/163,858
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Lawsonia intracellularis
US-10-449-462-50

Query Match 60.0%; Score 13.2; DB 17; Length 21;
Best Local Similarity 83.3%; Pred. No. 1.7e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          4 TGTTACAGGTAGAAAAGC 21
              || |||||  ||||||||
Db          2 TGGTACAGCAAGAAAAGC 19
```

RESULT 4
US-10-449-648-50
; Sequence 50, Application US/10449648
; Publication No. US20050143561A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer Products, Inc.
; TITLE OF INVENTION: LAWSONIA INTRACELLULARIS PROTEINS AND RELATED METHODS AND
; TITLE OF INVENTION: MATERIALS
; FILE REFERENCE: 3153.00187/PC10589A
; CURRENT APPLICATION NUMBER: US/10/449,648
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: US/09/689,065B
; PRIOR FILING DATE: 2000-10-12
; PRIOR APPLICATION NUMBER: US Prov. 60/160,922
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: US Prov. 60/163,858
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Lawsonia intracellularis
US-10-449-648-50

Query Match 60.0%; Score 13.2; DB 22; Length 21;
Best Local Similarity 83.3%; Pred. No. 1.7e+04;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          4 TGTTACAGGTAGAAAAGC 21
              || |||||  ||||||||
Db          2 TGGTACAGCAAGAAAAGC 19
```

RESULT 5
US-09-988-626-157/c
; Sequence 157, Application US/09988626
; Publication No. US20030044959A1
; GENERAL INFORMATION:
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.F.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
; FILE REFERENCE: 2318-258
; CURRENT APPLICATION NUMBER: US/09/988,626
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/564,805
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/107,468
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: 09/434,382
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 157
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-988-626-157

Query Match 58.2%; Score 12.8; DB 10; Length 19;
Best Local Similarity 87.5%; Pred. No. 2.6e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          3 ATGTTACAGGTAGAAA 18
              |||| ||||| |||||
Db         19 ATGTCACAGGCAGAAA 4
```

RESULT 6
US-09-988-687-157/c
; Sequence 157, Application US/09988687
; Publication No. US20030045704A1
; GENERAL INFORMATION:
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.F.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
; FILE REFERENCE: 2318-258
; CURRENT APPLICATION NUMBER: US/09/988,687
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/564,805
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/107,468
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: 09/434,382
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 157
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-988-687-157

Query Match 58.2%; Score 12.8; DB 10; Length 19;
Best Local Similarity 87.5%; Pred. No. 2.6e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          3 ATGTTACAGGTAGAAA 18
              |||| ||||| |||||
Db         19 ATGTCACAGGCAGAAA 4
```

RESULT 7
US-09-988-686-157/c
; Sequence 157, Application US/09988686
; Publication No. US20030120052A1
; GENERAL INFORMATION:
; APPLICANT: Tavtigian, Sean V.
; APPLICANT: Teng, David H.F.
; APPLICANT: Simard, Jacques
; APPLICANT: Rommens, Johanna M.
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Chromosome 17p-Linked Prostate Cancer Susceptibility
; TITLE OF INVENTION: Gene and a Paralog and Orthologous Genes
; FILE REFERENCE: 2318-258
; CURRENT APPLICATION NUMBER: US/09/988,686
; CURRENT FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 09/564,805
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: US 60/107,468
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: 09/434,382
; PRIOR FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 240
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 157
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-988-686-157

Query Match 58.2%; Score 12.8; DB 10; Length 19;
Best Local Similarity 87.5%; Pred. No. 2.6e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          3 ATGTTACAGGTAGAAA 18
              |||| ||||| |||||
Db         19 ATGTCACAGGCAGAAA 4
```

RESULT 8
US-09-906-158-75/c
; Sequence 75, Application US/09906158
; Publication No. US20030078217A1
; GENERAL INFORMATION:
; APPLICANT: Brett P. Monia
; APPLICANT: Susan M. Freier
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR-BETA 3 EXPRESS
; FILE REFERENCE: RTS-0257
; CURRENT APPLICATION NUMBER: US/09/906,158
; CURRENT FILING DATE: 2001-07-14
; NUMBER OF SEQ ID NOS: 168
; SEQ ID NO 75
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-906-158-75

Query Match 58.2%; Score 12.8; DB 10; Length 20;
Best Local Similarity 87.5%; Pred. No. 2.6e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          7 TACAGGTAGAAAAGCC 22
              |||||| |||||| ||
```

```
Db         18 TACAGGGAGAAAATCC 3


RESULT 9
US-10-388-263-524/c
; Sequence 524, Application US/10388263
; Publication No. US20030228597A1
; GENERAL INFORMATION:
;  APPLICANT: Cowsert, Lex M.
;  APPLICANT:  Baker, Brenda F.
;  APPLICANT:  McNeil, John
;  APPLICANT:  Freier, Susan M.
;  APPLICANT:  Sasmor, Henri M.
;  APPLICANT:  Brooks, Douglas G.
;  APPLICANT:  Ohashi, Cara
;  APPLICANT:  Wyatt, Jacqueline R.
;  APPLICANT:  Borchers, Alexander
;  APPLICANT:  Vickers, Timothy A.
;  TITLE OF INVENTION: IDENTIFICATION OF GENETIC TARGETS FOR
;  TITLE OF INVENTION:  MODULATION BY OLIGONUCLEOTIDES AND
;  TITLE OF INVENTION:  GENERATION OF OLIGONUCLEOTIDES FOR GENE MODULATION
;  FILE REFERENCE: ISIS-4503
;  CURRENT APPLICATION NUMBER: US/10/388,263
;  CURRENT FILING DATE:  2003-03-12
;  NUMBER OF SEQ ID NOS: 947
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 524
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-388-263-524

  Query Match             58.2%;  Score 12.8;  DB 17;  Length 20;
  Best Local Similarity   87.5%;  Pred. No. 2.6e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 TACAGGTAGAAAAGCC 22
              |||||| |||||| ||
Db         18 TACAGGGAGAAAATCC 3


RESULT 10
US-10-388-360-230/c
; Sequence 230, Application US/10388360
; Publication No. US20030225528A1
; GENERAL INFORMATION:
;  APPLICANT: GENOMIC HEALTH
;  APPLICANT:  Baker, Joffre B.
;  APPLICANT:  Cronin, Maureen T.
;  APPLICANT:  Kiefer, Michael C.
;  APPLICANT:  Shak, Steve
;  APPLICANT:  Walker, Michael Graham
;  TITLE OF INVENTION: GENE EXPRESSION PROFILING IN BIOPSIED TUMOR TISSUES
;  FILE REFERENCE: 39740-0001US
;  CURRENT APPLICATION NUMBER: US/10/388,360
;  CURRENT FILING DATE:  2003-03-12
;  PRIOR APPLICATION NUMBER: US 60/412,049
;  PRIOR FILING DATE: 2002-09-18
;  PRIOR APPLICATION NUMBER: US 60/364,890
;  PRIOR FILING DATE: 2002-03-13
;  NUMBER OF SEQ ID NOS: 384
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 230
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-388-360-230

  Query Match             58.2%;  Score 12.8;  DB 17;  Length 21;
  Best Local Similarity   87.5%;  Pred. No. 2.6e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 TACAGGTAGAAAAGCC 22
              | | ||||||||||||
Db         21 TTCTGGTAGAAAAGCC 6


RESULT 11
US-10-758-307-191/c
; Sequence 191, Application US/10758307
; Publication No. US20040209290A1
; GENERAL INFORMATION:
;  APPLICANT: GENOMIC HEALTH, INC.
;  APPLICANT:  RUSH UNIVERSITY MEDICAL CENTER
;  APPLICANT:  Cobleigh, Melody
;  APPLICANT:  Shak, Steven
;  APPLICANT:  Baker, Joffre
;  APPLICANT:  Cronin, Maureen
;  TITLE OF INVENTION: GENE EXPRESSION MARKERS FOR BREAST
;  TITLE OF INVENTION:  CANCER PROGNOSIS
;  FILE REFERENCE: 39740/0008 US
;  CURRENT APPLICATION NUMBER: US/10/758,307
;  CURRENT FILING DATE:  2004-01-14
;  PRIOR APPLICATION NUMBER: US 60/440,861
;  PRIOR FILING DATE: 2003-01-15
;  NUMBER OF SEQ ID NOS: 440
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 191
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: reverse primer
US-10-758-307-191

  Query Match             58.2%;  Score 12.8;  DB 20;  Length 21;
  Best Local Similarity   87.5%;  Pred. No. 2.6e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 TACAGGTAGAAAAGCC 22
              | | ||||||||||||
Db         21 TTCTGGTAGAAAAGCC 6


RESULT 12
US-10-690-880-48/c
; Sequence 48, Application US/10690880
; Publication No. US20050014165A1
; GENERAL INFORMATION:
;  APPLICANT: LEE, NANCY M
;  APPLICANT:  CHEN, LING C
;  TITLE OF INVENTION: BIOMARKER PANEL FOR COLORECTAL CANCER
;  FILE REFERENCE: CPMC-01000US1
;  CURRENT APPLICATION NUMBER: US/10/690,880
;  CURRENT FILING DATE:  2003-10-22
;  NUMBER OF SEQ ID NOS: 88
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 48
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: primer
US-10-690-880-48

  Query Match             58.2%;  Score 12.8;  DB 21;  Length 21;
  Best Local Similarity   87.5%;  Pred. No. 2.6e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 TACAGGTAGAAAAGCC 22
              | | ||||||||||||
Db         21 TTCTGGTAGAAAAGCC 6
```

```
RESULT 13
US-10-714-195-188/c
; Sequence 188, Application US/10714195
; Publication No. US20050019785A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Joffre
;  APPLICANT:  Cronin, Maureen
;  APPLICANT:  Shak, Steve
;  APPLICANT:  Baselga, Jose
;  TITLE OF INVENTION: GENE EXPRESSION PROFILING OF EGFR
;  TITLE OF INVENTION:  POSITIVE CANCER
;  FILE REFERENCE: 39740-0005
;  CURRENT APPLICATION NUMBER: US/10/714,195
;  CURRENT FILING DATE:  2003-11-14
;  PRIOR APPLICATION NUMBER: 60/427090
;  PRIOR FILING DATE: 2003-11-15
;  NUMBER OF SEQ ID NOS: 372
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 188
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: primer
US-10-714-195-188

  Query Match             58.2%;  Score 12.8;  DB 21;  Length 21;
  Best Local Similarity   87.5%;  Pred. No. 2.6e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 TACAGGTAGAAAAGCC 22
              | | ||||||||||||
Db         21 TTCTGGTAGAAAAGCC 6


RESULT 14
US-10-852-797-80/c
; Sequence 80, Application US/10852797
; Publication No. US20050064455A1
; GENERAL INFORMATION:
;  APPLICANT: Genomic Health, Inc.
;  APPLICANT:  Baker, Joffre
;  APPLICANT:  Miller, Kathy D.
;  APPLICANT:  Shak, Steven
;  APPLICANT:  Sledge, George
;  APPLICANT:  Soule, Sharon
;  TITLE OF INVENTION: Gene Expression Markers for Predicting
;  TITLE OF INVENTION:  Response to Chemotherapy
;  FILE REFERENCE: 39740-0010
;  CURRENT APPLICATION NUMBER: US/10/852,797
;  CURRENT FILING DATE:  2004-05-24
;  PRIOR APPLICATION NUMBER: 60/473,970
;  PRIOR FILING DATE: 2003-05-28
;  NUMBER OF SEQ ID NOS: 372
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 80
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: reverse primer
US-10-852-797-80

  Query Match             58.2%;  Score 12.8;  DB 21;  Length 21;
  Best Local Similarity   87.5%;  Pred. No. 2.6e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 TACAGGTAGAAAAGCC 22
              | | ||||||||||||
Db         21 TTCTGGTAGAAAAGCC 6


RESULT 15
US-10-831-901A-12579/c
; Sequence 12579, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
;  APPLICANT: Crooke, Stanley T.
;  APPLICANT:  Ecker, David J.
;  APPLICANT:  Sampath, Rangarajan
;  APPLICANT:  Freier, Susan M.
;  APPLICANT:  Massire, Christian
;  APPLICANT:  Hofstadler, Steven A.
;  APPLICANT:  Lowery, Kristin Sannes
;  APPLICANT:  Swayze, Eric
;  APPLICANT:  Baker, Brenda F.
;  APPLICANT:  Bennett, C. Frank
;  TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
;  TITLE OF INVENTION:  Acute Respiratory Syndrome (SARS)
;  FILE REFERENCE: ISIS0083-100 (BIOL0008US)
;  CURRENT APPLICATION NUMBER: US/10/831,901A
;  CURRENT FILING DATE:  2004-04-26
;  PRIOR APPLICATION NUMBER: 60/466,426
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: 60/468,562
;  PRIOR FILING DATE: 2003-05-06
;  PRIOR APPLICATION NUMBER: 60/467,770
;  PRIOR FILING DATE: 2003-04-30
;  PRIOR APPLICATION NUMBER: 60/468,627
;  PRIOR FILING DATE: 2003-05-06
;  PRIOR APPLICATION NUMBER: 60/477,637
;  PRIOR FILING DATE: 2003-06-10
;  PRIOR APPLICATION NUMBER: 60/483,579
;  PRIOR FILING DATE: 2003-06-27
;  NUMBER OF SEQ ID NOS: 30063
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12579
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense compound
US-10-831-901A-12579

  Query Match             57.3%;  Score 12.6;  DB 21;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.2e+04;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 TGTTACAGGTAGAAAAGCC 22
              |||||||| |   || ||||
Db         19 TGTTACAGCTCTAAGAGCC 1


RESULT 16
US-10-831-901A-12580/c
; Sequence 12580, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
;  APPLICANT: Crooke, Stanley T.
;  APPLICANT:  Ecker, David J.
;  APPLICANT:  Sampath, Rangarajan
;  APPLICANT:  Freier, Susan M.
;  APPLICANT:  Massire, Christian
;  APPLICANT:  Hofstadler, Steven A.
;  APPLICANT:  Lowery, Kristin Sannes
;  APPLICANT:  Swayze, Eric
;  APPLICANT:  Baker, Brenda F.
;  APPLICANT:  Bennett, C. Frank
;  TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
;  TITLE OF INVENTION:  Acute Respiratory Syndrome (SARS)
;  FILE REFERENCE: ISIS0083-100 (BIOL0008US)
;  CURRENT APPLICATION NUMBER: US/10/831,901A
;  CURRENT FILING DATE:  2004-04-26
;  PRIOR APPLICATION NUMBER: 60/466,426
;  PRIOR FILING DATE: 2003-04-28
```

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;  PRIOR APPLICATION NUMBER: 60/468,562
;  PRIOR FILING DATE: 2003-05-06
;  PRIOR APPLICATION NUMBER: 60/467,770
;  PRIOR FILING DATE: 2003-04-30
;  PRIOR APPLICATION NUMBER: 60/468,627
;  PRIOR FILING DATE: 2003-05-06
;  PRIOR APPLICATION NUMBER: 60/477,637
;  PRIOR FILING DATE: 2003-06-10
;  PRIOR APPLICATION NUMBER: 60/483,579
;  PRIOR FILING DATE: 2003-06-27
;  NUMBER OF SEQ ID NOS: 30063
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 12580
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense compound
US-10-831-901A-12580

  Query Match             57.3%;  Score 12.6;  DB 21;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 3.2e+04;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 TGTTACAGGTAGAAAAGCC 22
              |||||||| |  || ||||
Db         20 TGTTACAGCTCTAAGAGCC 2


RESULT 17
US-10-883-218-177/c
; Sequence 177, Application US/10883218
; Publication No. US20050124567A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  Haeberli, Peter
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of TRPM7 Gene Expression
;  TITLE OF INVENTION:  Using Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/195 (MBHB04-535)
;  CURRENT APPLICATION NUMBER: US/10/883,218
;  CURRENT FILING DATE:  2004-07-01
;  PRIOR APPLICATION NUMBER: PCT/US04/16390
;  PRIOR FILING DATE: 2003-05-24
;  PRIOR APPLICATION NUMBER: US 10/826,966
;  PRIOR FILING DATE: 2004-04-16
;  PRIOR APPLICATION NUMBER: US 10/757,803
;  PRIOR FILING DATE: 2004-01-14
;  PRIOR APPLICATION NUMBER: US 10/720,448
;  PRIOR FILING DATE: 2003-11-24
;  PRIOR APPLICATION NUMBER: US 10/693,059
;  PRIOR FILING DATE: 2003-10-23
;  PRIOR APPLICATION NUMBER: US 10/444,853
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: US 10/427,160
;  PRIOR FILING DATE: 2003-04-30
;  PRIOR APPLICATION NUMBER: PCT/US03/05346
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: PCT/US03/05028
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 930
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 177
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target Sequence/siNA sense r
US-10-883-218-177

  Query Match             56.4%;  Score 12.4;  DB 22;  Length 19;
  Best Local Similarity   92.9%;  Pred. No. 4e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 TTACAGGTAGAAAA 19
              |||||| |||||||
Db         15 TTACAGCTAGAAAA 2


RESULT 18
US-10-883-218-579
; Sequence 579, Application US/10883218
; Publication No. US20050124567A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  Haeberli, Peter
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of TRPM7 Gene Expression
;  TITLE OF INVENTION:  Using Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/195 (MBHB04-535)
;  CURRENT APPLICATION NUMBER: US/10/883,218
;  CURRENT FILING DATE:  2004-07-01
;  PRIOR APPLICATION NUMBER: PCT/US04/16390
;  PRIOR FILING DATE: 2003-05-24
;  PRIOR APPLICATION NUMBER: US 10/826,966
;  PRIOR FILING DATE: 2004-04-16
;  PRIOR APPLICATION NUMBER: US 10/757,803
;  PRIOR FILING DATE: 2004-01-14
;  PRIOR APPLICATION NUMBER: US 10/720,448
;  PRIOR FILING DATE: 2003-11-24
;  PRIOR APPLICATION NUMBER: US 10/693,059
;  PRIOR FILING DATE: 2003-10-23
;  PRIOR APPLICATION NUMBER: US 10/444,853
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: US 10/427,160
;  PRIOR FILING DATE: 2003-04-30
;  PRIOR APPLICATION NUMBER: PCT/US03/05346
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: PCT/US03/05028
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US 60/358,580
;  PRIOR FILING DATE: 2002-02-20
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 930
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 579
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  siNA antisense region
US-10-883-218-579

  Query Match             56.4%;  Score 12.4;  DB 22;  Length 19;
  Best Local Similarity   71.4%;  Pred. No. 4e+04;
  Matches   10;  Conservative    3;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 TTACAGGTAGAAAA 19
              ::|||| :||||||
Db          5 UUACAGCUAGAAAA 18


RESULT 19
US-10-219-834-44
; Sequence 44, Application US/10219834
; Publication No. US20030096751A1
; GENERAL INFORMATION:
;  APPLICANT: Bristol-Myers Squibb Company
;  TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR POLYNUCLEOTIDES AND METHODS OF USE THE
;  FILE REFERENCE: D0191 NP
;  CURRENT APPLICATION NUMBER: US/10/219,834
;  CURRENT FILING DATE:  2002-08-15
;  PRIOR APPLICATION NUMBER: US 60/313,658
```

; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: US 60/340,703
; PRIOR FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: US 60/318,675
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US 60/355,596
; PRIOR FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: US 60/333,417
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 60/338,367
; PRIOR FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 192
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-219-834-44

Query Match 56.4%; Score 12.4; DB 14; Length 20;
Best Local Similarity 92.9%; Pred. No. 4.1e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CAGGTAGAAAAGCC 22
|||| |||||||||
Db 2 CAGGAAGAAAAGCC 15

RESULT 20
US-10-436-715-92
; Sequence 92, Application US/10436715
; Publication No. US20040018976A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING NOVEL HUMAN G-PROTEIN COUPLED RECEPTORS,
; TITLE OF INVENTION: AND SPLICE VARIANTS THEREOF
; FILE REFERENCE: D0262 NP
; CURRENT APPLICATION NUMBER: US/10/436,715
; CURRENT FILING DATE: 2003-05-13
; PRIOR APPLICATION NUMBER: U.S. 60/380,336
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 471
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 92
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-436-715-92

Query Match 56.4%; Score 12.4; DB 17; Length 20;
Best Local Similarity 92.9%; Pred. No. 4.1e+04;
Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 9 CAGGTAGAAAAGCC 22
|||| |||||||||
Db 2 CAGGAAGAAAAGCC 15

RESULT 21
US-10-349-143-4779
; Sequence 4779, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Daniel
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Chumakov, Ilya
; TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
; FILE REFERENCE: GENSET.020CP1
; CURRENT APPLICATION NUMBER: US/10/349,143
; CURRENT FILING DATE: 2003-01-21
; PRIOR APPLICATION NUMBER: US/09/422,978
; PRIOR FILING DATE: 1999-10-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
; NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4779
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: primer_bind
; LOCATION: 1..18
; OTHER INFORMATION: upstream amplification primer 99-17762 for SEQ 845,
US-10-349-143-4779

Query Match 55.5%; Score 12.2; DB 17; Length 18;
Best Local Similarity 82.4%; Pred. No. 5e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 TGTTACAGGTAGAAAAG 20
||| | ||||||| |||
Db 1 TGTGAGAGGTAGAGAAG 17

RESULT 22
US-10-922-626-197/c
; Sequence 197, Application US/10922626
; Publication No. US20050159380A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Theraputics
; APPLICANT: Guerciolini, Roberto
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Angiopoietin Gene
; TITLE OF INVENTION: Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/226 (MBHB04-673)
; CURRENT APPLICATION NUMBER: US/10/922,626
; CURRENT FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: PCT/US04/13456
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US 10/780,447
; PRIOR FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: US 60/292,217
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/362,016
; PRIOR FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US 60/363,883
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/311,865
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: US 10/727,780
; PRIOR FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: US 60/543,480
; PRIOR FILING DATE: 2004-02-10
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 686
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 197
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Target Sequence/siNA sense r
US-10-922-626-197

Query Match 55.5%; Score 12.2; DB 22; Length 19;
Best Local Similarity 82.4%; Pred. No. 5.1e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          6 TTACAGGTAGAAAAGCC 22
              ||||||| ||| ||| |
Db         19 TTACAGGCAGAGAAGAC 3
```

RESULT 23
US-10-922-626-438
; Sequence 438, Application US/10922626
; Publication No. US20050159380A1
; GENERAL INFORMATION:
; APPLICANT: Sirna Theraputics
; APPLICANT: Guerciolini, Roberto
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: RNA Interference Mediated Inhibition of Angiopoietin Gene
; TITLE OF INVENTION: Expression Using Short Interfering Nucleic Acid (siNA)
; FILE REFERENCE: 400/226 (MBHB04-673)
; CURRENT APPLICATION NUMBER: US/10/922,626
; CURRENT FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: PCT/US04/16390
; PRIOR FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 10/826,966
; PRIOR FILING DATE: 2004-04-16
; PRIOR APPLICATION NUMBER: PCT/US04/13456
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: US 10/780,447
; PRIOR FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: US 60/292,217
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/362,016
; PRIOR FILING DATE: 2002-03-06
; PRIOR APPLICATION NUMBER: US 60/363,883
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: US 60/311,865
; PRIOR FILING DATE: 2001-08-13
; PRIOR APPLICATION NUMBER: US 10/727,780
; PRIOR FILING DATE: 2003-12-03
; PRIOR APPLICATION NUMBER: US 60/543,480
; PRIOR FILING DATE: 2004-02-10
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 686
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 438
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: siNA antisense region
US-10-922-626-438

Query Match 55.5%; Score 12.2; DB 22; Length 19;
Best Local Similarity 70.6%; Pred. No. 5.1e+04;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```
Qy          6 TTACAGGTAGAAAAGCC 22
              ::||||| ||| ||| |
Db          1 UUACAGGCAGAGAAGAC 17
```

RESULT 24
US-09-791-942-44/c
; Sequence 44, Application US/09791942
; Patent No. US20020147166A1
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Robert Rothlein
; APPLICANT: Takashi Kei Kishimoto
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF TALIN EXPRESSION
; FILE REFERENCE: RTS-0099
; CURRENT APPLICATION NUMBER: US/09/791,942
; CURRENT FILING DATE: 2001-02-22
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 44
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-791-942-44

Query Match 55.5%; Score 12.2; DB 9; Length 20;
Best Local Similarity 82.4%; Pred. No. 5.1e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          4 TGTTACAGGTAGAAAAG 20
              |||| |||| || ||||
Db         19 TGTTGCAGGCAGCAAAG 3
```

RESULT 25
US-09-888-361-50
; Sequence 50, Application US/09888361
; Publication No. US20030064944A1
; GENERAL INFORMATION:
; APPLICANT: Susan Murray
; APPLICANT: Jacqueline Wyatt
; TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA RECEPTOR
; TITLE OF INVENTION: EXPRESSION
; FILE REFERENCE: RTS-0158
; CURRENT APPLICATION NUMBER: US/09/888,361
; CURRENT FILING DATE: 2001-06-21
; NUMBER OF SEQ ID NOS: 163
; SEQ ID NO 50
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-888-361-50

Query Match 55.5%; Score 12.2; DB 10; Length 20;
Best Local Similarity 82.4%; Pred. No. 5.1e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          5 GTTACAGGTAGAAAAGC 21
              || |||||| ||||| |
Db          1 GTCACAGGTGGAAAATC 17
```

RESULT 26
US-10-415-463-44/c
; Sequence 44, Application US/10415463
; Publication No. US20040110705A1
; GENERAL INFORMATION:
; APPLICANT: Isis Pharmaceuticals, Inc.
; APPLICANT: C. Frank Bennett
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF TALIN EXPRESSION
; FILE REFERENCE: RTSP-0198
; CURRENT APPLICATION NUMBER: US/10/415,463
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: 09/702,251
; PRIOR FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 44
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-415-463-44

Query Match 55.5%; Score 12.2; DB 19; Length 20;
Best Local Similarity 82.4%; Pred. No. 5.1e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          4 TGTTACAGGTAGAAAAG 20
              |||| |||| || ||||
Db         19 TGTTGCAGGCAGCAAAG 3


RESULT 27
US-10-889-101-72
; Sequence 72, Application US/10889101
; Publication No. US20050107324A1
; GENERAL INFORMATION:
;  APPLICANT: Bennett, C. Frank
;  APPLICANT:  Dobie, Kenneth W.
;  APPLICANT:  Jain, Ravi
;  TITLE OF INVENTION: MODULATION OF CEACAM1 EXPRESSION
;  FILE REFERENCE: ISIS0101-100 (RTS-0655US)
;  CURRENT APPLICATION NUMBER: US/10/889,101
;  CURRENT FILING DATE:  2004-07-12
;  PRIOR APPLICATION NUMBER: 60/486,652
;  PRIOR FILING DATE: 2003-07-12
;  NUMBER OF SEQ ID NOS: 298
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 72
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Compound
US-10-889-101-72

  Query Match             55.5%;  Score 12.2;  DB 21;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 5.1e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 ATGTTACAGGTAGAAAA 19
              ||  |||||||||| ||
Db          3 ATCCTACAGGTAGACAA 19


RESULT 28
US-10-889-101-218/c
; Sequence 218, Application US/10889101
; Publication No. US20050107324A1
; GENERAL INFORMATION:
;  APPLICANT: Bennett, C. Frank
;  APPLICANT:  Dobie, Kenneth W.
;  APPLICANT:  Jain, Ravi
;  TITLE OF INVENTION: MODULATION OF CEACAM1 EXPRESSION
;  FILE REFERENCE: ISIS0101-100 (RTS-0655US)
;  CURRENT APPLICATION NUMBER: US/10/889,101
;  CURRENT FILING DATE:  2004-07-12
;  PRIOR APPLICATION NUMBER: 60/486,652
;  PRIOR FILING DATE: 2003-07-12
;  NUMBER OF SEQ ID NOS: 298
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 218
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
US-10-889-101-218

  Query Match             55.5%;  Score 12.2;  DB 21;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 5.1e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 ATGTTACAGGTAGAAAA 19
              ||  |||||||||| ||
Db         18 ATCCTACAGGTAGACAA 2


RESULT 29
US-10-705-715-50
; Sequence 50, Application US/10705715
; Publication No. US20040147472A1
; GENERAL INFORMATION:
;  APPLICANT: Susan Murray
;  APPLICANT:  Jacqueline Wyatt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TRANSFORMING GROWTH FACTOR BETA RECEPTOR
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: RTS-0158
;  CURRENT APPLICATION NUMBER: US/10/705,715
;  CURRENT FILING DATE:  2003-11-10
;  PRIOR APPLICATION NUMBER: US/09/888,361
;  PRIOR FILING DATE: 2001-06-21
;  NUMBER OF SEQ ID NOS: 163
; SEQ ID NO 50
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-705-715-50

  Query Match             55.5%;  Score 12.2;  DB 22;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 5.1e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 GTTACAGGTAGAAAAGC 21
              || |||||| ||||| |
Db          1 GTCACAGGTGGAAAATC 17


RESULT 30
US-10-333-429-274/c
; Sequence 274, Application US/10333429
; Publication No. US20040048265A1
; GENERAL INFORMATION:
;  APPLICANT: GENSET
;  TITLE OF INVENTION: Obesity Associated Biallelic Marker Maps
;  FILE REFERENCE: G-083US02PCT
;  CURRENT APPLICATION NUMBER: US/10/333,429
;  CURRENT FILING DATE:  2003-01-17
;  PRIOR APPLICATION NUMBER: PCT/IB01/01477
;  PRIOR FILING DATE: 2001-06-28
;  PRIOR APPLICATION NUMBER: US 60/219,704
;  PRIOR FILING DATE: 2000-07-18
;  NUMBER OF SEQ ID NOS: 579
;  SOFTWARE: Patent.pm
; SEQ ID NO 274
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..21
;   OTHER INFORMATION: upstream amplification primer 99-44259 for SEQ 103,
US-10-333-429-274

  Query Match             55.5%;  Score 12.2;  DB 18;  Length 21;
  Best Local Similarity   82.4%;  Pred. No. 5.1e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 GTTACAGGTAGAAAAGC 21
              ||| ||| || ||||||
Db         19 GTTTCAGATAAAAAAGC 3


RESULT 31
US-10-751-736-831/c
; Sequence 831, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Martinez, Robert
;  APPLICANT:  Brown, Eugene
;  APPLICANT:  Liu, Wei
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
```

```
;  TITLE OF INVENTION:  CANCERS
;  FILE REFERENCE: AM100927 (031896-002000)
;  CURRENT APPLICATION NUMBER: US/10/751,736
;  CURRENT FILING DATE:  2003-01-06
;  PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
;  PRIOR FILING DATE: 2003-01-06
;  NUMBER OF SEQ ID NOS: 54873
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 831
;   LENGTH: 21
;   TYPE: RNA
;   ORGANISM: RNAi
US-10-751-736-831

  Query Match             55.5%;  Score 12.2;  DB 20;  Length 21;
  Best Local Similarity   82.4%;  Pred. No. 5.1e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 ATGTTACAGGTAGAAAA 19
              ||| | |||||| ||||
Db         17 ATGGTGCAGGTATAAAA 1


RESULT 32
US-10-751-736-1680/c
; Sequence 1680, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Martinez, Robert
;  APPLICANT:  Brown, Eugene
;  APPLICANT:  Liu, Wei
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
;  TITLE OF INVENTION:  CANCERS
;  FILE REFERENCE: AM100927 (031896-002000)
;  CURRENT APPLICATION NUMBER: US/10/751,736
;  CURRENT FILING DATE:  2003-01-06
;  PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
;  PRIOR FILING DATE: 2003-01-06
;  NUMBER OF SEQ ID NOS: 54873
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1680
;   LENGTH: 21
;   TYPE: RNA
;   ORGANISM: RNAi
US-10-751-736-1680

  Query Match             55.5%;  Score 12.2;  DB 20;  Length 21;
  Best Local Similarity   82.4%;  Pred. No. 5.1e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 ATGTTACAGGTAGAAAA 19
              ||| | |||||| ||||
Db         17 ATGGTGCAGGTATAAAA 1


RESULT 33
US-10-751-736-10500
; Sequence 10500, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Martinez, Robert
;  APPLICANT:  Brown, Eugene
;  APPLICANT:  Liu, Wei
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
;  TITLE OF INVENTION:  CANCERS
;  FILE REFERENCE: AM100927 (031896-002000)
;  CURRENT APPLICATION NUMBER: US/10/751,736
;  CURRENT FILING DATE:  2003-01-06
;  PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
;  PRIOR FILING DATE: 2003-01-06
;  NUMBER OF SEQ ID NOS: 54873
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10500
;   LENGTH: 21
;   TYPE: RNA
;   ORGANISM: RNAi
US-10-751-736-10500

  Query Match             55.5%;  Score 12.2;  DB 20;  Length 21;
  Best Local Similarity   64.7%;  Pred. No. 5.1e+04;
  Matches   11;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          6 TTACAGGTAGAAAAGCC 22
              ::|| ||:|||||  ||
Db          1 UUACCGGUAGAAACACC 17


RESULT 34
US-10-751-736-15982
; Sequence 15982, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Martinez, Robert
;  APPLICANT:  Brown, Eugene
;  APPLICANT:  Liu, Wei
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
;  TITLE OF INVENTION:  CANCERS
;  FILE REFERENCE: AM100927 (031896-002000)
;  CURRENT APPLICATION NUMBER: US/10/751,736
;  CURRENT FILING DATE:  2003-01-06
;  PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
;  PRIOR FILING DATE: 2003-01-06
;  NUMBER OF SEQ ID NOS: 54873
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15982
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-751-736-15982

  Query Match             55.5%;  Score 12.2;  DB 20;  Length 21;
  Best Local Similarity   82.4%;  Pred. No. 5.1e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCATGTTACAGGTAGAA 17
              |||||| || || ||||
Db          3 GCATGTCACTGGAAGAA 19


RESULT 35
US-10-751-736-15983
; Sequence 15983, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Martinez, Robert
;  APPLICANT:  Brown, Eugene
;  APPLICANT:  Liu, Wei
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
;  TITLE OF INVENTION:  CANCERS
;  FILE REFERENCE: AM100927 (031896-002000)
;  CURRENT APPLICATION NUMBER: US/10/751,736
;  CURRENT FILING DATE:  2003-01-06
;  PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
;  PRIOR FILING DATE: 2003-01-06
;  NUMBER OF SEQ ID NOS: 54873
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 15983
;   LENGTH: 21
;   TYPE: RNA
;   ORGANISM: RNAi
US-10-751-736-15983
```

```
  Query Match             55.5%;  Score 12.2;  DB 20;  Length 21;
  Best Local Similarity   70.6%;  Pred. No. 5.1e+04;
  Matches   12;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCATGTTACAGGTAGAA 17
              |||:|: || || ||||
Db          1 GCAUGUCACUGGAAGAA 17


RESULT 36
US-10-751-736-40680/c
; Sequence 40680, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Martinez, Robert
;  APPLICANT:  Brown, Eugene
;  APPLICANT:  Liu, Wei
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
;  TITLE OF INVENTION:  CANCERS
;  FILE REFERENCE: AM100927 (031896-002000)
;  CURRENT APPLICATION NUMBER: US/10/751,736
;  CURRENT FILING DATE:  2003-01-06
;  PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
;  PRIOR FILING DATE: 2003-01-06
;  NUMBER OF SEQ ID NOS: 54873
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 40680
;   LENGTH: 21
;   TYPE: RNA
;   ORGANISM: RNAi
US-10-751-736-40680

  Query Match             55.5%;  Score 12.2;  DB 20;  Length 21;
  Best Local Similarity   82.4%;  Pred. No. 5.1e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GCATGTTACAGGTAGAA 17
              || |||  |||||||||
Db         17 GCGTGTGGCAGGTAGAA 1


RESULT 37
US-10-349-143-9693/c
; Sequence 9693, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/10/349,143
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: US/09/422,978
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 9693
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..20
;   OTHER INFORMATION: downstream amplification primer 99-669 for SEQ 1828, in complemen
US-10-349-143-9693

  Query Match             54.5%;  Score 12;  DB 17;  Length 20;
  Best Local Similarity   75.0%;  Pred. No. 6.4e+04;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GCATGTTACAGGTAGAAAAG 20
              | ||||   ||||| |||||
Db         20 GTATGTCTGAGGTATAAAAG 1


RESULT 38
US-09-969-373-4522
; Sequence 4522, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
;  APPLICANT: Effertz, Roger J.
;  APPLICANT:  Hauge, Brian M.
;  TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
;  FILE REFERENCE: 38-10(52679)A
;  CURRENT APPLICATION NUMBER: US/09/969,373
;  CURRENT FILING DATE:  2001-10-02
;  PRIOR APPLICATION NUMBER: US 09/754,853
;  PRIOR FILING DATE: 2001-01-05
;  PRIOR APPLICATION NUMBER: US 09/760,427
;  PRIOR FILING DATE: 2001-01-13
;  PRIOR APPLICATION NUMBER: US 09/855,768
;  PRIOR FILING DATE: 2001-05-15
;  NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 4522
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Glycine max
US-09-969-373-4522

  Query Match             53.6%;  Score 11.8;  DB 9;  Length 19;
  Best Local Similarity   86.7%;  Pred. No. 7.9e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 TGTTACAGGTAGAAA 18
              |||| |||||| |||
Db          3 TGTTGCAGGTACAAA 17


RESULT 39
US-09-969-373-4524
; Sequence 4524, Application US/09969373
; Patent No. US20020133852A1
; GENERAL INFORMATION:
;  APPLICANT: Effertz, Roger J.
;  APPLICANT:  Hauge, Brian M.
;  TITLE OF INVENTION: Soybean SSRs and Methods of Genotyping
;  FILE REFERENCE: 38-10(52679)A
;  CURRENT APPLICATION NUMBER: US/09/969,373
;  CURRENT FILING DATE:  2001-10-02
;  PRIOR APPLICATION NUMBER: US 09/754,853
;  PRIOR FILING DATE: 2001-01-05
;  PRIOR APPLICATION NUMBER: US 09/760,427
;  PRIOR FILING DATE: 2001-01-13
;  PRIOR APPLICATION NUMBER: US 09/855,768
;  PRIOR FILING DATE: 2001-05-15
;  NUMBER OF SEQ ID NOS: 4593
; SEQ ID NO 4524
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Glycine max
US-09-969-373-4524

  Query Match             53.6%;  Score 11.8;  DB 9;  Length 19;
  Best Local Similarity   86.7%;  Pred. No. 7.9e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 TGTTACAGGTAGAAA 18
              |||| |||||| |||
Db          3 TGTTGCAGGTACAAA 17
```

```
RESULT 40
US-10-349-143-6072
; Sequence 6072, Application US/10349143
; Publication No. US20040005584A1
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT:  Blumenfeld, Marta
;  APPLICANT:  Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/10/349,143
;  CURRENT FILING DATE:  2003-01-21
;  PRIOR APPLICATION NUMBER: US/09/422,978
;  PRIOR FILING DATE: 1999-10-20
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/298,850
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-21
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/109,732
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-23
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/082,614
;  PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6072
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..19
;   OTHER INFORMATION: upstream amplification primer 99-8748 for SEQ 2138,
US-10-349-143-6072

  Query Match             53.6%;  Score 11.8;  DB 17;  Length 19;
  Best Local Similarity   86.7%;  Pred. No. 7.9e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 GTTACAGGTAGAAAA 19
              |||| |||| |||||
Db          1 GTTAGAGGTTGAAAA 15


Search completed: August 12, 2005, 10:02:51
Job time : 373 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 12, 2005, 05:54:16 ; Search time 1779 Seconds
(without alignments)
470.722 Million cell updates/sec

Title: US-09-743-825-7
Perfect score: 22
Sequence: 1 gcatgttacaggtagaaaagcc 22

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 18786

Minimum DB seq length: 0
Maximum DB seq length: 22

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	13.8	62.7	22	8	AZ659094	AZ659094 1M0536E16
c	2	11.2	50.9	20	9	TA359F10Q	AL495341 T. brucei
c	3	11	50.0	20	8	AZ452265	AZ452265 1M0252H06
	4	10.8	49.1	20	9	CL681335	CL681335 PRI0130d_
	5	10.8	49.1	22	8	AZ651001	AZ651001 1M0521O23
	6	10.6	48.2	20	8	AZ775974	AZ775974 2M0009H14
	7	10.6	48.2	21	9	CL436392	CL436392 PST2884-N
c	8	10.4	47.3	22	8	AZ990555	AZ990555 2M0274N14
c	9	10.2	46.4	21	8	AZ649514	AZ649514 1M0519A09
	10	10	45.5	19	1	AI545076	AI545076 fb70d07.y
c	11	10	45.5	19	8	AZ775273	AZ775273 2M0007F04
c	12	10	45.5	20	1	AU008116	AU008116 AU008116
	13	10	45.5	20	8	AZ585902	AZ585902 1M0391M24
	14	10	45.5	21	8	AZ828233	AZ828233 2M0105B09
c	15	10	45.5	21	8	AZ828233	AZ828233 2M0105B09
	16	9.8	44.5	13	9	CL437394	CL437394 PST5288-N
c	17	9.8	44.5	19	7	CF316655	CF316655 HD--06-A1
c	18	9.8	44.5	19	8	AZ377971	AZ377971 1M0132I03
	19	9.8	44.5	19	8	AZ808350	AZ808350 2M0071P14
c	20	9.8	44.5	20	8	AZ625409	AZ625409 1M0464C20
c	21	9.8	44.5	20	8	AZ799032	AZ799032 2M0056K07
c	22	9.8	44.5	20	9	AJ596498	AJ596498 Arabidops
	23	9.8	44.5	21	8	AZ430939	AZ430939 1M0215E12
	24	9.8	44.5	21	8	AZ483078	AZ483078 1M0308H04
	25	9.8	44.5	22	8	AZ786362	AZ786362 2M0031N16
	26	9.6	43.6	19	9	CL668834	CL668834 PRI0158d_
	27	9.6	43.6	20	8	AZ396022	AZ396022 1M0160J20
	28	9.6	43.6	20	8	AZ787298	AZ787298 2M0033O16
c	29	9.6	43.6	20	9	CL687844	CL687844 PRI0147d_
c	30	9.6	43.6	21	9	AG197947	AG197947 Pan trogl
c	31	9.4	42.7	19	8	AZ312945	AZ312945 1M0029P03
	32	9.4	42.7	19	8	AZ774536	AZ774536 2M0004P01
	33	9.4	42.7	20	1	AJ796099	AJ796099 AJ796099
c	34	9.4	42.7	21	8	AZ428984	AZ428984 1M0212P03
c	35	9.4	42.7	22	8	AZ942905	AZ942905 2M0203K13
c	36	9.4	42.7	22	9	TA82F07Q	AL459970 T. brucei
c	37	9.2	41.8	19	7	CO780477	CO780477 BL009D_A0
c	38	9.2	41.8	19	8	AZ612157	AZ612157 1M0438L21
	39	9.2	41.8	19	8	AZ817291	AZ817291 2M0086P05
c	40	9.2	41.8	21	1	AU008312	AU008312 AU008312
	41	9.2	41.8	21	8	AZ348213	AZ348213 1M0084N15
c	42	9.2	41.8	21	8	AZ760232	AZ760232 1M0553N15
c	43	9.2	41.8	22	8	AZ357874	AZ357874 1M0099D13
	44	9.2	41.8	22	8	AZ807992	AZ807992 2M0071C14
	45	9.2	41.8	22	9	AJ590809	AJ590809 Arabidops
c	46	9.2	41.8	22	9	TA246F04Q	AL488803 T. brucei
c	47	9.2	41.8	22	9	CL670376	CL670376 PRI0161d_
c	48	9	40.9	19	7	CF295672	CF295672 30DGS--05
	49	9	40.9	19	7	CF337272	CF337272 JMT--07-K
c	50	9	40.9	19	8	AZ865832	AZ865832 2M0176D09
	51	9	40.9	20	1	AU256704	AU256704 AU256704
	52	9	40.9	20	7	D18242	D18242 MUSGS00522
	53	9	40.9	20	8	AZ328275	AZ328275 1M0052A01
c	54	9	40.9	20	8	AZ489135	AZ489135 1M0319H15
	55	9	40.9	20	8	AZ499543	AZ499543 1M0337F19
	56	9	40.9	20	8	AZ782333	AZ782333 2M0022I01
c	57	9	40.9	22	8	AZ345854	AZ345854 1M0080F16
c	58	8.8	40.0	16	2	AW250981	AW250981 2822267.3
c	59	8.8	40.0	19	5	BQ789814	BQ789814 hage002aF
c	60	8.8	40.0	19	8	AZ328922	AZ328922 1M0052L22
c	61	8.8	40.0	19	8	AZ357958	AZ357958 1M0099D23
	62	8.8	40.0	19	8	AZ585367	AZ585367 1M0390D06
c	63	8.8	40.0	20	8	AZ368917	AZ368917 1M0119A16
c	64	8.8	40.0	20	8	AZ462631	AZ462631 1M0269F12
c	65	8.8	40.0	20	8	AZ490568	AZ490568 1M0323B07
c	66	8.8	40.0	21	5	BX553324	BX553324 BX553324
c	67	8.8	40.0	21	8	AZ439800	AZ439800 1M0230A09
c	68	8.8	40.0	21	8	AZ598000	AZ598000 1M0412F01
c	69	8.8	40.0	21	8	AZ765823	AZ765823 1M0563A05
	70	8.8	40.0	21	8	AZ776420	AZ776420 2M0010G02
c	71	8.8	40.0	22	6	CD529328	CD529328 02I12 Ara
c	72	8.8	40.0	22	8	AZ345846	AZ345846 1M0080B18
c	73	8.8	40.0	22	8	AZ392578	AZ392578 1M0155F13
	74	8.8	40.0	22	8	AZ501345	AZ501345 1M0340I11
	75	8.8	40.0	22	8	AZ610074	AZ610074 1M0435J11
	76	8.8	40.0	22	8	AZ819251	AZ819251 2M0089G18
	77	8.8	40.0	22	8	AZ990555	AZ990555 2M0274N14
c	78	8.6	39.1	17	6	C21103	C21103 HUMGS000262
c	79	8.6	39.1	19	8	AZ581163	AZ581163 1M0369M20
	80	8.6	39.1	19	8	AZ623493	AZ623493 1M0461M13
c	81	8.6	39.1	20	8	AZ308068	AZ308068 1M0010N08
	82	8.6	39.1	20	8	AZ407675	AZ407675 1M0178E04
	83	8.6	39.1	20	8	AZ772089	AZ772089 1M0574P11
	84	8.6	39.1	21	1	AU257209	AU257209 AU257209
c	85	8.6	39.1	21	8	AZ402083	AZ402083 1M0169A15
	86	8.6	39.1	21	8	AZ514444	AZ514444 1M0361L17
c	87	8.6	39.1	22	1	AI219622	AI219622 qg10d07.x
c	88	8.6	39.1	22	7	CF314827	CF314827 HD--03-I0
	89	8.6	39.1	22	8	AZ483608	AZ483608 1M0309N19
c	90	8.6	39.1	22	8	AZ824702	AZ824702 2M0099P20
	91	8.6	39.1	22	8	AZ979907	AZ979907 2M0256E17
	92	8.4	38.2	15	9	AJ589581	AJ589581 Arabidops
c	93	8.4	38.2	15	9	AJ591909	AJ591909 Arabidops
	94	8.4	38.2	16	9	CL683179	CL683179 PRI0136a_
c	95	8.4	38.2	19	8	AZ397615	AZ397615 1M0162M07
c	96	8.4	38.2	19	8	AZ597767	AZ597767 1M0411C22
	97	8.4	38.2	19	8	AZ782384	AZ782384 2M0022I09

c 98	8.4	38.2	19	8	AZ788165	AZ788165	2M0035P02
c 99	8.4	38.2	20	1	AU254575	AU254575	AU254575
c 100	8.4	38.2	20	8	AZ331643	AZ331643	1M0059P12

ALIGNMENTS

RESULT 1
AZ659094
LOCUS AZ659094 22 bp DNA linear GSS 14-DEC-2000
DEFINITION 1M0536E16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0536E16 F, genomic survey sequence.
ACCESSION AZ659094
VERSION AZ659094.1 GI:11796240
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0536 row: E column: 16
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 22.
FEATURES Location/Qualifiers
source 1. .22
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0536E16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
ORIGIN

Query Match 62.7%; Score 13.8; DB 8; Length 22;
Best Local Similarity 88.2%; Pred. No. 5.3e+04;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          3 ATGTTACAGGTAGAAAA 19
              ||| |||||||||| |||
Db          6 ATGATACAGGTAGTAAA 22
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RESULT 2
TA359F10Q/c
LOCUS TA359F10Q 20 bp DNA linear GSS 13-DEC-2000
DEFINITION T. brucei sheared genomic DNA clone 359f10, reverse sequence, genomic survey sequence.
ACCESSION AL495341
VERSION AL495341.1 GI:11871728
KEYWORDS GSS.
SOURCE Trypanosoma brucei
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
REFERENCE 1 (bases 1 to 20)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and nh1@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (
4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES Location/Qualifiers
source 1. .20
/organism="Trypanosoma brucei"
/mol_type="genomic DNA"
/strain="TREU927"
/db_xref="taxon:5691"
/clone="359f10"
ORIGIN

Query Match 50.9%; Score 11.2; DB 9; Length 20;
Best Local Similarity 81.2%; Pred. No. 9.5e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          6 TTACAGGTAGAAAAGC 21
              | ||||| | ||||||
Db         19 TCACAGGCACAAAAGC 4
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RESULT 3
AZ452265/c
LOCUS AZ452265 20 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0252H06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0252H06 F, genomic survey sequence.
ACCESSION AZ452265
VERSION AZ452265.1 GI:10608897
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,

```
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0252  row: H  column: 06
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0252H06"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             50.0%;  Score 11;  DB 8;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.2e+06;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          8 ACAGGTAGAAA 18
              ||||||||||
Db         13 ACAGGTAGAAA 3


RESULT 4
CL681335
LOCUS       CL681335                  20 bp    DNA     linear   GSS 09-JUL-2004
DEFINITION  PRI0130d_E07_2 - PRI0130d.BR (20) Note: Recurring String Mixed
            stage fosmid library of P. pacificus var. California Pristionchus
            pacificus genomic, genomic survey sequence.
ACCESSION   CL681335
VERSION     CL681335.1  GI:50188343
KEYWORDS    GSS.
SOURCE      Pristionchus pacificus
  ORGANISM  Pristionchus pacificus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
            Neodiplogasteridae; Pristionchus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
  TITLE     AppaDB: an AcedB database for the nematode satellite organism
            Pristionchus pacificus
  JOURNAL   Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT     Contact: Sommer RJ
            Evolutionary Biology
            Max-Planck-Institute for Developmental Biology
            Spemannstr. 37-39, Tuebingen D-72076, Germany
            Tel: 00497071601371
            Fax: 00497071601498
            Email: ralf.sommer@tuebingen.mpg.de
            This library was generated at Caltech, Pasadena, USA and end
            sequenced at Vancouver, Canada.
            Seq primer: T7
            Class: fosmid ends.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Pristionchus pacificus"
                     /mol_type="genomic DNA"
                     /strain="California"
                     /db_xref="taxon:54126"
                     /clone_lib="Mixed stage fosmid library of P. pacificus
                     var. California"
                     /note="Vector: pEpifos-5 Fosmid vector"
ORIGIN

  Query Match             49.1%;  Score 10.8;  DB 9;  Length 20;
  Best Local Similarity   85.7%;  Pred. No. 1.5e+06;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 TGTTACAGGTAGAA 17
              ||| ||| ||||||
Db          7 TGTGACACGTAGAA 20


RESULT 5
AZ651001
LOCUS       AZ651001                  22 bp    DNA     linear   GSS 14-DEC-2000
DEFINITION  1M0521O23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0521O23 F, genomic survey sequence.
ACCESSION   AZ651001
VERSION     AZ651001.1  GI:11786054
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0521  row: O  column: 23
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
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/db_xref="taxon:10090"
/clone="UUGC1M0521O23"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 49.1%; Score 10.8; DB 8; Length 22;
Best Local Similarity 85.7%; Pred. No. 1.5e+06;
Matches 12; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          4 TGTTACAGGTAGAA 17
              || ||||||| |||
Db          6 TGCTACAGGTTGAA 19
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RESULT 6
AZ775974
LOCUS AZ775974 20 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0009H14F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0009H14 F, genomic survey sequence.
ACCESSION AZ775974
VERSION AZ775974.1 GI:12903069
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0009 row: H column: 14
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0009H14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 48.2%; Score 10.6; DB 8; Length 20;
Best Local Similarity 76.5%; Pred. No. 1.8e+06;
Matches 13; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy          3 ATGTTACAGGTAGAAAA 19
              ||| ||||||   ||||
Db          3 ATGATACAGGAGTAAAA 19
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RESULT 7
CL436392
LOCUS CL436392 21 bp DNA linear GSS 18-MAR-2004
DEFINITION PST2884-NL.Seq MICB1 Mus musculus genomic clone PST2884-NL.Seq similar to 2700016D05Rik, genomic survey sequence.
ACCESSION CL436392
VERSION CL436392.1 GI:45571141
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 21)
AUTHORS Hicks,G.G.
TITLE www.EScells.ca
JOURNAL Unpublished (2002)
COMMENT Contact: Hicks GG
Mammalian Functional Genomics Centre
Manitoba Institute of Cell Biology, Universitry of Manitoba
ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
Tel: 204 787 2133
Fax: 204 787 2190
Email: hicksgg@cc.umanitoba.ca
U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional sequence information and target gene cloning can be generated. ES cell line harboring insertion mutation of target gene is available. Sequence analysis available from http://140.193.242.7/esdb/public_search_frame.php?PST=PST2884-NL.Seq
Class: Gene Trap.
FEATURES Location/Qualifiers
source 1. .21
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129 sv"
/db_xref="taxon:10090"
/clone="PST2884-NL.Seq"
/sex="Male"

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                     /cell_type="Embryonic stem cell"
                     /cell_line="D3H (J1 subclone)"
                     /clone_lib="MICB1"
                     /note="Vector: U3NeoSV1"
ORIGIN

  Query Match             48.2%;  Score 10.6;  DB 9;  Length 21;
  Best Local Similarity   76.5%;  Pred. No. 1.9e+06;
  Matches   13;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 CATGTTACAGGTAGAAA 18
              |||||  |  |||||||
Db          1 CATGTCTCTAGTAGAAA 17


RESULT 8
AZ990555/c
LOCUS       AZ990555                  22 bp    DNA     linear   GSS 27-APR-2001
DEFINITION  2M0274N14F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
            clone UUGC2M0274N14 F, genomic survey sequence.
ACCESSION   AZ990555
VERSION     AZ990555.1  GI:13861782
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0274  row: N  column: 14
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0274N14"
                     /sex="Female"
                     /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC2M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (female) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             47.3%;  Score 10.4;  DB 8;  Length 22;
  Best Local Similarity   91.7%;  Pred. No. 2.3e+06;
  Matches   11;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 TACAGGTAGAAA 18
              | ||||||||||
Db         13 TGCAGGTAGAAA 2


RESULT 9
AZ649514/c
LOCUS       AZ649514                  21 bp    DNA     linear   GSS 14-DEC-2000
DEFINITION  1M0519A09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0519A09 F, genomic survey sequence.
ACCESSION   AZ649514
VERSION     AZ649514.1  GI:11783070
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0519  row: A  column: 09
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0519A09"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
```

purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
ORIGIN

Query Match 46.4%; Score 10.2; DB 8; Length 21;
Best Local Similarity 80.0%; Pred. No. 2.9e+06;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          6 TTACAGGTAGAAAAG 20
              || ||||||  ||||
Db         16 TTGCAGGTATTAAAG 2
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RESULT 10
AI545076
LOCUS AI545076 19 bp mRNA linear EST 07-JUN-2001
DEFINITION fb70d07.y1 Zebrafish WashU MPIMG EST Danio rerio cDNA clone IMAGE:3717229 5' similar to TR:O23327 O23327 HYPOTHETICAL 108.0 KD PROTEIN. ;, mRNA sequence.
ACCESSION AI545076
VERSION AI545076.1 GI:4462449
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
REFERENCE 1 (bases 1 to 19)
AUTHORS Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
TITLE WashU Zebrafish EST Project 1998
JOURNAL Unpublished (1998)
COMMENT Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: zbrafish@watson.wustl.edu
cDNA Library Preparation: Matthew Clark. cDNA Library Arrayed by: Matthew Clark. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: Genome Systems, St. Louis, Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address: www.rzpd.de)
Trace considered overall poor quality
Possible reversed clone: similarity on wrong strand
Seq primer: T3 ET from Amersham
High quality sequence stop: 1
POLYA=No.
FEATURES Location/Qualifiers
source 1. .19
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:3717229"
/sex="mixed"
/tissue_type="26 somite embryos, adult livers, shield stage embryos"
/lab_host="XL1-blue MRF"
/clone_lib="Zebrafish WashU MPIMG EST"
/note="Vector: pSPORT1; Site_1: NotI; Site_2: SalI; 1st strand cDNA was primed with a Not I - oligo(dT)15 primer [5'pGACTAGTTCTAGATCGCGAGCGGCCGCCCTTTTTTTTTTTTTTT3']; double-stranded cDNA was ligated to Sal I adaptors (BRL), digested with Not I and cloned into the Not I and Sal I sites of the pSPORT1 vector (BRL). Library was constructed by Matthew Clark (Lehrach lab; ICRF, London and Max Planck Institut fuer Molekulare Genetik,Berlin). cDNAs for EST analysis were selected following oligonucleotide hybridization fingerprinting of arrayed clones from zebrafish late somitogenesis (26 ss), adult liver or embryonic shield stage (5.6 h) libraries. Fingerprint data were used to computationally cluster cDNAs, and a single cDNA from each cluster was chosen for sequencing. In some cases multiple members of the same cluster were sequenced to assess clustering parameters or single clones were sequenced additional times to assess quality control."
ORIGIN

Query Match 45.5%; Score 10; DB 1; Length 19;
Best Local Similarity 72.2%; Pred. No. 3.6e+06;
Matches 13; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Qy          1 GCATGTTACAGGTAGAAA 18
              ||||| |||| | |  ||
Db          2 GCATGGTACATGGATGAA 19
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RESULT 11
AZ775273/c
LOCUS AZ775273 19 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0007F04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0007F04 R, genomic survey sequence.
ACCESSION AZ775273
VERSION AZ775273.1 GI:12901587
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0007 row: F column: 04
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0007F04"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

```
  Query Match             45.5%;  Score 10;  DB 8;  Length 19;
  Best Local Similarity   72.2%;  Pred. No. 3.6e+06;
  Matches   13;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          4 TGTTACAGGTAGAAAAGC 21
              ||  ||||| | ||| ||
Db         18 TGCCACAGGGAAAAACGC 1
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RESULT 12
AU008116/c
LOCUS AU008116 20 bp mRNA linear EST 31-JUL-1998
DEFINITION AU008116 Schizosaccharomyces pombe late log phase cDNA Schizosaccharomyces pombe cDNA clone spc02889, mRNA sequence.
ACCESSION AU008116
VERSION AU008116.1 GI:3344574
KEYWORDS EST.
SOURCE Schizosaccharomyces pombe (fission yeast)
ORGANISM Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.
REFERENCE 1 (bases 1 to 20)
AUTHORS Morimyo,M. and Mita,K.
TITLE Identification of expressed sequence tags of Schizosaccharomyces pombe
JOURNAL Unpublished (1998)
COMMENT Contact: Mitsuoki Morimyo
Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: morimyo@nirs.go.jp.
FEATURES Location/Qualifiers
source 1. .20
/organism="Schizosaccharomyces pombe"
/mol_type="mRNA"
/strain="972"
/db_xref="taxon:4896"
/clone="spc02889"
/sex="h minus"
/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"

ORIGIN

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  Query Match             45.5%;  Score 10;  DB 1;  Length 20;
  Best Local Similarity   72.2%;  Pred. No. 3.6e+06;
  Matches   13;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GCATGTTACAGGTAGAAA 18
              || ||||| ||| | | |
Db         20 GCGTGTTAAAGGAATACA 3
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RESULT 13
AZ585902
LOCUS AZ585902 20 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0391M24F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0391M24 F, genomic survey sequence.
ACCESSION AZ585902
VERSION AZ585902.1 GI:11708092
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0391 row: M column: 24
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0391M24"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

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  Query Match             45.5%;  Score 10;  DB 8;  Length 20;
  Best Local Similarity   72.2%;  Pred. No. 3.6e+06;
  Matches   13;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          4 TGTTACAGGTAGAAAAGC 21
              || ||||||   |||| |
Db          1 TGATACAGGAGTAAAACC 18
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RESULT 14
AZ828233
LOCUS       AZ828233                 21 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0105B09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0105B09 F, genomic survey sequence.
ACCESSION   AZ828233
VERSION     AZ828233.1  GI:12998141
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0105  row: B  column: 09
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0105B09"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             45.5%;  Score 10;  DB 8;  Length 21;
  Best Local Similarity   72.2%;  Pred. No. 3.6e+06;
  Matches   13;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 CATGTTACAGGTAGAAAA 19
              | ||| ||| || ||||
Db          2 CCTGTAACAATTAAAAAA 19
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RESULT 15
AZ828233/c
LOCUS       AZ828233                 21 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0105B09F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0105B09 F, genomic survey sequence.
ACCESSION   AZ828233
VERSION     AZ828233.1  GI:12998141
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0105  row: B  column: 09
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0105B09"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             45.5%;  Score 10;  DB 8;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3.6e+06;
  Matches   10;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          4 TGTTACAGGT 13
              ||||||||||
Db         10 TGTTACAGGT 1
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RESULT 16
CL437394
LOCUS       CL437394                 13 bp    DNA     linear   GSS 18-MAR-2004
DEFINITION  PST5288-NL.Seq MICB1 Mus musculus genomic clone PST5288-NL.Seq,
            genomic survey sequence.
ACCESSION   CL437394
VERSION     CL437394.1  GI:45573060
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Hicks,G.G.
  TITLE     www.EScells.ca
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hicks GG
            Mammalian Functional Genomics Centre
            Manitoba Institute of Cell Biology, Universitry of Manitoba
            ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
            Tel: 204 787 2133
            Fax: 204 787 2190
            Email: hicksgg@cc.umanitoba.ca
            U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
            sequence information and target gene cloning can be generated. ES
            cell line harboring insertion mutation of target gene is available.
            Sequence analysis available from
            http://140.193.242.7/esdb/public_search_frame.php?PST=PST5288-NL.Se
            q
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="129 sv"
                     /db_xref="taxon:10090"
                     /clone="PST5288-NL.Seq"
                     /sex="Male"
                     /cell_type="Embryonic stem cell"
                     /cell_line="D3H (J1 subclone)"
                     /clone_lib="MICB1"
                     /note="Vector: U3NeoSV1"
ORIGIN

  Query Match             44.5%;  Score 9.8;  DB 9;  Length 13;
  Best Local Similarity   84.6%;  Pred. No. 4.2e+06;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 CATGTTACAGGTA 14
              ||||||| | |||
Db          1 CATGTTAAAAGTA 13


RESULT 17
CF316655/c
LOCUS       CF316655                 19 bp    mRNA    linear   EST 15-AUG-2003
DEFINITION  HD--06-A14.g1 OsHDAC1-overexpressing transgenic rice plasmid cDNA
            library (HD) Oryza sativa (japonica cultivar-group) cDNA clone
            HD--06-A14, mRNA sequence.
ACCESSION   CF316655
VERSION     CF316655.1  GI:33688416
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="HD--06-A14"
                     /tissue_type="callus"
                     /dev_stage="proliferated callus on 2N6 media for 2 weeks"
                     /lab_host="E.coli DH10B"
                     /clone_lib="OsHDAC1-overexpressing transgenic rice plasmid
                     cDNA library (HD)"
                     /note="Vector: pCR4-TOPO; Site_1: EcoRI; Callus was
                     treated with ABA(20um) for 1hr. Oligo-capped mRNA was
                     reverse transcribed and then used for PCR. mRNA was
                     derived from rice Histone Deacetylase overexpression
                     line."
ORIGIN

  Query Match             44.5%;  Score 9.8;  DB 7;  Length 19;
  Best Local Similarity   84.6%;  Pred. No. 4.5e+06;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 ACAGGTAGAAAAG 20
              ||||| | |||||
Db         13 ACAGGAATAAAAG 1


RESULT 18
AZ377971/c
LOCUS       AZ377971                 19 bp    DNA     linear   GSS 02-OCT-2000
DEFINITION  1M0132I03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0132I03 R, genomic survey sequence.
ACCESSION   AZ377971
VERSION     AZ377971.1  GI:10491671
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0132  row: I  column: 03
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
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/clone="UUGC1M0132I03"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 44.5%; Score 9.8; DB 8; Length 19;
Best Local Similarity 84.6%; Pred. No. 4.5e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          3 ATGTTACAGGTAG 15
              ||||| || ||||
Db         18 ATGTTGCATGTAG 6
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RESULT 19
AZ808350
LOCUS AZ808350 19 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0071P14R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0071P14 R, genomic survey sequence.
ACCESSION AZ808350
VERSION AZ808350.1 GI:12973606
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0071 row: P column: 14
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"

/clone="UUGC2M0071P14"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 44.5%; Score 9.8; DB 8; Length 19;
Best Local Similarity 84.6%; Pred. No. 4.5e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          7 TACAGGTAGAAAA 19
              ||||  |||||||
Db          3 TACACATAGAAAA 15
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RESULT 20
AZ625409/c
LOCUS AZ625409 20 bp DNA linear GSS 13-DEC-2000
DEFINITION 1M0464C20R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0464C20 R, genomic survey sequence.
ACCESSION AZ625409
VERSION AZ625409.1 GI:11747599
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0464 row: C column: 20
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"

/clone="UUGC1M0464C20"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 44.5%; Score 9.8; DB 8; Length 20;
Best Local Similarity 84.6%; Pred. No. 4.5e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          1 GCATGTTACAGGT 13
              ||||| ||| |||
Db         13 GCATGGTACTGGT 1
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RESULT 21
AZ799032/c
LOCUS AZ799032 20 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0056K07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0056K07 F, genomic survey sequence.
ACCESSION AZ799032
VERSION AZ799032.1 GI:12949733
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0056 row: K column: 07
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0056K07"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 44.5%; Score 9.8; DB 8; Length 20;
Best Local Similarity 84.6%; Pred. No. 4.5e+06;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          9 CAGGTAGAAAAGC 21
              |||| |||||| |
Db         14 CAGGCAGAAAAAC 2
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RESULT 22
AJ596498/c
LOCUS AJ596498 20 bp DNA linear GSS 15-JAN-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 435B03, genomic survey sequence.
ACCESSION AJ596498
VERSION AJ596498.1 GI:37946126
KEYWORDS GSS; left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G., Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE 22363535
PUBMED 12446565
REFERENCE 2 (bases 1 to 20)
AUTHORS Balzergue,S.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
FEATURES Location/Qualifiers

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     source          1. .20
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="435B03"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature    1. .20
                     /note="T-DNA flanking sequence
                     left border"
ORIGIN

  Query Match             44.5%;  Score 9.8;  DB 9;  Length 20;
  Best Local Similarity   84.6%;  Pred. No. 4.5e+06;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 TACAGGTAGAAAA 19
              | ||||||| ||||
Db         16 TTCAGGTATAAAA 4


RESULT 23
AZ430939
LOCUS       AZ430939                 21 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0215E12R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0215E12 R, genomic survey sequence.
ACCESSION   AZ430939
VERSION     AZ430939.1  GI:10554952
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0215  row: E  column: 12
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0215E12"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             44.5%;  Score 9.8;  DB 8;  Length 21;
  Best Local Similarity   84.6%;  Pred. No. 4.5e+06;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 TACAGGTAGAAAA 19
              |||||||| | ||
Db          8 TACAGGTATACAA 20


RESULT 24
AZ483078
LOCUS       AZ483078                 21 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0308H04R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0308H04 R, genomic survey sequence.
ACCESSION   AZ483078
VERSION     AZ483078.1  GI:10646729
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0308  row: H  column: 04
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0308H04"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
```

adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

```
  Query Match             44.5%;  Score 9.8;  DB 8;  Length 21;
  Best Local Similarity   84.6%;  Pred. No. 4.5e+06;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          9 CAGGTAGAAAAGC 21
              || ||| ||||||
Db          5 CATGTAAAAAAGC 17
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RESULT 25
AZ786362
LOCUS AZ786362 22 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0031N16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0031N16 R, genomic survey sequence.
ACCESSION AZ786362
VERSION AZ786362.1 GI:12924044
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
  ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 22)
  AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
  JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0031 row: N column: 16
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 22.
FEATURES Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0031N16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

```
  Query Match             44.5%;  Score 9.8;  DB 8;  Length 22;
  Best Local Similarity   84.6%;  Pred. No. 4.6e+06;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 TACAGGTAGAAAA 19
              ||| |||| ||||
Db          6 TACCGGTAAAAAA 18
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RESULT 26
CL668834
LOCUS CL668834 19 bp DNA linear GSS 09-JUL-2004
DEFINITION PRI0158d_C09 - PRI0158d.B21 (19) Note: Recurring String Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.
ACCESSION CL668834
VERSION CL668834.1 GI:50164652
KEYWORDS GSS.
SOURCE Pristionchus pacificus
  ORGANISM Pristionchus pacificus
Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchus.
REFERENCE 1 (bases 1 to 19)
  AUTHORS Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
  TITLE AppaDB: an AcedB database for the nematode satellite organism Pristionchus pacificus
  JOURNAL Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT Contact: Sommer RJ
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.
FEATURES Location/Qualifiers
     source 1. .19
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"
/strain="California"
/db_xref="taxon:54126"
/clone_lib="Mixed stage fosmid library of P. pacificus var. California"
/note="Vector: pEpifos-5 Fosmid vector"
ORIGIN

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  Query Match             43.6%;  Score 9.6;  DB 9;  Length 19;
  Best Local Similarity   75.0%;  Pred. No. 5.6e+06;
  Matches   12;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          6 TTACAGGTAGAAAAGC 21
              ||| | ||||||  ||
Db          4 TTAAAAGTAGAACGGC 19
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RESULT 27
AZ396022
LOCUS AZ396022 20 bp DNA linear GSS 03-OCT-2000

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DEFINITION  1M0160J20F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0160J20 F, genomic survey sequence.
ACCESSION   AZ396022
VERSION     AZ396022.1  GI:10511094
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0160  row: J  column: 20
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0160J20"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             43.6%;  Score 9.6;  DB 8;  Length 20;
  Best Local Similarity   75.0%;  Pred. No. 5.6e+06;
  Matches   12;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 ATGTTACAGGTAGAAA 18
              ||||||||    ||||
Db          5 ATGTTACATCGTGAAA 20


RESULT 28
AZ787298
LOCUS       AZ787298                  20 bp    DNA     linear   GSS 16-FEB-2001
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DEFINITION  2M0033O16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0033O16 F, genomic survey sequence.
ACCESSION   AZ787298
VERSION     AZ787298.1  GI:12925926
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0033  row: O  column: 16
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0033O16"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             43.6%;  Score 9.6;  DB 8;  Length 20;
  Best Local Similarity   75.0%;  Pred. No. 5.6e+06;
  Matches   12;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          6 TTACAGGTAGAAAAGC 21
              ||||||   || ||||
Db          2 TTACAGCATGATAAGC 17


RESULT 29
CL687844/c
LOCUS       CL687844                  20 bp    DNA     linear   GSS 09-JUL-2004
```

```
DEFINITION  PRI0147d_G03_2 - PRI0147d.BR (20) Mixed stage fosmid library of P.
            pacificus var. California Pristionchus pacificus genomic, genomic
            survey sequence.
ACCESSION   CL687844
VERSION     CL687844.1  GI:50196717
KEYWORDS    GSS.
SOURCE      Pristionchus pacificus
  ORGANISM  Pristionchus pacificus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
            Neodiplogasteridae; Pristionchus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
  TITLE     AppaDB: an AcedB database for the nematode satellite organism
            Pristionchus pacificus
  JOURNAL   Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT     Contact: Sommer RJ
            Evolutionary Biology
            Max-Planck-Institute for Developmental Biology
            Spemannstr. 37-39, Tuebingen D-72076, Germany
            Tel: 00497071601371
            Fax: 00497071601498
            Email: ralf.sommer@tuebingen.mpg.de
            This library was generated at Caltech, Pasadena, USA and end
            sequenced at Vancouver, Canada.
            Seq primer: T7
            Class: fosmid ends.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Pristionchus pacificus"
                     /mol_type="genomic DNA"
                     /strain="California"
                     /db_xref="taxon:54126"
                     /clone_lib="Mixed stage fosmid library of P. pacificus
                     var. California"
                     /note="Vector: pEpifos-5 Fosmid vector"
ORIGIN

  Query Match             43.6%;  Score 9.6;  DB 9;  Length 20;
  Best Local Similarity   75.0%;  Pred. No. 5.6e+06;
  Matches   12;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 ATGTTACAGGTAGAAA 18
              | || | ||| |||||
Db         20 AGGTAAGAGGGAGAAA 5


RESULT 30
AG197947/c
LOCUS       AG197947                 21 bp    DNA     linear   GSS 06-MAR-2004
DEFINITION  Pan troglodytes DNA, clone: RP43-078H02.T7, genomic survey
            sequence.
ACCESSION   AG197947
VERSION     AG197947.1  GI:45230123
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1
  AUTHORS   Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
            Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
  TITLE     BAC end sequences of Library RP-43
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 21)
  AUTHORS   Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
            Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
            Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
            52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
            (E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,
            Tel:82-42-866-7181, Fax:82-42-860-4409)
COMMENT     Clones are derived from the chimpanzee BAC library RP-43 This BAC
            end was generated during the R&D process and may have higher chance
            of clone tracking errors.
             PRIMERS
                 Sequencing: T7
             LIBRARY
                 Vector    : pBACe3.6
                 R.Site 1  : EcoRI
                 R.Site 2  : EcoRI.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
                     /clone="RP43-078H02.T7"
                     /sex="male"
                     /cell_type="lymphocytes"
                     /clone_lib="RP-43 Chimpanzee Male BAC Library"
ORIGIN

  Query Match             43.6%;  Score 9.6;  DB 9;  Length 21;
  Best Local Similarity   75.0%;  Pred. No. 5.7e+06;
  Matches   12;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          7 TACAGGTAGAAAAGCC 22
              || ||||||  ||| |
Db         21 TAGAGGTAGGCAAGTC 6


RESULT 31
AZ312945/c
LOCUS       AZ312945                 19 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0029P03F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0029P03 F, genomic survey sequence.
ACCESSION   AZ312945
VERSION     AZ312945.1  GI:10357381
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0029  row: P  column: 03
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0029P03"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
```

Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

```
  Query Match             42.7%;  Score 9.4;  DB 8;  Length 19;
  Best Local Similarity   90.9%;  Pred. No. 7e+06;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 CAGGTAGAAAA 19
              || ||||||||
Db         11 CATGTAGAAAA 1
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RESULT 32
AZ774536
LOCUS AZ774536 19 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0004P01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0004P01 F, genomic survey sequence.
ACCESSION AZ774536
VERSION AZ774536.1 GI:12900089
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0004 row: P column: 01
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0004P01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson

Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."

ORIGIN

```
  Query Match             42.7%;  Score 9.4;  DB 8;  Length 19;
  Best Local Similarity   68.4%;  Pred. No. 7e+06;
  Matches   13;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          3 ATGTTACAGGTAGAAAAGC 21
              || ||| |   | |||||||
Db          1 ATCTTAAAAAAAAAAAAGC 19
```

RESULT 33
AJ796099
LOCUS AJ796099 20 bp mRNA linear EST 11-AUG-2004
DEFINITION AJ796099 Antirrhinum majus whole plant Antirrhinum majus cDNA clone 018_3_09_p24, mRNA sequence.
ACCESSION AJ796099
VERSION AJ796099.1 GI:51111427
KEYWORDS EST.
SOURCE Antirrhinum majus (snapdragon)
ORGANISM Antirrhinum majus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; lamiids; Lamiales; Plantaginaceae; Antirrhineae; Antirrhinum.
REFERENCE 1 (bases 1 to 20)
AUTHORS Zachgo,S., Stueber,K., Saedler,H., Sommer,H. and Schwarz-Sommer,Z.
TITLE Antirrhinum EST collection
JOURNAL Unpublished (2003)
COMMENT Contact: Schwarz-Sommer Z
Molekulare Pflanzengenetik
MPI fuer Zuechtungsforschung
Carl-von-Linne Weg 10, D-50829, Germany.
FEATURES Location/Qualifiers
source 1. .20
/organism="Antirrhinum majus"
/mol_type="mRNA"
/db_xref="taxon:4151"
/clone="018_3_09_p24"
/tissue_type="whole plant"
/clone_lib="Antirrhinum majus whole plant"

ORIGIN

```
  Query Match             42.7%;  Score 9.4;  DB 1;  Length 20;
  Best Local Similarity   68.4%;  Pred. No. 7e+06;
  Matches   13;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          3 ATGTTACAGGTAGAAAAGC 21
              || ||  || ||||  |||
Db          2 ATATTGGAGCTAGAGGAGC 20
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RESULT 34
AZ428984/c
LOCUS AZ428984 21 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0212P03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic

```
            clone UUGC1M0212P03 R, genomic survey sequence.
ACCESSION   AZ428984
VERSION     AZ428984.1  GI:10552913
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0212  row: P  column: 03
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0212P03"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match           42.7%;  Score 9.4;  DB 8;  Length 21;
  Best Local Similarity   68.4%;  Pred. No. 7.1e+06;
  Matches   13;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 CATGTTACAGGTAGAAAAG 20
              ||| || || ||   ||||
Db         21 CATATTTCACGTCATAAAG 3


RESULT 35
AZ942905/c
LOCUS       AZ942905                 22 bp    DNA     linear   GSS 26-APR-2001
DEFINITION  2M0203K13F Mouse 10kb plasmid UUGC2M library Mus musculus genomic

            clone UUGC2M0203K13 F, genomic survey sequence.
ACCESSION   AZ942905
VERSION     AZ942905.1  GI:13806556
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0203  row: K  column: 13
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 22.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0203K13"
                     /sex="Female"
                     /lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC2M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (female) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match           42.7%;  Score 9.4;  DB 8;  Length 22;
  Best Local Similarity   90.9%;  Pred. No. 7.1e+06;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         10 AGGTAGAAAAG 20
              ||| |||||||
Db         13 AGGAAGAAAAG 3


RESULT 36
TA82F07Q/c
LOCUS       TA82F07Q                 22 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  T. brucei sheared genomic DNA clone 82f07, reverse sequence,
```

```
            genomic survey sequence.
ACCESSION   AL459970
VERSION     AL459970.1  GI:11860295
KEYWORDS    GSS.
SOURCE      Trypanosoma brucei
  ORGANISM  Trypanosoma brucei
            Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
            Trypanosoma.
REFERENCE   1  (bases 1 to 22)
  AUTHORS   Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
            Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
            Melville,S.E., Rajandream,M.A. and Barrell,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing
            project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
            Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
            nh1@sanger.ac.uk
COMMENT     Constructed at the Institute for Genomic Research (TIGR),
            Rockville, MD. Genomic DNA isolated from a cloned population of
            Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
            to give a tight size distribution (
            4 kb). The v + i method used for the library construction is
            described in detail in Smith, H. and Venter, J.C. (Making small
            insert libraries for whole genome shotgun sequencing projects. In
            Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
            Barrell, Oxford University Press, 1999).
            Email: nelsayed@tigr.org
            Details of T. brucei sequencing at the Sanger Centre are available
            at http://www.sanger.ac.uk/Projects/T_brucei/.
FEATURES             Location/Qualifiers
     source          1. .22
                     /organism="Trypanosoma brucei"
                     /mol_type="genomic DNA"
                     /strain="TREU927"
                     /db_xref="taxon:5691"
                     /clone="82f07"
ORIGIN

  Query Match             42.7%;  Score 9.4;  DB 9;  Length 22;
  Best Local Similarity   90.9%;  Pred. No. 7.1e+06;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GCATGTTACAG 11
              | |||||||||
Db         19 GAATGTTACAG 9


RESULT 37
CO780477/c
LOCUS       CO780477                 19 bp    mRNA    linear   EST 05-AUG-2004
DEFINITION  BL009D_A05 6-Day Axolotl Tail Blastema (6DAxBL) Ambystoma mexicanum
            cDNA 5' similar to hypothetical protein, mRNA sequence.
ACCESSION   CO780477
VERSION     CO780477.1  GI:50996457
KEYWORDS    EST.
SOURCE      Ambystoma mexicanum (axolotl)
  ORGANISM  Ambystoma mexicanum
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
            Ambystoma.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Habermann,B., Bebin,A.G., Herklotz,S., Volkmer,M., Eckelt,K.,
            Pehlke,K., Epperlein,H.H., Schackert,H.K., Wiebe,G. and Tanaka,E.M.
  TITLE     An Ambystoma mexicanum EST sequencing project: Analysis of 17,352
            expressed sequence tags from embryonic and regenerating blastema
            cDNA libraries
  JOURNAL   Genome Biol. (2004) In press
COMMENT     Contact: Elly M. Tanaka
            Tanaka Lab
            Max Planck Institute of Molecular Cell Biology and Genetics,
            Dresden
            Pfotenhauerstrasse 108,01307 Dresden, Germany
            Tel: 0049 351 210 2620
            Fax: 0049 351 210 1489
            Email: tanaka@mpi-cbg.de
            Plate: BL009D  row: 05  column: A
            Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Ambystoma mexicanum"
                     /mol_type="mRNA"
                     /db_xref="taxon:8296"
                     /tissue_type="Tail Blastema"
                     /cell_type="regenerating tail blastema"
                     /clone_lib="6-Day Axolotl Tail Blastema (6DAxBL)"
                     /note="Vector: pCMVSport6; Site_1: NotI; Site_2: SalI;
                     Unnormalized cDNA plasmid library prepared by Invitrogen.
                     Size fractionated mRNA was polydT primed and cloned into
                     NotI-SalI site of pCMVSport6. Bacterial host is
                     EMDH10B-TONA. Average insert size is 1.67 kB.
                     TAG_LIB=6DAxBL"
ORIGIN

  Query Match             41.8%;  Score 9.2;  DB 7;  Length 19;
  Best Local Similarity   78.6%;  Pred. No. 8.7e+06;
  Matches   11;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          8 ACAGGTAGAAAAGC 21
              ||  |||||||| |
Db         17 ACGAGTAGAAAAAC 4


RESULT 38
AZ612157/c
LOCUS       AZ612157                 19 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0438L21R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0438L21 R, genomic survey sequence.
ACCESSION   AZ612157
VERSION     AZ612157.1  GI:11734347
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0438  row: L  column: 21
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
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                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0438L21"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
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musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 41.8%; Score 9.2; DB 8; Length 19;
Best Local Similarity 78.6%; Pred. No. 8.7e+06;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          7 TACAGGTAGAAAAG 20
              | || ||||||| |
Db         17 TCCAAGTAGAAACG 4
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RESULT 39
AZ817291
LOCUS AZ817291 19 bp DNA linear GSS 20-FEB-2001
DEFINITION 2M0086P05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0086P05 R, genomic survey sequence.
ACCESSION AZ817291
VERSION AZ817291.1 GI:12987199
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0086 row: P column: 05
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.
FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0086P05"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.

musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 41.8%; Score 9.2; DB 8; Length 19;
Best Local Similarity 78.6%; Pred. No. 8.7e+06;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 9 CAGGTAGAAAAGCC 22
|||| | ||||| |
Db 4 CAGGCACAAAAGGC 17

RESULT 40
AU008312/c
LOCUS AU008312 21 bp mRNA linear EST 31-JUL-1998
DEFINITION AU008312 Schizosaccharomyces pombe late log phase cDNA Schizosaccharomyces pombe cDNA clone spc03191, mRNA sequence.
ACCESSION AU008312
VERSION AU008312.1 GI:3344770
KEYWORDS EST.
SOURCE Schizosaccharomyces pombe (fission yeast)
ORGANISM Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.
REFERENCE 1 (bases 1 to 21)
AUTHORS Morimyo,M. and Mita,K.
TITLE Identification of expressed sequence tags of Schizosaccharomyces pombe
JOURNAL Unpublished (1998)
COMMENT Contact: Mitsuoki Morimyo
Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: morimyo@nirs.go.jp.
FEATURES Location/Qualifiers
source 1. .21
/organism="Schizosaccharomyces pombe"
/mol_type="mRNA"
/strain="972"
/db_xref="taxon:4896"
/clone="spc03191"
/sex="h minus"
/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/note="Vector: M13mp19; The cDNA library of Schizosaccharomyces pombe was prepared by cloning cDNA into the SmaI site of M13mp19 DNA and the direction of DNA sequences was not always from 5' to 3'. The cDNA data of Schizosaccharomyces pombe are available for searching on the World Wide Web. (URL, http://www.nirs.go.jp)"

ORIGIN

Query Match 41.8%; Score 9.2; DB 1; Length 21;
Best Local Similarity 73.3%; Pred. No. 8.9e+06;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy          6 TTACAGGTAGAAAAG 20
              | ||| | || ||||
Db         18 TNACAAGCAGGAAAG 4
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Search completed: August 12, 2005, 09:54:57
Job time : 1787 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 12, 2005, 09:25:17 ; Search time 1566 Seconds
(without alignments)
649.783 Million cell updates/sec

Title: US-09-743-825-8
Perfect score: 21
Sequence: 1 ctggcgtatctgaagagtctg 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 892778

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	13	61.9	20	6	AR116690	AR116690 Sequence
	2	13	61.9	20	6	AR275648	AR275648 Sequence
c	3	12.8	61.0	17	6	AR402108	AR402108 Sequence
c	4	12.8	61.0	17	6	BD067608	BD067608 Enzymatic
c	5	12.8	61.0	20	6	A17234	A17234 Oligonucleo
c	6	12.8	61.0	20	6	AR027617	AR027617 Sequence
c	7	12.2	58.1	17	6	AR402109	AR402109 Sequence
c	8	12.2	58.1	17	6	AX690585	AX690585 Sequence
c	9	12.2	58.1	17	6	BD067609	BD067609 Enzymatic
	10	12.2	58.1	20	6	AR070817	AR070817 Sequence
	11	12.2	58.1	20	6	AR104505	AR104505 Sequence
c	12	12.2	58.1	20	6	AX962823	AX962823 Sequence
c	13	12	57.1	17	6	AX737882	AX737882 Sequence
	14	11.8	56.2	16	6	AR328335	AR328335 Sequence
	15	11.8	56.2	17	6	AR007304	AR007304 Sequence
	16	11.8	56.2	17	6	AR053990	AR053990 Sequence
	17	11.8	56.2	17	6	AR135992	AR135992 Sequence
	18	11.8	56.2	17	6	I22067	I22067 Sequence 4
	19	11.8	56.2	17	6	AR327036	AR327036 Sequence
c	20	11.8	56.2	17	6	AR402107	AR402107 Sequence
c	21	11.8	56.2	17	6	AX217836	AX217836 Sequence
c	22	11.8	56.2	17	6	BD067607	BD067607 Enzymatic
c	23	11.8	56.2	20	6	AR160744	AR160744 Sequence
	24	11.8	56.2	20	6	AR310829	AR310829 Sequence
c	25	11.8	56.2	21	6	BD238283	BD238283 Accelerat
c	26	11.8	56.2	21	6	AX804694	AX804694 Sequence
c	27	11.8	56.2	21	11	DOGC00505A	L77539 Canis famil
c	28	11.6	55.2	18	6	CQ786885	CQ786885 Sequence
c	29	11.6	55.2	20	4	DOGP17601	L24208 Dog (Clone:
	30	11.6	55.2	20	6	BD138203	BD138203 Antisense
	31	11.6	55.2	20	6	CQ794181	CQ794181 Sequence
	32	11.6	55.2	20	6	CQ800150	CQ800150 Sequence
	33	11.6	55.2	20	6	CQ831775	CQ831775 Sequence
	34	11.6	55.2	20	6	AR230770	AR230770 Sequence
c	35	11.6	55.2	20	6	AR312230	AR312230 Sequence
c	36	11.6	55.2	20	6	AR535425	AR535425 Sequence
c	37	11.6	55.2	20	6	AX093430	AX093430 Sequence
	38	11.6	55.2	20	6	AX167860	AX167860 Sequence
c	39	11.6	55.2	20	6	AX361094	AX361094 Sequence
c	40	11.6	55.2	20	6	BD015694	BD015694 Novel pro
c	41	11.6	55.2	20	6	BD094847	BD094847 Novel pro
c	42	11.6	55.2	20	6	BD096030	BD096030 Use of di
c	43	11.6	55.2	20	6	BD128305	BD128305 Utilizati
c	44	11.6	55.2	21	6	AR530713	AR530713 Sequence
c	45	11.6	55.2	21	6	AX096738	AX096738 Sequence
c	46	11.4	54.3	19	6	AR294751	AR294751 Sequence
c	47	11.4	54.3	20	6	AR055756	AR055756 Sequence
c	48	11.4	54.3	20	6	AX613897	AX613897 Sequence
c	49	11.2	53.3	17	6	AR402110	AR402110 Sequence
	50	11.2	53.3	17	6	AX578318	AX578318 Sequence
	51	11.2	53.3	17	6	AX578319	AX578319 Sequence
c	52	11.2	53.3	17	6	AX690584	AX690584 Sequence
c	53	11.2	53.3	17	6	AX690586	AX690586 Sequence
c	54	11.2	53.3	17	6	BD067610	BD067610 Enzymatic
	55	11.2	53.3	18	6	AR293947	AR293947 Sequence
	56	11.2	53.3	19	6	AR011904	AR011904 Sequence
c	57	11.2	53.3	19	6	AR292924	AR292924 Sequence
c	58	11.2	53.3	19	6	AX129248	AX129248 Sequence
c	59	11.2	53.3	19	6	AX129249	AX129249 Sequence
	60	11.2	53.3	19	6	AX571920	AX571920 Sequence
	61	11.2	53.3	20	6	AR129618	AR129618 Sequence
	62	11.2	53.3	20	6	AR129619	AR129619 Sequence
	63	11.2	53.3	20	6	AR129620	AR129620 Sequence
c	64	11.2	53.3	20	6	AR130183	AR130183 Sequence
	65	11.2	53.3	20	6	BD184497	BD184497 Method an
c	66	11.2	53.3	20	6	CQ858917	CQ858917 Sequence
	67	11.2	53.3	20	6	AR311962	AR311962 Sequence
	68	11.2	53.3	20	6	AX296902	AX296902 Sequence
	69	11.2	53.3	20	6	AX742644	AX742644 Sequence
c	70	11.2	53.3	20	11	DOGHOX7B	L77371 Canis famil
	71	11.2	53.3	21	6	BD241765	BD241765 Embryonic
	72	11.2	53.3	21	6	AR299909	AR299909 Sequence
	73	11.2	53.3	21	6	AR492271	AR492271 Sequence
c	74	11.2	53.3	21	6	AX250343	AX250343 Sequence
	75	11.2	53.3	21	6	AX928320	AX928320 Sequence
	76	11	52.4	12	6	AR167790	AR167790 Sequence
	77	11	52.4	12	6	E29674	E29674 Method for
	78	11	52.4	12	6	E38780	E38780 Method and
	79	11	52.4	12	6	E64206	E64206 Method for
	80	11	52.4	18	6	A51815	A51815 Sequence 11
	81	11	52.4	18	6	A51816	A51816 Sequence 12
	82	11	52.4	18	6	AR008099	AR008099 Sequence
	83	11	52.4	18	6	AR153938	AR153938 Sequence
c	84	11	52.4	20	6	AR172951	AR172951 Sequence
c	85	11	52.4	20	6	AR313970	AR313970 Sequence
c	86	11	52.4	20	6	AR337698	AR337698 Sequence
	87	11	52.4	20	6	AX404238	AX404238 Sequence
c	88	11	52.4	20	6	BD131971	BD131971 Oligonucl
c	89	11	52.4	21	6	CQ787036	CQ787036 Sequence
	90	11	52.4	21	6	AR531283	AR531283 Sequence
	91	11	52.4	21	6	AX097308	AX097308 Sequence
c	92	10.8	51.4	15	6	AR132841	AR132841 Sequence

93	10.8	51.4	17	6	BD255269	BD255269	Regulatio
94	10.8	51.4	17	6	BD255495	BD255495	Regulatio
95	10.8	51.4	17	6	BD255496	BD255496	Regulatio
96	10.8	51.4	17	6	BD255497	BD255497	Regulatio
97	10.8	51.4	17	6	AR186193	AR186193	Sequence
98	10.8	51.4	17	6	AR322824	AR322824	Sequence
99	10.8	51.4	17	6	AX217098	AX217098	Sequence
c 100	10.8	51.4	17	6	AX217837	AX217837	Sequence

ALIGNMENTS

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RESULT 1
AR116690
LOCUS       AR116690                  20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 3 from patent US 6133434.
ACCESSION   AR116690
VERSION     AR116690.1  GI:14097012
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Buell,G.Nutter., Surprenant,A. and Kawashima,E.
  TITLE     Purinergic receptor
  JOURNAL   Patent: US 6133434-A 3 17-OCT-2000;
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GGCGTATCTGAAG 15
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Db          1 GGCGTATCTGAAG 13


RESULT 2
AR275648
LOCUS       AR275648                  20 bp    DNA     linear   PAT 10-APR-2003
DEFINITION  Sequence 3 from patent US 6509163.
ACCESSION   AR275648
VERSION     AR275648.1  GI:29709099
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Buell,G.N., Surprenant,A. and Kawashima,E.
  TITLE     Methods of screening modulators of mammalian P2X7 purinergic
            receptors
  JOURNAL   Patent: US 6509163-A 3 21-JAN-2003;
FEATURES             Location/Qualifiers
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1.2e+05;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GGCGTATCTGAAG 15
              |||||||||||||
Db          1 GGCGTATCTGAAG 13


RESULT 3
AR402108/c
LOCUS       AR402108                  17 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 448 from patent US 6623962.
ACCESSION   AR402108
VERSION     AR402108.1  GI:40149558
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Akhtar,S., Fell,P. and McSwiggen,J.A.
  TITLE     Enzymatic nucleic acid treatment of diseases of conditions related
            to levels of epidermal growth factor receptors
  JOURNAL   Patent: US 6623962-A 448 23-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .17
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ORIGIN

  Query Match             61.0%;  Score 12.8;  DB 6;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 1.6e+05;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 GTATCTGAAGAGTCTG 21
              |||||  |||||||||
Db         16 GTATCGAAAGAGTCTG 1


RESULT 4
BD067608/c
LOCUS       BD067608                  17 bp    RNA     linear   PAT 27-AUG-2002
DEFINITION  Enzymatic nucleic acid treatment of diseases or conditions related
            to levels of epidermal growth factor receptors.
ACCESSION   BD067608
VERSION     BD067608.1  GI:22613211
KEYWORDS    JP 2001511003-A/448.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Akhtar,S., Fell,P. and Mcswiggen,J.A.
  TITLE     Enzymatic nucleic acid treatment of diseases or conditions related
            to levels of epidermal growth factor receptors
  JOURNAL   Patent: JP 2001511003-A 448 07-AUG-2001;
            RIBOZYME PHARMACEUTICALS INC,ASTON UNIV
COMMENT     OS   Unidentified
            PN   JP 2001511003-A/448
            PD   07-AUG-2001
            PF   14-JAN-1998 JP 1998532913
            PR   31-JAN-1997 US    60/036476,04-DEC-1997 US    08/985162 PI
            SAGHIR AKHTAR,PATRICIA FELL,JAMES A MCSWIGGEN PC
            C12N9/00,C07K14/71
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Enzymatic nucleic acid treatment of diseases or conditions  CC
                   related to
            CC   levels of epidermal growth factor receptors
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .17
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                     /db_xref="taxon:32644"
ORIGIN

  Query Match             61.0%;  Score 12.8;  DB 6;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 1.6e+05;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 GTATCTGAAGAGTCTG 21
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```
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Db         16 GTATCGAAAGAGTCTG 1


RESULT 5
A17234/c
LOCUS       A17234                    20 bp    DNA     linear   PAT 31-MAR-1994
DEFINITION  Oligonucleotide 20-mer BB9513 (SEQ ID NO: 134).
ACCESSION   A17234
VERSION     A17234.1  GI:513003
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   .
  TITLE     STEM CELL INHIBITING PROTEINS
  JOURNAL   Patent: WO 9313206-A 134 08-JUL-1993;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             61.0%;  Score 12.8;  DB 6;  Length 20;
  Best Local Similarity   87.5%;  Pred. No. 1.5e+05;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CTGGCGTATCTGAAGA 16
              ||| || |||||||||
Db         17 CTGACGCATCTGAAGA 2


RESULT 6
AR027617/c
LOCUS       AR027617                  20 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 134 from patent US 5856301.
ACCESSION   AR027617
VERSION     AR027617.1  GI:5938437
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Craig,S., Hunter,M.George., Edwards,R.Mark., Czaplewski,L.George.
            and Gilbert,R.James.
  TITLE     Stem cell inhibiting proteins
  JOURNAL   Patent: US 5856301-A 134 05-JAN-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             61.0%;  Score 12.8;  DB 6;  Length 20;
  Best Local Similarity   87.5%;  Pred. No. 1.5e+05;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CTGGCGTATCTGAAGA 16
              ||| || |||||||||
Db         17 CTGACGCATCTGAAGA 2


RESULT 7
AR402109/c
LOCUS       AR402109                  17 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 449 from patent US 6623962.
ACCESSION   AR402109
VERSION     AR402109.1  GI:40149559
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Akhtar,S., Fell,P. and McSwiggen,J.A.
  TITLE     Enzymatic nucleic acid treatment of diseases of conditions related
            to levels of epidermal growth factor receptors
  JOURNAL   Patent: US 6623962-A 449 23-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             58.1%;  Score 12.2;  DB 6;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 3.3e+05;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 GCGTATCTGAAGAGTCT 20
              | |||||  ||||||||
Db         17 GGGTATCGAAAGAGTCT 1


RESULT 8
AX690585/c
LOCUS       AX690585                  17 bp    DNA     linear   PAT 31-MAR-2003
DEFINITION  Sequence 3317 from Patent EP1281758.
ACCESSION   AX690585
VERSION     AX690585.1  GI:29413466
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Shannon,M., Gu,Y. and Nguyen,C.T.
  TITLE     Four human zinc-finger-containing proteins : mdz3, mdz4, mdz7 and
            mdz12
  JOURNAL   Patent: EP 1281758-A 3317 05-FEB-2003;
            Aeomica, Inc. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             58.1%;  Score 12.2;  DB 6;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 3.3e+05;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CTGGCGTATCTGAAGAG 17
              |||| || | |||||||
Db         17 CTGGAGTCTTTGAAGAG 1


RESULT 9
BD067609/c
LOCUS       BD067609                  17 bp    RNA     linear   PAT 27-AUG-2002
DEFINITION  Enzymatic nucleic acid treatment of diseases or conditions related
            to levels of epidermal growth factor receptors.
ACCESSION   BD067609
VERSION     BD067609.1  GI:22613212
KEYWORDS    JP 2001511003-A/449.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Akhtar,S., Fell,P. and Mcswiggen,J.A.
  TITLE     Enzymatic nucleic acid treatment of diseases or conditions related
            to levels of epidermal growth factor receptors
  JOURNAL   Patent: JP 2001511003-A 449 07-AUG-2001;
            RIBOZYME PHARMACEUTICALS INC,ASTON UNIV
COMMENT     OS   Unidentified
            PN   JP 2001511003-A/449
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            PD   07-AUG-2001
            PF   14-JAN-1998 JP 1998532913
            PR   31-JAN-1997 US    60/036476,04-DEC-1997 US    08/985162 PI
            SAGHIR AKHTAR,PATRICIA FELL,JAMES A MCSWIGGEN PC
            C12N9/00,C07K14/71
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Enzymatic nucleic acid treatment of diseases or conditions  CC
                 related to
            CC   levels of epidermal growth factor receptors
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             58.1%;  Score 12.2;  DB 6;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 3.3e+05;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 GCGTATCTGAAGAGTCT 20
              | |||||  ||||||||
Db         17 GGGTATCGAAAGAGTCT 1


RESULT 10
AR070817
LOCUS       AR070817                  20 bp    DNA     linear   PAT 18-FEB-2000
DEFINITION  Sequence 8 from patent US 5908773.
ACCESSION   AR070817
VERSION     AR070817.1  GI:7221705
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cesarman,E., Arvanitakis,L., Knowles,D.M. and Mesri,E.
  TITLE     KSHV positive cell lines
  JOURNAL   Patent: US 5908773-A 8 01-JUN-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             58.1%;  Score 12.2;  DB 6;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 3.3e+05;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 CGTATCTGAAGAGTCTG 21
              || | || |||||||||
Db          1 CGGAGCTAAAGAGTCTG 17


RESULT 11
AR104505
LOCUS       AR104505                  20 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 8 from patent US 6093806.
ACCESSION   AR104505
VERSION     AR104505.1  GI:12817213
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cesarman,E. and Knowles,D.M.
  TITLE     DNA encoding proteins of Kaposi's sarcoma associated herpesvirus
  JOURNAL   Patent: US 6093806-A 8 25-JUL-2000;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             58.1%;  Score 12.2;  DB 6;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 3.3e+05;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 CGTATCTGAAGAGTCTG 21
              || | || |||||||||
Db          1 CGGAGCTAAAGAGTCTG 17


RESULT 12
AX962823/c
LOCUS       AX962823                  20 bp    DNA     linear   PAT 14-JAN-2004
DEFINITION  Sequence 79 from Patent WO03104458.
ACCESSION   AX962823
VERSION     AX962823.1  GI:40881936
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Baker,B.F., Freier,S.M. and Dobie,K.W.
  TITLE     Antisense modulation of il-1 receptor-associated kinase-1
            expression
  JOURNAL   Patent: WO 03104458-A 79 18-DEC-2003;
            ISIS PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Antisense Oligonucleotide"
ORIGIN

  Query Match             58.1%;  Score 12.2;  DB 6;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 3.3e+05;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 GCGTATCTGAAGAGTCT 20
              ||||| ||| || ||||
Db         17 GCGTAGCTGGAGGGTCT 1


RESULT 13
AX737882/c
LOCUS       AX737882                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 3472 from Patent WO03025177.
ACCESSION   AX737882
VERSION     AX737882.1  GI:30517170
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 3472 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             57.1%;  Score 12;  DB 6;  Length 17;
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  Best Local Similarity   100.0%;  Pred. No. 4.2e+05;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 TATCTGAAGAGT 18
              ||||||||||||
Db         17 TATCTGAAGAGT 6


RESULT 14
AR328335
LOCUS       AR328335                  16 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 5737 from patent US 6566127.
ACCESSION   AR328335
VERSION     AR328335.1  GI:33714143
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 5737 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="unknown"
                     /mol_type="unassigned RNA"
ORIGIN

  Query Match             56.2%;  Score 11.8;  DB 6;  Length 16;
  Best Local Similarity   86.7%;  Pred. No. 5.5e+05;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GGCGTATCTGAAGAG 17
              | |||| ||||||||
Db          2 GACGTAACTGAAGAG 16


RESULT 15
AR007304
LOCUS       AR007304                  17 bp    DNA     linear   PAT 04-DEC-1998
DEFINITION  Sequence 18 from patent US 5750390.
ACCESSION   AR007304
VERSION     AR007304.1  GI:3966788
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Thompson,J.D. and Draper,K.G.
  TITLE     Method and reagent for treatment of diseases caused by expression
            of the bcl-2 gene
  JOURNAL   Patent: US 5750390-A 18 12-MAY-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             56.2%;  Score 11.8;  DB 6;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5.5e+05;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 GTATCTGAAGAGTCT 20
              || |||||||| |||
Db          3 GTCTCTGAAGACTCT 17


RESULT 16
AR053990
LOCUS       AR053990                  17 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 4 from patent US 5834302.
ACCESSION   AR053990
VERSION     AR053990.1  GI:5978852
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Racaniello,V., Tatem,J.Marie. and Weeks-Levy,C.L.
  TITLE     Method for producing RNA viruses from CDNA
  JOURNAL   Patent: US 5834302-A 4 10-NOV-1998;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             56.2%;  Score 11.8;  DB 6;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5.5e+05;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GGCGTATCTGAAGAG 17
              |||||||||||  ||
Db          1 GGCGTATCTGACAAG 15


RESULT 17
AR135992
LOCUS       AR135992                  17 bp    DNA     linear   PAT 16-JUN-2001
DEFINITION  Sequence 4 from patent US 6136570.
ACCESSION   AR135992
VERSION     AR135992.1  GI:14476664
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Racaniello,V., Tatem,J.Marie. and Weeks-Levy,C.L.
  TITLE     Method for producing RNA viruses from cDNA
  JOURNAL   Patent: US 6136570-A 4 24-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             56.2%;  Score 11.8;  DB 6;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 5.5e+05;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GGCGTATCTGAAGAG 17
              |||||||||||  ||
Db          1 GGCGTATCTGACAAG 15


RESULT 18
I22067
LOCUS       I22067                    17 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 4 from patent US 5525715.
ACCESSION   I22067
VERSION     I22067.1  GI:1602421
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Racaniello,V., Tatem,J.M. and Weeks-Levy,C.L.
  TITLE     Method for producing RNA viruses from cDNA
  JOURNAL   Patent: US 5525715-A 4 11-JUN-1996;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN
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  Query Match            56.2%;  Score 11.8;  DB 6;  Length 17;
  Best Local Similarity  86.7%;  Pred. No. 5.5e+05;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GGCGTATCTGAAGAG 17
              ||||||||||  ||
Db          1 GGCGTATCTGACAAG 15


RESULT 19
AR327036
LOCUS       AR327036                  17 bp    RNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 4438 from patent US 6566127.
ACCESSION   AR327036
VERSION     AR327036.1  GI:33712844
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Pavco,P., McSwiggen,J.A., Stinchcomb,D.T. and Escobedo,J.
  TITLE     Method and reagent for the treatment of diseases or conditions
            related to levels of vascular endothelial growth factor receptor
  JOURNAL   Patent: US 6566127-A 4438 20-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned RNA"
ORIGIN

  Query Match            56.2%;  Score 11.8;  DB 6;  Length 17;
  Best Local Similarity  86.7%;  Pred. No. 5.5e+05;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GGCGTATCTGAAGAG 17
              | ||||  ||||||||
Db          1 GACGTAACTGAAGAG 15


RESULT 20
AR402107/c
LOCUS       AR402107                  17 bp    DNA     linear   PAT 18-DEC-2003
DEFINITION  Sequence 447 from patent US 6623962.
ACCESSION   AR402107
VERSION     AR402107.1  GI:40149557
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Akhtar,S., Fell,P. and McSwiggen,J.A.
  TITLE     Enzymatic nucleic acid treatment of diseases of conditions related
            to levels of epidermal growth factor receptors
  JOURNAL   Patent: US 6623962-A 447 23-SEP-2003;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match            56.2%;  Score 11.8;  DB 6;  Length 17;
  Best Local Similarity  86.7%;  Pred. No. 5.5e+05;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 TATCTGAAGAGTCTG 21
              ||||  |||||||||
Db         17 TATCGAAAGAGTCTG 3


RESULT 21
AX217836/c
LOCUS       AX217836                  17 bp    RNA     linear   PAT 07-SEP-2001
DEFINITION  Sequence 3278 from Patent WO0159103.
ACCESSION   AX217836
VERSION     AX217836.1  GI:15527897
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Blatt,L., Mcswiggen,J. and Chowrira,B.M.
  TITLE     Method and reagent for the modulation and diagnosis of cd20 and
            nogo gene expression
  JOURNAL   Patent: WO 0159103-A 3278 16-AUG-2001;
            RIBOZYME PHARMACEUTICALS, INC. (US) ; Blatt, Lawrence (US) ;
            McSwiggen, James (US) ; Chowrira, Bharat M. (US)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32630"
                     /note="Nucleic Acid"
ORIGIN

  Query Match            56.2%;  Score 11.8;  DB 6;  Length 17;
  Best Local Similarity  86.7%;  Pred. No. 5.5e+05;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 GCGTATCTGAAGAGT 18
              |||||| || |||||
Db         16 GCGTATGTGCAGAGT 2


RESULT 22
BD067607/c
LOCUS       BD067607                  17 bp    RNA     linear   PAT 27-AUG-2002
DEFINITION  Enzymatic nucleic acid treatment of diseases or conditions related
            to levels of epidermal growth factor receptors.
ACCESSION   BD067607
VERSION     BD067607.1  GI:22613210
KEYWORDS    JP 2001511003-A/447.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Akhtar,S., Fell,P. and Mcswiggen,J.A.
  TITLE     Enzymatic nucleic acid treatment of diseases or conditions related
            to levels of epidermal growth factor receptors
  JOURNAL   Patent: JP 2001511003-A 447 07-AUG-2001;
            RIBOZYME PHARMACEUTICALS INC,ASTON UNIV
COMMENT     OS   Unidentified
            PN   JP 2001511003-A/447
            PD   07-AUG-2001
            PF   14-JAN-1998 JP 1998532913
            PR   31-JAN-1997 US    60/036476,04-DEC-1997 US    08/985162 PI
            SAGHIR AKHTAR,PATRICIA FELL,JAMES A MCSWIGGEN PC
            C12N9/00,C07K14/71
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Enzymatic nucleic acid treatment of diseases or conditions  CC
                 related to
            CC   levels of epidermal growth factor receptors
            FH   Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic RNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match            56.2%;  Score 11.8;  DB 6;  Length 17;
  Best Local Similarity  86.7%;  Pred. No. 5.5e+05;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;
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Qy          7 TATCTGAAGAGTCTG 21
              ||||  |||||||||
Db         17 TATCGAAAGAGTCTG 3


RESULT 23
AR160744/c
LOCUS       AR160744                  20 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 38 from patent US 6255110.
ACCESSION   AR160744
VERSION     AR160744.1  GI:16225330
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Cowsert,L.M. and Wyatt,J.
  TITLE     Antisense modulation of ARA70 expression
  JOURNAL   Patent: US 6255110-A 38 03-JUL-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             56.2%;  Score 11.8;  DB 6;  Length 20;
  Best Local Similarity   86.7%;  Pred. No. 5.4e+05;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CTGGCGTATCTGAAG 15
              |||||  ||||||||
Db         16 CTGGCCAATCTGAAG 2


RESULT 24
AR310829
LOCUS       AR310829                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 1366 from patent US 6559294.
ACCESSION   AR310829
VERSION     AR310829.1  GI:31704255
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 1366 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             56.2%;  Score 11.8;  DB 6;  Length 20;
  Best Local Similarity   86.7%;  Pred. No. 5.4e+05;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 GCGTATCTGAAGAGT 18
              ||| |||||| ||||
Db          1 GCGGATCTGAGGAGT 15


RESULT 25
BD238283/c
LOCUS       BD238283                  21 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Accelerated identification of polymorphism of single nucleotide in
            genome sequencing and alignment of clones.
ACCESSION   BD238283
VERSION     BD238283.1  GI:33048053
KEYWORDS    JP 2002534098-A/118.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Barany,F., Liu,J., Kirk,B.W., Zirvi,M., Gerry,N.P. and Paty,P.B.
  TITLE     Accelerated identification of polymorphism of single nucleotide in
            genome sequencing and alignment of clones
  JOURNAL   Patent: JP 2002534098-A 118 15-OCT-2002;
            CORNELL RESEARCH FOUNDATION INC, SLOAN KETTERING INSTITUTE FOR
            CANCER RESEARCH
COMMENT     OS   Artificial Sequence
            PN   JP 2002534098-A/118
            PD   15-OCT-2002
            PF   05-JAN-2000 JP 2000592447
            PR   06-JAN-1999 US    60/114881
            PI   FRANCIS BARANY,JIANZHAO LIU,BRIAN W KIRK,MONIB ZIRVI,NORMAN P
            PI   GERRY,
            PI   PHILIP B PATY
            PC   C12N15/09,C12Q1/68,G01N33/53,G01N33/566,G01N37/00,G01N37/00//
            PC   G01N33/50,
            PC   C12N15/00
            CC   Description of Artificial Sequence: probe/primer FH   Key
              Location/Qualifiers
            FT   source          1. .21
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             56.2%;  Score 11.8;  DB 6;  Length 21;
  Best Local Similarity   86.7%;  Pred. No. 5.4e+05;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CTGGCGTATCTGAAG 15
              |||| || |||||||
Db         17 CTGGTGTGTCTGAAG 3


RESULT 26
AX804694/c
LOCUS       AX804694                  21 bp    DNA     linear   PAT 25-NOV-2003
DEFINITION  Sequence 862 from Patent WO03060160.
ACCESSION   AX804694
VERSION     AX804694.1  GI:38521835
KEYWORDS    .
SOURCE      Oreochromis niloticus (Nile tilapia)
  ORGANISM  Oreochromis niloticus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
            Labroidei; Cichlidae; Oreochromis.
REFERENCE   1
  AUTHORS   Lie,Y., Slettan,A., Hoeyum,M. and Lingaas,F.
  TITLE     Verification of food origin based on nucleic acid pattern
            recognition
  JOURNAL   Patent: WO 03060160-A 862 24-JUL-2003;
            Genomar ASA (NO)
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Oreochromis niloticus"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:8128"
ORIGIN

  Query Match             56.2%;  Score 11.8;  DB 6;  Length 21;
  Best Local Similarity   86.7%;  Pred. No. 5.4e+05;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GGCGTATCTGAAGAG 17
              ||||||| || ||||
Db         15 GGCGTATTTGGAGAG 1
```

```
RESULT 27
DOGC00505A/c
LOCUS       DOGC00505A               21 bp    DNA     linear   STS 10-APR-1996
DEFINITION  Canis familiaris STS microsatellite marker (repeat motif in
            reference clone (GT)9T(TG)4(TA)4(TG)7) DNA, sequence tagged site.
ACCESSION   L77539
VERSION     L77539.1  GI:1261663
KEYWORDS    STS; PCR identification; microsatellite; sequence tagged site.
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Yuzbasiyan-Gurkan,V., Cao,Y., Gurkan,M., Yuxun,W., Venta,P.J.,
            Brewer,G.J. and Blanton,S.H.
  TITLE     Microsatelite markers for the canine genome
  JOURNAL   Unpublished (1996)
COMMENT     Original source text: Canis familiaris female adult peripheral
            blood DNA.
            Hotstart, touchdown PCR. Starting at 60 C, decreasing by one degree
            for 10 cycles,  25 further cylces at  52.  Motif and size of
            product as found in the reference dog.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9615"
                     /sex="female"
                     /cell_type="white blood cells"
                     /tissue_type="peripheral blood"
                     /dev_stage="adult"
     STS             1. .21
                     /note="product size 230"
ORIGIN

  Query Match            56.2%;  Score 11.8;  DB 11;  Length 21;
  Best Local Similarity  86.7%;  Pred. No. 5.4e+05;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 TATCTGAAGAGTCTG 21
              |||||||||  ||||
Db         15 TATCTGAAGGCTCTG 1


RESULT 28
CQ786885/c
LOCUS       CQ786885                 18 bp    DNA     linear   PAT 24-MAR-2004
DEFINITION  Sequence 62 from Patent WO2004021010.
ACCESSION   CQ786885
VERSION     CQ786885.1  GI:45721877
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Nakamura,Y. and Furukawa,Y.
  TITLE     Method of diagnosing colon and gastric cancers
  JOURNAL   Patent: WO 2004021010-A 62 11-MAR-2004;
            Oncotherapy Science, Inc. (JP); Japan as represented by the
            president of the university o f Tokyo (JP)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Artificially synthesized S-oligonucleotide"
ORIGIN

  Query Match            55.2%;  Score 11.6;  DB 6;  Length 18;
  Best Local Similarity  77.8%;  Pred. No. 7e+05;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 GCGTATCTGAAGAGTCTG 21
              | | || ||||| |||||
Db         18 GTGGATGTGAAGTGTCTG 1


RESULT 29
DOGP17601/c
LOCUS       DOGP17601                20 bp    DNA     linear   MAM 16-JAN-1996
DEFINITION  Dog (Clone: CXX.176) primer for STS 176, 5' end.
ACCESSION   L24208
VERSION     L24208.1  GI:401855
KEYWORDS    PCR identification; PCR primer; STS.
SEGMENT     1 of 2
SOURCE      Canis familiaris (dog)
  ORGANISM  Canis familiaris
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Ostrander,E.A., Mapa,F.A., Yee,M. and Rine,J.
  TITLE     One hundred and one new simple sequence repeat-based markers for
            the canine genome
  JOURNAL   Mamm. Genome 6 (3), 192-195 (1995)
  MEDLINE   95268214
   PUBMED   7749226
COMMENT     Original source text: Canis familiaris (library: E. Ostrander, in
            pBluescript+) adult spleen DNA.
            Submitted by:   Fred Hutchinson Cancer Research Center
            Transplantation Biology Dept   1124 Columbia; Mailstop M318
            Seattle, WA 98104, USA   e-mail: EAOstrander@lbl.gov     PCR
            Buffer: PCR buffer (Perkin-Elmer/Cetus)   PCR Profile:
            Denaturation:    94 degrees C for 1.00 minute Annealing:       55
            or 59 degrees C for 0.45 minutes   Polymerization:  74 degrees C
            for 1.00 minutes   PCR Cycles:      33   Final Extension:  74
            degrees C for 5.00 minutes.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Canis familiaris"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9615"
                     /tissue_type="spleen"
                     /dev_stage="adult"
                     /tissue_lib="E. Ostrander, in pBluescript+"
     primer_bind     1. .20
ORIGIN

  Query Match            55.2%;  Score 11.6;  DB 4;  Length 20;
  Best Local Similarity  77.8%;  Pred. No. 6.9e+05;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 GCGTATCTGAAGAGTCTG 21
              | || |||| |||| |||
Db         19 GTGTCTCTGGAGAGCCTG 2


RESULT 30
BD138203
LOCUS       BD138203                 20 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Antisense modulation of human MDM2 expression.
ACCESSION   BD138203
VERSION     BD138203.1  GI:23233148
KEYWORDS    JP 2002508944-A/129.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Miraglia,L.J., Nero,P., Graham,M.J., Monia,B.P. and Cowsert,L.M.
  TITLE     Antisense modulation of human MDM2 expression
  JOURNAL   Patent: JP 2002508944-A 129 26-MAR-2002;
            ISIS PHARMACEUTICALS INC
COMMENT     OS   Unidentified
            PN   JP 2002508944-A/129
            PD   26-MAR-2002
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            PF   26-MAR-1999 JP 2000538025
            PR   26-MAR-1998 US    09/048810
            PI   LOREN J MIRAGLIA,PAMELA NERO,MARK J GRAHAM,BRETT P MONIA,LEX M

            PI   COWSERT
            PC   C12N15/09,A61K48/00,A61P9/10,A61P17/06,A61P35/00,C07H21/04//
            PC   C12Q1/68,
            PC   C12N15/00
            CC   Strandedness: Single;
            CC   Topology: Linear;
            CC   Antisense modulation of human MDM2 expression FH   Key
                Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Unidentified'.
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="unidentified"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:32644"
ORIGIN

  Query Match             55.2%;  Score 11.6;  DB 6;  Length 20;
  Best Local Similarity   77.8%;  Pred. No. 6.9e+05;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 TGGCGTATCTGAAGAGTC 19
              ||||||  ||| ||| ||
Db          1 TGGCGTCCCTGTAGATTC 18


RESULT 31
CQ794181
LOCUS       CQ794181                 20 bp    DNA     linear   PAT 19-APR-2004
DEFINITION  Sequence 101 from Patent EP1403384.
ACCESSION   CQ794181
VERSION     CQ794181.1  GI:46406823
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Meijer,C.J. and Snijders,P.J.
  TITLE     Method for detecting and typing of cutaneous HPV and primers and
            probes for use therein
  JOURNAL   Patent: EP 1403384-A 101 31-MAR-2004;
            Stichting Researchfonds Pathologie (NL)
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="type-specific detection probe RLBskinHPV 37"
ORIGIN

  Query Match             55.2%;  Score 11.6;  DB 6;  Length 20;
  Best Local Similarity   77.8%;  Pred. No. 6.9e+05;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CTGGCGTATCTGAAGAGT 18
              ||||  |||  |||||||
Db          3 CTGGTATATTGGAAGAGT 20


RESULT 32
CQ800150
LOCUS       CQ800150                 20 bp    DNA     linear   PAT 29-APR-2004
DEFINITION  Sequence 101 from Patent WO2004029302.
ACCESSION   CQ800150
VERSION     CQ800150.1  GI:46849070
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Meijer,C.J. and Snijders,P.J.
  TITLE     Method for detecting and typing of cutaneous hpv and primers and
            probes for use therein
  JOURNAL   Patent: WO 2004029302-A 101 08-APR-2004;
            Stichting Researchfonds Pathologie (NL)
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="type-specific detection probe RLBskinHPV 37"
ORIGIN

  Query Match             55.2%;  Score 11.6;  DB 6;  Length 20;
  Best Local Similarity   77.8%;  Pred. No. 6.9e+05;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CTGGCGTATCTGAAGAGT 18
              ||||  |||  |||||||
Db          3 CTGGTATATTGGAAGAGT 20


RESULT 33
CQ831775
LOCUS       CQ831775                 20 bp    DNA     linear   PAT 29-JUL-2004
DEFINITION  Sequence 29 from Patent WO2004056994.
ACCESSION   CQ831775
VERSION     CQ831775.1  GI:50831650
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Gouliaev,A.H., Holtmann,A., Pedersen,H. and Franch,T.
  TITLE     Quasirandom structure and function guided synthesis methods
  JOURNAL   Patent: WO 2004056994-A 29 08-JUL-2004;
            Nuevolution A/S (DK)
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="synthetic construct"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32630"
                      /note="The oligonucleotides were prepared by conventional
                      phosphoramidit e synthesis"
ORIGIN

  Query Match             55.2%;  Score 11.6;  DB 6;  Length 20;
  Best Local Similarity   77.8%;  Pred. No. 6.9e+05;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 GCGTATCTGAAGAGTCTG 21
              || ||| ||| || ||||
Db          1 GCCTATGTGACGAATCTG 18


RESULT 34
AR230770
LOCUS       AR230770                 20 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 30 from patent US 6451602.
ACCESSION   AR230770
VERSION     AR230770.1  GI:27271557
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Popoff,I. and Cowsert,L.M.
  TITLE     Antisense modulation of PARP expression
  JOURNAL   Patent: US 6451602-A 30 17-SEP-2002;
FEATURES              Location/Qualifiers
     source           1. .20
                      /organism="unknown"
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                     /mol_type="genomic DNA"
ORIGIN

  Query Match           55.2%;  Score 11.6;  DB 6;  Length 20;
  Best Local Similarity   77.8%;  Pred. No. 6.9e+05;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 GCGTATCTGAAGAGTCTG 21
              || |||| ||||| || |
Db          1 GCTTATCCGAAGACTCCG 18


RESULT 35
AR312230/c
LOCUS       AR312230                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 2767 from patent US 6559294.
ACCESSION   AR312230
VERSION     AR312230.1  GI:31705656
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 2767 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           55.2%;  Score 11.6;  DB 6;  Length 20;
  Best Local Similarity   77.8%;  Pred. No. 6.9e+05;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 GCGTATCTGAAGAGTCTG 21
              || | |||||| || |||
Db         20 GCTTCTCTGAACAGACTG 3


RESULT 36
AR535425/c
LOCUS       AR535425                  20 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 12 from patent US 6737245.
ACCESSION   AR535425
VERSION     AR535425.1  GI:53926637
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Francis,K.P., Contag,P.R. and Joh,D.J.
  TITLE     Luciferase expression cassettes and methods of use
  JOURNAL   Patent: US 6737245-A 12 18-MAY-2004;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           55.2%;  Score 11.6;  DB 6;  Length 20;
  Best Local Similarity   77.8%;  Pred. No. 6.9e+05;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 GCGTATCTGAAGAGTCTG 21
              || | ||||| |||| ||
Db         19 GCATCTCTGAGGAGTGTG 2


RESULT 37
AX093430/c
LOCUS       AX093430                  20 bp    DNA     linear   PAT 30-MAR-2001
DEFINITION  Sequence 12 from Patent WO0118195.
ACCESSION   AX093430
VERSION     AX093430.1  GI:13509880
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Francis,K.P., Contag,P.R. and Joh,D.J.
  TITLE     Luciferase expression cassettes and methods of use
  JOURNAL   Patent: WO 0118195-A 12 15-MAR-2001;
            Xenogen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="LUXA-REV"
ORIGIN

  Query Match           55.2%;  Score 11.6;  DB 6;  Length 20;
  Best Local Similarity   77.8%;  Pred. No. 6.9e+05;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 GCGTATCTGAAGAGTCTG 21
              || | ||||| |||| ||
Db         19 GCATCTCTGAGGAGTGTG 2


RESULT 38
AX167860
LOCUS       AX167860                  20 bp    DNA     linear   PAT 03-JUL-2001
DEFINITION  Sequence 44 from Patent WO0142307.
ACCESSION   AX167860
VERSION     AX167860.1  GI:14597179
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Saito,K., Ohe,N. and Satoh,H.
  TITLE     Mutant er_g(a) and test systems for transactivation
  JOURNAL   Patent: WO 0142307-A 44 14-JUN-2001;
            Sumitomo Chemical Company, Limited (JP)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Designed oligonucleotide primer for PCR"
ORIGIN

  Query Match           55.2%;  Score 11.6;  DB 6;  Length 20;
  Best Local Similarity   77.8%;  Pred. No. 6.9e+05;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 GCGTATCTGAAGAGTCTG 21
              || |  |||||| |||||
Db          2 GCTTCACTGAAGGGTCTG 19


RESULT 39
AX361094/c
LOCUS       AX361094                  20 bp    DNA     linear   PAT 15-FEB-2002
DEFINITION  Sequence 15 from Patent WO0208431.
ACCESSION   AX361094
VERSION     AX361094.1  GI:18693753
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
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  AUTHORS   Francis,K.P. and Purchio,A.F.
  TITLE     Compositions and methods for use thereof in modifying the genomes
            of microorganisms
  JOURNAL   Patent: WO 0208431-A 15 31-JAN-2002;
            Xenogen Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Primer LuxA-Rev"
ORIGIN

  Query Match             55.2%;  Score 11.6;  DB 6;  Length 20;
  Best Local Similarity   77.8%;  Pred. No. 6.9e+05;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 GCGTATCTGAAGAGTCTG 21
              || .| ||||| |||| ||
Db         19 GCATCTCTGAGGAGTGTG 2


RESULT 40
BD015694/c
LOCUS       BD015694                  20 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Novel protein and DNA thereof.
ACCESSION   BD015694
VERSION     BD015694.1  GI:22556831
KEYWORDS    JP 2001204480-A/9.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Nakanishi,A. and Morita,S.
  TITLE     Novel protein and DNA thereof
  JOURNAL   Patent: JP 2001204480-A 9 31-JUL-2001;
            TAKEDA CHEMICAL INDUSTRIES LTD
COMMENT     OS   Artificial Sequence
            PN   JP 2001204480-A/9
            PD   31-JUL-2001
            PF   14-NOV-2000 JP 2000347107
            PI   ATSUSHI NAKANISHI,SHIGERU MORITA
            PC   C12N15/09,A61K38/00,A61K45/00,A61K48/00,A61P11/00,A61P11/06,
            PC   A61P31/04,
            PC   A61P31/06,A61P31/12,A61P31/18,A61P37/02,A61P37/08,A61P43/00,
            PC   C07K16/40,
            PC   C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N9/34,G01N33/15,G01N33/
            PC   50//
            PC   C12P21/08,C12N15/00,A61K37/02,C12N5/00
            CC   Primer
            FH   Key             Location/Qualifiers
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            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match             55.2%;  Score 11.6;  DB 6;  Length 20;
  Best Local Similarity   77.8%;  Pred. No. 6.9e+05;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CTGGCGTATCTGAAGAGT 18
              ||| ||  ||||| ||||
Db         19 CTGACGGTTCTGAGGAGT 2


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Job time : 1571 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 12, 2005, 08:59:07 ; Search time 238 Seconds
(without alignments)
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Title: US-09-743-825-8
Perfect score: 21
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 2380332

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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2: geneseqn1990s:*
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4: geneseqn2001as:*
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6: geneseqn2002as:*
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11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	21	100.0	21	3	AAZ50445	Aaz50445 EST R0050
c	2	13.8	65.7	20	12	ADJ85951	Adj85951 Nucleic a
c	3	13.6	64.8	20	2	AAZ05689	Aaz05689 PCR prime
	4	13	61.9	20	4	AAC63691	Aac63691 Rat P2X_7
	5	13	61.9	20	9	ADA09833	Ada09833 Antisense
c	6	12.8	61.0	17	2	AAV97668	Aav97668 Human EGF
c	7	12.8	61.0	20	12	ADJ85562	Adj85562 Nucleic a
	8	12.8	61.0	20	12	ADK96254	Adk96254 Primer of
	9	12.8	61.0	21	10	ADF50105	Adf50105 Human BCL
c	10	12.8	61.0	21	10	ADF50117	Adf50117 Human BCL
c	11	12.8	61.0	21	10	ADF50125	Adf50125 Human BCL
c	12	12.8	61.0	21	10	ADF50109	Adf50109 Human BCL
	13	12.8	61.0	21	10	ADG29696	Adg29696 BCL2-targ
c	14	12.8	61.0	21	10	ADG29693	Adg29693 BCL2-targ
c	15	12.8	61.0	21	10	ADG29700	Adg29700 BCL2-targ
c	16	12.4	59.0	19	12	ADQ61043	Adq61043 Anti-FRK
	17	12.4	59.0	20	12	ADI79541	Adi79541 Human HMG
c	18	12.4	59.0	20	12	ADI79738	Adi79738 Human HMG
c	19	12.2	58.1	17	2	AAV97669	Aav97669 Human EGF
c	20	12.2	58.1	17	8	ADB02331	Adb02331 Human MDZ
	21	12.2	58.1	20	2	AAV29903	Aav29903 3' PCR pr
	22	12.2	58.1	20	2	AAV31711	Aav31711 Kaposi's
c	23	12.2	58.1	20	10	AAD61207	Aad61207 Human Shi
c	24	12.2	58.1	20	12	ADH50671	Adh50671 Human IRA
c	25	12	57.1	17	10	ADI50969	Adi50969 Human tum
c	26	12	57.1	20	4	AAC92623	Aac92623 Human nuc
c	27	12	57.1	20	12	ADP68593	Adp68593 Human PPA
	28	12	57.1	20	12	ADP68748	Adp68748 Human PPA
c	29	12	57.1	21	3	AAA46172	Aaa46172 PCR prime
c	30	12	57.1	21	4	AAF97151	Aaf97151 Human gen
	31	11.8	56.2	17	2	AAQ51964	Aaq51964 BCL-2 mRN
c	32	11.8	56.2	17	2	AAV97667	Aav97667 Human EGF
c	33	11.8	56.2	17	4	ABK03278	Abk03278 Human CD2
	34	11.8	56.2	17	12	ADF92273	Adf92273 Human cyt
	35	11.8	56.2	19	12	ADQ61034	Adq61034 Anti-FLT1
c	36	11.8	56.2	19	13	ADR79337	Adr79337 Human apo
c	37	11.8	56.2	19	13	ADR80012	Adr80012 Human apo
c	38	11.8	56.2	19	13	ADR75873	Adr75873 Human apo
c	39	11.8	56.2	19	13	ADR77702	Adr77702 Human apo
c	40	11.8	56.2	19	13	ADR78491	Adr78491 Human apo
c	41	11.8	56.2	19	13	ADR77068	Adr77068 Human apo
	42	11.8	56.2	20	2	AAX92065	Aax92065 PCR prime
c	43	11.8	56.2	20	4	AAH25254	Aah25254 Antisense
c	44	11.8	56.2	20	12	ADI29104	Adi29104 Antisense
	45	11.8	56.2	20	12	ADI29174	Adi29174 Human MAR
	46	11.8	56.2	20	13	ADQ88807	Adq88807 Human HIF
c	47	11.8	56.2	21	2	ADG77200	Adg77200 Canine di
c	48	11.8	56.2	21	3	AAA57654	Aaa57654 PCR prime
c	49	11.8	56.2	21	10	ADD20227	Add20227 Oreochrom
	50	11.8	56.2	21	12	ADJ97442	Adj97442 Human Flt
c	51	11.6	55.2	18	12	ADL66406	Adl66406 Human LEM
	52	11.6	55.2	20	2	AAZ37599	Aaz37599 Human mdm
c	53	11.6	55.2	20	2	AAX93441	Aax93441 PCR prime
	54	11.6	55.2	20	4	AAS45609	Aas45609 Human PAR
	55	11.6	55.2	20	4	AAH56991	Aah56991 Human oes
	56	11.6	55.2	20	4	AAF80753	Aaf80753 Human mdm
c	57	11.6	55.2	20	4	AAS00300	Aas00300 Primer LU
c	58	11.6	55.2	20	4	AAH42021	Aah42021 Disease t
c	59	11.6	55.2	20	5	AAH46137	Aah46137 Mouse Gob
	60	11.6	55.2	20	5	AAS29368	Aas29368 Human mdm
c	61	11.6	55.2	20	6	ABK48015	Abk48015 Transposo
c	62	11.6	55.2	20	6	ABQ81566	Abq81566 Luciferas
c	63	11.6	55.2	20	8	ABZ76183	Abz76183 A. thalia
	64	11.6	55.2	20	10	ADD21564	Add21564 Human mdm
c	65	11.6	55.2	20	10	ABX14046	Abx14046 PCR prime
	66	11.6	55.2	20	12	ADO51090	Ado51090 Human BCL
c	67	11.6	55.2	20	12	ADP85595	Adp85595 Human EMA
	68	11.6	55.2	21	2	AAT14321	Aat14321 Primer #1
c	69	11.4	54.3	19	3	AAZ72130	Aaz72130 Human bia
	70	11.4	54.3	20	9	ADA89290	Ada89290 Human IBD
	71	11.4	54.3	20	10	ADA66509	Ada66509 Transform
c	72	11.4	54.3	20	11	ADM65775	Adm65775 Human Y c
c	73	11.4	54.3	20	12	ADH58733	Adh58733 Human CDC
c	74	11.4	54.3	20	12	ADI79866	Adi79866 Mouse HMG
	75	11.4	54.3	20	12	ADI79673	Adi79673 Mouse HMG
	76	11.4	54.3	20	12	ADL17929	Adl17929 Antisense
	77	11.4	54.3	20	12	ADL61397	Adl61397 Human pro
	78	11.4	54.3	20	12	ADM14341	Adm14341 Human mPG
	79	11.4	54.3	20	12	ADM14657	Adm14657 Human mPG
	80	11.4	54.3	20	12	ADM14768	Adm14768 Human mPG
	81	11.4	54.3	20	12	ADM14234	Adm14234 Human mPG
	82	11.4	54.3	20	12	ADM14290	Adm14290 Human mPG
	83	11.4	54.3	20	12	ADM14923	Adm14923 Human mPG
	84	11.4	54.3	20	12	ADM14365	Adm14365 Human mPG
	85	11.4	54.3	20	12	ADM14507	Adm14507 Human mPG
	86	11.4	54.3	21	4	AAF97721	Aaf97721 Human gen
c	87	11.4	54.3	21	12	ADO27101	Ado27101 Human HIF
c	88	11.4	54.3	21	13	ADR74087	Adr74087 Allele sp
c	89	11.2	53.3	17	2	AAV97670	Aav97670 Human EGF
	90	11.2	53.3	17	6	ABK55785	Abk55785 Human CLC
	91	11.2	53.3	17	6	ABK55786	Abk55786 Human CLC
c	92	11.2	53.3	17	6	ACN02458	Acn02458 WNV Inozy
c	93	11.2	53.3	17	6	ACN00743	Acn00743 WNV Hamme

c	94	11.2	53.3	17	8	ADB02332	Adb02332 Human MDZ
c	95	11.2	53.3	17	8	ADB02330	Adb02330 Human MDZ
	96	11.2	53.3	17	11	ADL47815	Adl47815 Human IKK
	97	11.2	53.3	18	3	AAZ71326	Aaz71326 Human bia
	98	11.2	53.3	19	2	AAV27078	Aav27078 Primer YA
c	99	11.2	53.3	19	3	AAA82881	Aaa82881 cdk4 ribo
c	100	11.2	53.3	19	3	AAA82880	Aaa82880 cdk4 ribo

ALIGNMENTS

RESULT 1
AAZ50445
ID AAZ50445 standard; DNA; 21 BP.
XX
AC AAZ50445;
XX
DT 18-MAY-2000 (first entry)
XX
DE EST R00504-specific primer 2.
XX
KW PB39; human; prostate cancer; PC; chromosome 11p11.1-11.2; cancer;
KW prostate epithelium; splicing mechanism; early diagnosis; progression;
KW precancerous cell; metastatic potential; non-neoplastic prostate disease;
KW expressed sequence tag; EST; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200005376-A1.
XX
PD 03-FEB-2000.
XX
PF 23-JUL-1999; 99WO-US016831.
XX
PR 24-JUL-1998; 98US-0094137P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Chuaqui RF, Cole KA, Liotta LA;
XX
DR WPI; 2000-182700/16.
XX
PT Novel gene which is dysregulated in prostate cancer useful for diagnosing
PT cancer.
XX
PS Claim 5; Page 16; 51pp; English.
XX
CC The present sequence is the EST AAR00504-specific PCR primer, used for
CC amplification of sequences contained within the EST AAR00504. It is
CC useful to probe the gene overexpressed in prostate cancer epithelium and
CC to analyse the differential expression of the EST. The PB39 gene that is
CC dysregulated in prostate cancer is isolated from human pancreas cDNA
CC library and has homology to the EST AAR00504. PB39 gene is located on
CC chromosome 11p11.1-11.2. Abnormally high concentrations of PB39 are found
CC in prostate tissue derived from prostate cancer (PC) epithelium. PB39
CC sequence is useful for detection of precancerous or cancer cells in the
CC prostate. PB39 is useful for early diagnosis of the progression of
CC prostate cancer, especially in aggressive prostate carcinoma. It can also
CC distinguish PC from other non-neoplastic prostate disease. The diagnostic
CC method is selective and specific for various types of PC and also
CC facilitates identifying prostate cancer of differing aggressiveness and
CC metastatic potential
XX
SQ Sequence 21 BP; 4 A; 4 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 21; DB 3; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CTGGCGTATCTGAAGAGTCTG 21
              |||||||||||||||||||||
Db          1 CTGGCGTATCTGAAGAGTCTG 21
```

RESULT 2
ADJ85951/c
ID ADJ85951 standard; DNA; 20 BP.
XX
AC ADJ85951;
XX
DT 06-MAY-2004 (first entry)
XX
DE Nucleic acid analysis-related Tag probe SeqID1019.
XX
KW restriction endonuclease site; T3 promoter site; Tag gene; Poly A site;
KW T7 Promoter; nucleic acid analysis; synthetic Tag gene; assay control;
KW assay development; product development; product validation;
KW quality control; probe; ss.
XX
OS Synthetic.
OS Unidentified.
XX
PN WO2004007684-A2.
XX
PD 22-JAN-2004.
XX
PF 14-JUL-2003; 2003WO-US021990.
XX
PR 12-JUL-2002; 2002US-0395530P.
XX
PA (AFFY-) AFFYMETRIX INC.
XX
PI Christians FC;
XX
DR WPI; 2004-122923/12.
XX
PT New DNA molecules made by annealing and extending overlapping 60mer
PT oligonucleotides, useful in producing synthetic Tag genes useful as assay
PT controls, in assay development, product development and for quality
PT control.
XX
PS Disclosure; SEQ ID NO 1019; 91pp; English.
XX
CC This invention relates to a novel DNA molecule which comprises a DNA
CC molecule made up of the following elements in a 5' to 3' direction: a
CC first restriction endonuclease site; a T3 promoter site; at least one Tag
CC gene comprising at least 5 20mer Tag sequences; a Poly A site having at
CC least 21 consecutive A residues; a second restriction endonuclease site
CC which may be the same or different than the first restriction
CC endonuclease site; or a T7 Promoter on the opposite strand as the T3
CC promoter. The invention may be useful in nucleic acid analysis, in
CC particular to synthetic Tag genes useful as assay controls, in assay
CC development, product development and validation and for quality control.
CC The present sequence is that of a Tag oligonucleotide probe which may be
CC used during the creation of the novel DNA molecule of the invention.
XX
SQ Sequence 20 BP; 5 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 65.7%; Score 13.8; DB 12; Length 20;
Best Local Similarity 88.2%; Pred. No. 3.5e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          5 CGTATCTGAAGAGTCTG 21
              | |||||| ||||||||
Db         20 CATATCTGGAGAGTCTG 4
```

RESULT 3
AAZ05689/c
ID AAZ05689 standard; DNA; 20 BP.
XX
AC AAZ05689;
XX
DT 07-OCT-1999 (first entry)
XX

DE PCR primer used to amplify an ORF of Chlamydia trachomatis.
XX
KW Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis;
KW nongonococcal uretritis; epidymitis; cervicitis; salpingitis; PCR primer;
KW bartholinitis; pneumopathy; venereal lymphogranulomatosis; ss.
XX
OS Synthetic.
OS Chlamydia trachomatis.
XX
PN WO9928475-A2.
XX
PD 10-JUN-1999.
XX
PF 27-NOV-1998; 98WO-IB001939.
XX
PR 28-NOV-1997; 97FR-00015041.
PR 17-DEC-1997; 97FR-00016034.
PR 04-NOV-1998; 98US-0107077P.
XX
PA (GEST) GENSET.
XX
PI Griffais R;
XX
DR WPI; 1999-371125/31.
XX
PT Genome sequence of Chlamydia trachomatis.
XX
PS Disclosure; Page 1791; 1755pp; English.
XX
CC PCR primers AAZ01426-Z06209 were used to amplify open reading frames
CC (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). These ORFs
CC encode polypeptides (see AAY36754-Y37949) which can be used as vaccines
CC against Chlamydia trachomatis. Antisense and ribozyme sequences can also
CC be used to control growth of the microorganism. Chlamydia trachomatis is
CC responsible for a large number of diseases, e.g. eye diseases such as
CC conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion
CC conjunctivitis; genital diseases such as nongonococcal uretritis,
CC epidymitis, cervicitis, salpingitis, perihepatitis, bartholinitis;
CC pneumopathy in breast feeding infants; and venereal lymphogranulomatosis.
CC The polypeptides of the invention may be of use in treating these
CC diseases
XX
SQ Sequence 20 BP; 6 A; 7 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 64.8%; Score 13.6; DB 2; Length 20;
Best Local Similarity 80.0%; Pred. No. 4.4e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          2 TGGCGTATCTGAAGAGTCTG 21
              || ||| || |||||| |||
Db         20 TGTCGTTTCAGAAGAGGCTG 1
```

RESULT 4
AAC63691
ID AAC63691 standard; DNA; 20 BP.
XX
AC AAC63691;
XX
DT 13-FEB-2001 (first entry)
XX
DE Rat P2X_7/P2Z PCR primer #3.
XX
KW Rat; P2X_7; neuroprotective; nootropic; antiinflammatory; antirheumatic;
KW antiarthritic; antibacterial; antiviral; antiallergic; cytostatic;
KW cardiant; cerebroprotective; immunosuppressive; P2Z; purinergic receptor;
KW nervous system disorder; chronic inflammation; Alzheimer's disease;
KW rheumatoid arthritis; amyloidosis; bacterial; viral; microbial infection;
KW haematopoietic system disorder; immune response; autoimmune disorder;
KW allergy; lymphoproliferative disorder; cardiac; cerebral ischaemia;
KW tuberculosis; PCR primer; ss.
XX
OS Rattus sp.
XX
PN US6133434-A.
XX
PD 17-OCT-2000.
XX
PF 28-APR-1997; 97US-00842079.
XX
PR 28-APR-1997; 97US-00842079.
XX
PA (GLAX) GLAXO GROUP LTD.
XX
PI Buell GN, Kawashima E, Surprenant A;
XX
DR WPI; 2001-006153/01.
XX
PT Mammalian purinergic receptor (P2X7) useful for screening for modulators
PT which are useful for treating arthritic, respiratory disorders and
PT neurodegenerative disorders, and to generate receptors specific
PT antibodies.
XX
PS Example 1; Col 7-8; 40pp; English.
XX
CC The present invention relates to rat and human purinergic receptor
CC P2X_7/P2Z (AAC63693-C63694). The P2X_7 coding sequences can be used to
CC treat disorders of the nervous system, particularly diseases with a
CC component of chronic inflammation, such as Alzheimer's disease, diseases
CC involving acute or chronic inflammation such as rheumatoid arthritis,
CC amyloidosis, bacterial, viral and other microbial infections, disorders
CC of the haematopoietic system and immune response such as autoimmune
CC disorders, allergies and lymphoproliferative disorders, diseases
CC involving apoptotic cell death, such as cardiac and cerebral ischaemia
CC and microbial infections, particularly tuberculosis. The present sequence
CC is a PCR primer used to isolate the rat P2X_7 coding sequence
XX
SQ Sequence 20 BP; 4 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

Query Match 61.9%; Score 13; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          3 GGCGTATCTGAAG 15
              |||||||||||||
Db          1 GGCGTATCTGAAG 13
```

RESULT 5
ADA09833
ID ADA09833 standard; DNA; 20 BP.
XX
AC ADA09833;
XX
DT 06-NOV-2003 (first entry)
XX
DE Antisense nested PCR primer #1 for amplification of rat P2X7 (P2Z).
XX
KW PCR; ss; primer; permeabilising activity; P2X7 receptor; P2Z receptor;
KW receptor; ATP; antigen presenting cell; T lymphocyte;
KW mitogenic stimulation; multinucleated giant cell; adenosine triphosphate;
KW 3'-O-(4-benzoyl)benzoyl ATP; BzATP; fluorescent dye; propidium iodide;
KW nootropic; neuroprotective; immunosuppressive; cerebroprotective;
KW vasotropic; arthritic disorder; respiratory disorder;
KW neurodegenerative disease; Alzheimer's disease; inflammation;
KW rheumatoid arthritis; amyloidosis; infection; tuberculosis;
KW haematopoietic system; immune response; allergy;
KW lymphoproliferative disorder; apoptosis; ischaemia; rat;
KW autoimmune disorder.
XX
OS Rattus sp.
XX
PN US6509163-B1.
XX
PD 21-JAN-2003.

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XX
PF   15-AUG-2000; 2000US-00638857.
XX
PR   28-APR-1997;   97US-00842079.
XX
PA   (GLAX ) GLAXO GROUP LTD.
XX
PI   Buell GN,  Surprenant A,  Kawashima E;
XX
DR   WPI; 2003-502654/47.
XX
PT   Screening of compound for its ability to modulate permeabilizing activity
PT   of mammalian receptor useful for treating e.g. arthritis, and alzheimer's
PT   disease.
XX
PS   Example 1; SEQ ID NO 3; 43pp; English.
XX
CC   The invention discloses a method for screening a compound for its ability
CC   to modulate the permeabilising activity of a mammalian P2X7 (P2Z)
CC   receptor. The P2Z receptor is a cell surface receptor for ATP and has
CC   been implicated in the lysis of antigen presenting cells by cytotoxic T
CC   lymphocytes, in the mitogenic stimulation of human T lymphocytes, as well
CC   as in the formation of multinucleated giant cells. The preferred agonist
CC   is adenosine triphosphate (ATP) or 3'-O-(4-benzoyl)benzoyl ATP (BzATP)
CC   and the preferred method comprises monitoring the uptake into the cell of
CC   a detectable molecule, preferably a fluorescent dye (e.g. propidium
CC   iodide). The inventive method is useful for screening a compound for its
CC   ability to modulate the permeabilising activity of a mammalian P2X7
CC   receptor useful for treatment of arthritic and respiratory disorders and
CC   neurodegenerative diseases. It is particularly useful in the treatment of
CC   Alzheimer's disease, diseases involving acute or chronic inflammation
CC   including rheumatoid arthritis, amyloidosis, bacterial, viral and other
CC   microbial infections, e.g. tuberculosis, disorders of the haematopoietic
CC   system and immune response, including autoimmune disorders, allergies and
CC   lymphoproliferative disorders, diseases involving apoptotic cell death,
CC   such as cardiac and cerebral ischaemia. The sequence presented is a
CC   nested PCR primer used for the amplification of rat P2X7 cDNA.
XX
SQ   Sequence 20 BP; 4 A; 3 C; 7 G; 6 T; 0 U; 0 Other;

  Query Match             61.9%;  Score 13;  DB 9;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 9e+03;
  Matches   13;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          3 GGCGTATCTGAAG 15
              |||||||||||||
Db          1 GGCGTATCTGAAG 13


RESULT 6
AAV97668/c
ID   AAV97668 standard; RNA; 17 BP.
XX
AC   AAV97668;
XX
DT   17-MAR-1999  (first entry)
XX
DE   Human EGF-R target sequence nucleotide position 3858.
XX
KW   Human; epidermal growth factor receptor; EGFR; EGF-R; target sequence;
KW   hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;
KW   cancer; genetic drift; detection; mutation; ss.
XX
OS   Homo sapiens.
XX
PN   WO9833893-A2.
XX
PD   06-AUG-1998.
XX
PF   14-JAN-1998;   98WO-US000730.
XX
PR   31-JAN-1997;   97US-0036476P.
PR   04-DEC-1997;   97US-00985162.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (UYAS-) UNIV ASTON.
XX
PI   Akhtar S,  Fell P,  Mcswiggen JA;
XX
DR   WPI; 1998-437449/37.
XX
PT   Enzymatic nucleic acids - which cleave RNA derived from an epidermal
PT   growth factor receptor, useful for inhibiting cell proliferation and for
PT   treating cancers.
XX
PS   Claim 5; Page 77; 109pp; English.
XX
CC   The present invention describes enzymatic nucleic acid molecules (NAMs)
CC   which specifically cleave RNA derived from an epidermal growth factor
CC   receptor (EGF-R) gene. AAV97221 to AAV98043 and AAV98979 to AAV99090
CC   represent specifically claimed target sequence from human EGF-R. AAV98044
CC   to AAV98866 and AAV98867 to V9878 represent hammerhead ribozymes and
CC   hairpin ribozymes respectively for human EGF-R. The NAMs are useful for
CC   cleaving EGF-R RNA in the treatment of a condition associated with EGFR
CC   expression levels e.g. to inhibit cell proliferation in the prevention or
CC   treatment of cancers. The NAMs can also be used as diagnostic tools to
CC   examine genetic drift and mutations within diseased cells or to detect
CC   the presence of EGF-R RNA in a cell
XX
SQ   Sequence 17 BP; 4 A; 6 C; 2 G; 0 T; 5 U; 0 Other;

  Query Match             61.0%;  Score 12.8;  DB 2;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 1.1e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 GTATCTGAAGAGTCTG 21
              |||||  |||||||||
Db         16 GTATCGAAAGAGTCTG 1


RESULT 7
ADJ85562/c
ID   ADJ85562 standard; DNA; 20 BP.
XX
AC   ADJ85562;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Nucleic acid analysis-related Tag probe SeqID630.
XX
KW   restriction endonuclease site; T3 promoter site; Tag gene; Poly A site;
KW   T7 Promoter; nucleic acid analysis; synthetic Tag gene; assay control;
KW   assay development; product development; product validation;
KW   quality control; probe; ss.
XX
OS   Synthetic.
OS   Unidentified.
XX
PN   WO2004007684-A2.
XX
PD   22-JAN-2004.
XX
PF   14-JUL-2003; 2003WO-US021990.
XX
PR   12-JUL-2002; 2002US-0395530P.
XX
PA   (AFFY-) AFFYMETRIX INC.
XX
PI   Christians FC;
XX
DR   WPI; 2004-122923/12.
XX
PT   New DNA molecules made by annealing and extending overlapping 60mer
PT   oligonucleotides, useful in producing synthetic Tag genes useful as assay
PT   controls, in assay development, product development and for quality
PT   control.
```

```
XX
PS   Disclosure; SEQ ID NO 630; 91pp; English.
XX
CC   This invention relates to a novel DNA molecule which comprises a DNA
CC   molecule made up of the following elements in a 5' to 3' direction: a
CC   first restriction endonuclease site; a T3 promoter site; at least one Tag
CC   gene comprising at least 5 20mer Tag sequences; a Poly A site having at
CC   least 21 consecutive A residues; a second restriction endonuclease site
CC   which may be the same or different than the first restriction
CC   endonuclease site; or a T7 Promoter on the opposite strand as the T3
CC   promoter. The invention may be useful in nucleic acid analysis, in
CC   particular to synthetic Tag genes useful as assay controls, in assay
CC   development, product development and validation and for quality control.
CC   The present sequence is that of a Tag oligonucleotide probe which may be
CC   used during the creation of the novel DNA molecule of the invention.
XX
SQ   Sequence 20 BP; 5 A; 4 C; 6 G; 5 T; 0 U; 0 Other;

  Query Match             61.0%;  Score 12.8;  DB 12;  Length 20;
  Best Local Similarity   87.5%;  Pred. No. 1.1e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 GCGTATCTGAAGAGTC 19
              ||||||||| | ||||
Db         17 GCGTATCTGCATAGTC 2


RESULT 8
ADK96254
ID   ADK96254 standard; DNA; 20 BP.
XX
AC   ADK96254;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Primer of the invention #1974.
XX
KW   human; single nucleotide polymorphism; SNP; ss; primer.
XX
OS   Synthetic.
XX
PN   JP2003259875-A.
XX
PD   16-SEP-2003.
XX
PF   08-MAR-2002; 2002JP-00064373.
XX
PR   08-MAR-2002; 2002JP-00064373.
XX
PA   (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.
XX
DR   WPI; 2004-093977/10.
XX
PT   Novel polynucleotide useful for PCR amplification along with two DNA
PT   fragment from another set of sequences, or for detecting single
PT   nucleotide polymorphism in human gene.
XX
PS   Claim 2; SEQ ID NO 5283; 2627pp; Japanese.
XX
CC   The present invention relates to a polynucleotide isolated from a human
CC   gene and is useful for detecting a single nucleotide polymorphism in a
CC   human gene or for diagnosing of disease. The invention enables the
CC   detection of a single nucleotide polymorphism in a human gene. The
CC   present sequence represents a primer of the invention.
XX
SQ   Sequence 20 BP; 5 A; 3 C; 8 G; 4 T; 0 U; 0 Other;

  Query Match             61.0%;  Score 12.8;  DB 12;  Length 20;
  Best Local Similarity   87.5%;  Pred. No. 1.1e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CTGGCGTATCTGAAGA 16
              ||||| || |||||||
Db          3 CTGGCATAGCTGAAGA 18


RESULT 9
ADF50105
ID   ADF50105 standard; RNA; 21 BP.
XX
AC   ADF50105;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Human BCL2 siNA target sequence SEQ ID NO:833.
XX
KW   ss; siNA; human; BCL2; short interfering nucleic acid; RNA interference;
KW   cytostatic; immunosuppressive; virucide; anti-HIV; cancer;
KW   autoimmune disease; viral infection; HIV.
XX
OS   Homo sapiens.
XX
PN   WO2003070969-A2.
XX
PD   28-AUG-2003.
XX
PF   18-FEB-2003; 2003WO-US004908.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   18-JUL-2002; 2002US-0396905P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L;
XX
DR   WPI; 2003-712622/67.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of cancer or autoimmune disease, downregulates expression of
PT   the BCL2 gene.
XX
PS   Example 3; SEQ ID NO 833; 148pp; English.
XX
CC   The invention relates to a novel short interfering nucleic acid (siNA)
CC   that downregulates expression of the BCL2 gene by RNA interference. A
CC   siNA of the invention has cytostatic, immunosuppressive, virucide, and
CC   anti-HIV activity. The siNA are useful for modulation (inhibition) of
CC   expression or activity of BCL2 by RNA interference. siNA are used to
CC   modulate expression of BCL2 genes, in cells, tissue explants or
CC   organisms, e.g. for treating cancer, autoimmune diseases and viral
CC   infections (including by HIV) but also for drug screening, diagnosis,
CC   target identification and validation, genetic engineering,
CC   pharmacogenomics, studying gene function and gene mapping (e.g. of single
CC   -nucleotide polymorphisms). The sequences shown in ADF49273-ADF50143
CC   represent siNA of the invention.
XX
SQ   Sequence 21 BP; 3 A; 5 C; 5 G; 2 T; 6 U; 0 Other;

  Query Match             61.0%;  Score 12.8;  DB 10;  Length 21;
  Best Local Similarity   56.2%;  Pred. No. 1.2e+04;
  Matches    9;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 GTATCTGAAGAGTCTG 21
              |: :|:||||| :|:|
Db          4 GUCUCUGAAGACUCUG 19


RESULT 10
ADF50117/c
ID   ADF50117 standard; RNA; 21 BP.
```

```
XX
AC   ADF50117;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Human BCL2 siNA target sequence SEQ ID NO:845.
XX
KW   ss; siNA; human; BCL2; short interfering nucleic acid; RNA interference;
KW   cytostatic; immunosuppressive; virucide; anti-HIV; cancer;
KW   autoimmune disease; viral infection; HIV.
XX
OS   Homo sapiens.
XX
PN   WO2003070969-A2.
XX
PD   28-AUG-2003.
XX
PF   18-FEB-2003; 2003WO-US004908.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   18-JUL-2002; 2002US-0396905P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L;
XX
DR   WPI; 2003-712622/67.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of cancer or autoimmune disease, downregulates expression of
PT   the BCL2 gene.
XX
PS   Example 3; SEQ ID NO 845; 148pp; English.
XX
CC   The invention relates to a novel short interfering nucleic acid (siNA)
CC   that downregulates expression of the BCL2 gene by RNA interference. A
CC   siNA of the invention has cytostatic, immunosuppressive, virucide, and
CC   anti-HIV activity. The siNA are useful for modulation (inhibition) of
CC   expression or activity of BCL2 by RNA interference. siNA are used to
CC   modulate expression of BCL2 genes, in cells, tissue explants or
CC   organisms, e.g. for treating cancer, autoimmune diseases and viral
CC   infections (including by HIV) but also for drug screening, diagnosis,
CC   target identification and validation, genetic engineering,
CC   pharmacogenomics, studying gene function and gene mapping (e.g. of single
CC   -nucleotide polymorphisms). The sequences shown in ADF49273-ADF50143
CC   represent siNA of the invention.
XX
SQ   Sequence 21 BP; 6 A; 5 C; 5 G; 2 T; 3 U; 0 Other;

  Query Match             61.0%;  Score 12.8;  DB 10;  Length 21;
  Best Local Similarity   87.5%;  Pred. No. 1.2e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 GTATCTGAAGAGTCTG 21
              || |||||||| ||||
Db         16 GTCTCTGAAGACTCTG 1


RESULT 11
ADF50125/c
ID   ADF50125 standard; RNA; 21 BP.
XX
AC   ADF50125;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Human BCL2 siNA target sequence SEQ ID NO:853.
XX
KW   ss; siNA; human; BCL2; short interfering nucleic acid; RNA interference;
KW   cytostatic; immunosuppressive; virucide; anti-HIV; cancer;
KW   autoimmune disease; viral infection; HIV.
XX
OS   Homo sapiens.
XX
PN   WO2003070969-A2.
XX
PD   28-AUG-2003.
XX
PF   18-FEB-2003; 2003WO-US004908.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   18-JUL-2002; 2002US-0396905P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Mcswiggen J,  Beigelman L;
XX
DR   WPI; 2003-712622/67.
XX
PT   New short interfering nucleic acid, useful e.g. for treatment and
PT   diagnosis of cancer or autoimmune disease, downregulates expression of
PT   the BCL2 gene.
XX
PS   Example 3; SEQ ID NO 853; 148pp; English.
XX
CC   The invention relates to a novel short interfering nucleic acid (siNA)
CC   that downregulates expression of the BCL2 gene by RNA interference. A
CC   siNA of the invention has cytostatic, immunosuppressive, virucide, and
CC   anti-HIV activity. The siNA are useful for modulation (inhibition) of
CC   expression or activity of BCL2 by RNA interference. siNA are used to
CC   modulate expression of BCL2 genes, in cells, tissue explants or
CC   organisms, e.g. for treating cancer, autoimmune diseases and viral
CC   infections (including by HIV) but also for drug screening, diagnosis,
CC   target identification and validation, genetic engineering,
CC   pharmacogenomics, studying gene function and gene mapping (e.g. of single
CC   -nucleotide polymorphisms). The sequences shown in ADF49273-ADF50143
CC   represent siNA of the invention.
XX
SQ   Sequence 21 BP; 6 A; 5 C; 5 G; 2 T; 3 U; 0 Other;

  Query Match             61.0%;  Score 12.8;  DB 10;  Length 21;
  Best Local Similarity   87.5%;  Pred. No. 1.2e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 GTATCTGAAGAGTCTG 21
              || |||||||| ||||
Db         16 GTCTCTGAAGACTCTG 1


RESULT 12
ADF50109/c
ID   ADF50109 standard; RNA; 21 BP.
XX
AC   ADF50109;
XX
DT   12-FEB-2004  (first entry)
XX
DE   Human BCL2 siNA target sequence SEQ ID NO:837.
XX
KW   ss; siNA; human; BCL2; short interfering nucleic acid; RNA interference;
KW   cytostatic; immunosuppressive; virucide; anti-HIV; cancer;
KW   autoimmune disease; viral infection; HIV.
XX
OS   Homo sapiens.
```

XX
PN WO2003070969-A2.
XX
PD 28-AUG-2003.
XX
PF 18-FEB-2003; 2003WO-US004908.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 18-JUL-2002; 2002US-0396905P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Mcswiggen J, Beigelman L;
XX
DR WPI; 2003-712622/67.
XX
PT New short interfering nucleic acid, useful e.g. for treatment and
PT diagnosis of cancer or autoimmune disease, downregulates expression of
PT the BCL2 gene.
XX
PS Example 3; SEQ ID NO 837; 148pp; English.
XX
CC The invention relates to a novel short interfering nucleic acid (siNA)
CC that downregulates expression of the BCL2 gene by RNA interference. A
CC siNA of the invention has cytostatic, immunosuppressive, virucide, and
CC anti-HIV activity. The siNA are useful for modulation (inhibition) of
CC expression or activity of BCL2 by RNA interference. siNA are used to
CC modulate expression of BCL2 genes, in cells, tissue explants or
CC organisms, e.g. for treating cancer, autoimmune diseases and viral
CC infections (including by HIV) but also for drug screening, diagnosis,
CC target identification and validation, genetic engineering,
CC pharmacogenomics, studying gene function and gene mapping (e.g. of single
CC -nucleotide polymorphisms). The sequences shown in ADF49273-ADF50143
CC represent siNA of the invention.
XX
SQ Sequence 21 BP; 6 A; 5 C; 5 G; 2 T; 3 U; 0 Other;

Query Match 61.0%; Score 12.8; DB 10; Length 21;
Best Local Similarity 87.5%; Pred. No. 1.2e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GTATCTGAAGAGTCTG 21
|| |||||||| ||||
Db 16 GTCTCTGAAGACTCTG 1

RESULT 13
ADG29696
ID ADG29696 standard; RNA; 21 BP.
XX
AC ADG29696;
XX
DT 26-FEB-2004 (first entry)
XX
DE BCL2-targeted siNA DNA-RNA hybrid - SEQ ID 262.
XX
KW double-stranded short interfering nucleic acid; siNA;
KW antiarteriosclerotic; neuroprotective; nootropic; antiparkinsonian;
KW anticonvulsant; pulmonary disease; restenosis; atherosclerosis;
KW Alzheimer's; Parkinson's; epilepsy; dementia; huntington's;
KW amyotrophic lateral sclerosis; gene therapy; ss; DNA-RNA hybrid; BCL2.
XX
OS Unidentified.
OS Synthetic.
XX
PN WO2003074654-A2.
XX
PD 12-SEP-2003.
XX
PF 20-FEB-2003; 2003WO-US005028.
XX
PR 20-FEB-2002; 2002US-0358580P.
PR 11-MAR-2002; 2002US-0363124P.
PR 06-JUN-2002; 2002US-0386782P.
PR 29-AUG-2002; 2002US-0406784P.
PR 05-SEP-2002; 2002US-0408378P.
PR 09-SEP-2002; 2002US-0409293P.
PR 15-JAN-2003; 2003US-0440129P.
XX
PA (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI Mcswiggen J, Beigelman L, Chowrira B, Pavco P, Fosnaugh K;
PI Jamison S, Usman N, Thompson J;
XX
DR WPI; 2003-731676/69.
XX
PT New double-stranded short interfering nucleic acid molecule, useful for
PT down-regulating the expression of an endogenous mammalian target gene or
PT for treating diseases that respond to modulation of gene expression or
PT activity.
XX
PS Example 24; SEQ ID NO 262; 593pp; English.
XX
CC The invention relates to a double-stranded short interfering nucleic acid
CC (siNA) molecule that down-regulates expression of an endogenous mammalian
CC target gene comprising one or more chemical modifications and each strand
CC of the double-stranded siNA comprises about 21 nucleotides. The siNA of
CC the invention demonstrates antiarteriosclerotic, neuroprotective,
CC nootropic, antiparkinsonian and anticonvulsant activities and may be
CC useful for down-regulating the expression of an endogenous mammalian
CC target gene and therefore in the treatment of any disease or condition
CC that responds to modulation of gene expression or activity in a cell,
CC tissue or organism. The disease or condition may include pulmonary
CC diseases such as restenosis, atherosclerosis, Alzheimer's disease,
CC Parkinson's disease, epilepsy, dementia, huntington's disease or
CC amyotrophic lateral sclerosis. Furthermore, the siNA may be utilised for
CC gene therapy applications. The current sequence is that of the siNA DNA-
CC RNA hybrid of the invention.
XX
SQ Sequence 21 BP; 3 A; 5 C; 5 G; 2 T; 6 U; 0 Other;

Query Match 61.0%; Score 12.8; DB 10; Length 21;
Best Local Similarity 56.2%; Pred. No. 1.2e+04;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GTATCTGAAGAGTCTG 21
|: :|:||||| :|:|
Db 4 GUCUCUGAAGACUCUG 19

RESULT 14
ADG29693/c
ID ADG29693 standard; RNA; 21 BP.
XX
AC ADG29693;
XX
DT 26-FEB-2004 (first entry)
XX
DE BCL2-targeted siNA DNA-RNA hybrid - SEQ ID 259.
XX
KW double-stranded short interfering nucleic acid; siNA;
KW antiarteriosclerotic; neuroprotective; nootropic; antiparkinsonian;
KW anticonvulsant; pulmonary disease; restenosis; atherosclerosis;
KW Alzheimer's; Parkinson's; epilepsy; dementia; huntington's;
KW amyotrophic lateral sclerosis; gene therapy; ss; DNA-RNA hybrid; BCL2.
XX
OS Unidentified.
OS Synthetic.
XX
PN WO2003074654-A2.

```
XX
PD   12-SEP-2003.
XX
PF   20-FEB-2003; 2003WO-US005028.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI   Mcswiggen J,  Beigelman L,  Chowrira B,  Pavco P,  Fosnaugh K;
PI   Jamison S,  Usman N,  Thompson J;
XX
DR   WPI; 2003-731676/69.
XX
PT   New double-stranded short interfering nucleic acid molecule, useful for
PT   down-regulating the expression of an endogenous mammalian target gene or
PT   for treating diseases that respond to modulation of gene expression or
PT   activity.
XX
PS   Example 24; SEQ ID NO 259; 593pp; English.
XX
CC   The invention relates to a double-stranded short interfering nucleic acid
CC   (siNA) molecule that down-regulates expression of an endogenous mammalian
CC   target gene comprising one or more chemical modifications and each strand
CC   of the double-stranded siNA comprises about 21 nucleotides. The siNA of
CC   the invention demonstrates antiarteriosclerotic, neuroprotective,
CC   nootropic, antiparkinsonian and anticonvulsant activities and may be
CC   useful for down-regulating the expression of an endogenous mammalian
CC   target gene and therefore in the treatment of any disease or condition
CC   that responds to modulation of gene expression or activity in a cell,
CC   tissue or organism. The disease or condition may include pulmonary
CC   diseases such as restenosis, atherosclerosis, Alzheimer's disease,
CC   Parkinson's disease, epilepsy, dementia, huntington's disease or
CC   amyotrophic lateral sclerosis. Furthermore, the siNA may be utilised for
CC   gene therapy applications. The current sequence is that of the siNA DNA-
CC   RNA hybrid of the invention.
XX
SQ   Sequence 21 BP; 6 A; 5 C; 5 G; 2 T; 3 U; 0 Other;

  Query Match             61.0%;  Score 12.8;  DB 10;  Length 21;
  Best Local Similarity   87.5%;  Pred. No. 1.2e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 GTATCTGAAGAGTCTG 21
              || |||||||| ||||
Db         16 GTCTCTGAAGACTCTG 1


RESULT 15
ADG29700/c
ID   ADG29700 standard; RNA; 21 BP.
XX
AC   ADG29700;
XX
DT   26-FEB-2004  (first entry)
XX
DE   BCL2-targeted siNA DNA-RNA hybrid - SEQ ID 266.
XX
KW   double-stranded short interfering nucleic acid; siNA;
KW   antiarteriosclerotic; neuroprotective; nootropic; antiparkinsonian;
KW   anticonvulsant; pulmonary disease; restenosis; atherosclerosis;
KW   Alzheimer's; Parkinson's; epilepsy; dementia; huntington's;
KW   amyotrophic lateral sclerosis; gene therapy; ss; DNA-RNA hybrid; BCL2.
XX
OS   Unidentified.
OS   Synthetic.
XX
```

```
PN   WO2003074654-A2.
XX
PD   12-SEP-2003.
XX
PF   20-FEB-2003; 2003WO-US005028.
XX
PR   20-FEB-2002; 2002US-0358580P.
PR   11-MAR-2002; 2002US-0363124P.
PR   06-JUN-2002; 2002US-0386782P.
PR   29-AUG-2002; 2002US-0406784P.
PR   05-SEP-2002; 2002US-0408378P.
PR   09-SEP-2002; 2002US-0409293P.
PR   15-JAN-2003; 2003US-0440129P.
XX
PA   (SIRN-) SIRNA THERAPEUTICS INC.
XX
PI   Mcswiggen J,  Beigelman L,  Chowrira B,  Pavco P,  Fosnaugh K;
PI   Jamison S,  Usman N,  Thompson J;
XX
DR   WPI; 2003-731676/69.
XX
PT   New double-stranded short interfering nucleic acid molecule, useful for
PT   down-regulating the expression of an endogenous mammalian target gene or
PT   for treating diseases that respond to modulation of gene expression or
PT   activity.
XX
PS   Example 24; SEQ ID NO 266; 593pp; English.
XX
CC   The invention relates to a double-stranded short interfering nucleic acid
CC   (siNA) molecule that down-regulates expression of an endogenous mammalian
CC   target gene comprising one or more chemical modifications and each strand
CC   of the double-stranded siNA comprises about 21 nucleotides. The siNA of
CC   the invention demonstrates antiarteriosclerotic, neuroprotective,
CC   nootropic, antiparkinsonian and anticonvulsant activities and may be
CC   useful for down-regulating the expression of an endogenous mammalian
CC   target gene and therefore in the treatment of any disease or condition
CC   that responds to modulation of gene expression or activity in a cell,
CC   tissue or organism. The disease or condition may include pulmonary
CC   diseases such as restenosis, atherosclerosis, Alzheimer's disease,
CC   Parkinson's disease, epilepsy, dementia, huntington's disease or
CC   amyotrophic lateral sclerosis. Furthermore, the siNA may be utilised for
CC   gene therapy applications. The current sequence is that of the siNA DNA-
CC   RNA hybrid of the invention.
XX
SQ   Sequence 21 BP; 6 A; 5 C; 5 G; 2 T; 3 U; 0 Other;

  Query Match             61.0%;  Score 12.8;  DB 10;  Length 21;
  Best Local Similarity   87.5%;  Pred. No. 1.2e+04;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 GTATCTGAAGAGTCTG 21
              || |||||||| ||||
Db         16 GTCTCTGAAGACTCTG 1


RESULT 16
ADQ61043/c
ID   ADQ61043 standard; RNA; 19 BP.
XX
AC   ADQ61043;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Anti-FRK siRNA related DNA sequence SEQ ID NO:745.
XX
KW   ss; siRNA; gene silencing; Bcl-2; optimised; short interfering RNA;
KW   RNA interference.
XX
OS   Synthetic.
XX
PN   WO2004045543-A2.
XX
PD   03-JUN-2004.
```

XX
PF 14-NOV-2003; 2003WO-US036787.
XX
PR 14-NOV-2002; 2002US-0426137P.
PR 10-SEP-2003; 2003US-0502050P.
XX
PA (DHAR-) DHARMACON INC.
XX
PI Anastasia K, Angela R, Devin L, William M, Stephen S;
XX
DR WPI; 2004-420527/39.
XX
PT Selecting siRNA by selecting an siRNA molecule of 19-25 nucleoside bases
PT by selecting a target gene and measuring the functionality of the
PT nucleotide sequences that are complementary to a stretch of nucleotides
PT of the target sequence.
XX
PS Example 12; SEQ ID NO 745; 199pp; English.
XX
CC The invention relates to a novel method for selecting siRNA (short
CC interfering RNA) comprising selecting an siRNA molecule of 19-25
CC nucleoside bases by selecting a target gene and measuring the
CC functionality of sequences of 19-25 nucleotides in length that are
CC substantially complementary to a stretch of nucleotides of the target
CC sequence, where the functionality is dependent upon non-target specific
CC criteria. Also claimed are methods for gene-silencing, developing an
CC siRNA algorithm for selecting siRNA, selecting an siRNA with improved
CC functionality, selecting hyperfunctional siRNA, an siRNA molecule
CC effective at silencing Bcl-2, and a kit for gene silencing comprising the
CC siRNA. The siRNA molecule comprises a sequence substantially similar to a
CC sequence consisting of GGGAGAUAGUGAUGAAGUA; GAAGUACAUCCAUUAUAAG;
CC GUACGACAACCGGGAGAUA; AGAUAGUGAUGAAGUACAU; UGAAGACUCUGCUCAGUUU;
CC CAUGCGGCCUCUGUUUGA; UGCGGCCUCUGUUUGAUUU; GAGAUAGUGAUGAAGUACA;
CC GGAGAUAGUGAUGAAGUAC; and GAAGACUCUGCUCAGUUUG. The siRNA molecule
CC comprises a sense strand and an anti-sense strand. The siRNA molecule
CC comprises a hairpin. The siRNA molecule comprises between 18 and 30 base
CC pairs. The kit comprises at least two siRNA, comprising a first optimised
CC siRNA and a second optimised siRNA. The method is useful in selecting
CC siRNA for generating a gene silencing reagent. The present sequence is
CC used in the exemplification of the invention. The sequence is shown in
CC the specification as DNA, but described as siRNA.
XX
SQ Sequence 19 BP; 7 A; 4 C; 2 G; 6 T; 0 U; 0 Other;

```
  Query Match             59.0%;  Score 12.4;  DB 12;  Length 19;
  Best Local Similarity   92.9%;  Pred. No. 1.8e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 ATCTGAAGAGTCTG 21
              || ||||||||||||
Db         18 ATATGAAGAGTCTG 5
```

RESULT 17
ADI79541
ID ADI79541 standard; DNA; 20 BP.
XX
AC ADI79541;
XX
DT 22-APR-2004 (first entry)
XX
DE Human HMG-CoA reductase antisense oligonucleotide, SEQ ID No 64.
XX
KW HMG-CoA reductase; 3-hydroxy-3-methylglutaryl-Coenzyme A;
KW HMG-CoA reductase; cardiant; antiarteriosclerotic; antilipaemic;
KW antisense gene therapy; cardiovascular disorder; cholesterol metabolism;
KW human; ss.
XX
OS Homo sapiens.
XX
PN US2004006031-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00190366.
XX
PR 02-JUL-2002; 2002US-00190366.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Dean NM, Freier SM, Dobie KW;
XX
DR WPI; 2004-081743/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding HMG-CoA reductase, useful for treating
PT atherosclerosis, or a disease involving cholesterol metabolism or
PT angiogenesis.
XX
PS Example 15; SEQ ID NO 64; 110pp; English.
XX
CC The invention relates to novel compounds of 8-80 nucleobases in length
CC targeted to, and which specifically hybridises with, a nucleic acid
CC molecule encoding 3-hydroxy-3-methylglutaryl-Coenzyme A (HMG-CoA)
CC reductase, and inhibits the expression of HMG-CoA reductase. The novel
CC compounds have cardiant, antiarteriosclerotic, and antilipaemic
CC activities. The compound can be used to treat disorders by antisense gene
CC therapy. The compounds, compositions and methods are useful for treating
CC a disease or condition associated with HMG-CoA reductase, such as a
CC cardiovascular disorder e.g. atherosclerosis, or a disease or condition
CC involving cholesterol metabolism. They are also useful in research and
CC diagnostics for modulating the expression of HMG-CoA reductase. This
CC polynucleotide sequence represents an antisense oligonucleotide of the
CC invention.
XX
SQ Sequence 20 BP; 5 A; 3 C; 7 G; 5 T; 0 U; 0 Other;

```
  Query Match             59.0%;  Score 12.4;  DB 12;  Length 20;
  Best Local Similarity   92.9%;  Pred. No. 1.8e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 ATCTGAAGAGTCTG 21
              |||||| |||||||
Db          3 ATCTGAGGAGTCTG 16
```

RESULT 18
ADI79738/c
ID ADI79738 standard; DNA; 20 BP.
XX
AC ADI79738;
XX
DT 22-APR-2004 (first entry)
XX
DE Human HMG-CoA reductase antisense oligonucleotide, SEQ ID No 261.
XX
KW HMG-CoA reductase; 3-hydroxy-3-methylglutaryl-Coenzyme A;
KW HMG-CoA reductase; cardiant; antiarteriosclerotic; antilipaemic;
KW antisense gene therapy; cardiovascular disorder; cholesterol metabolism;
KW human; ss.
XX
OS Homo sapiens.
XX
PN US2004006031-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00190366.
XX
PR 02-JUL-2002; 2002US-00190366.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Dean NM, Freier SM, Dobie KW;
XX
DR WPI; 2004-081743/08.

```
XX
PT   New compounds, particularly antisense oligonucleotides targeted to a
PT   nucleic acid encoding HMG-CoA reductase, useful for treating
PT   atherosclerosis, or a disease involving cholesterol metabolism or
PT   angiogenesis.
XX
PS   Example 16; SEQ ID NO 261; 110pp; English.
XX
CC   The invention relates to novel compounds of 8-80 nucleobases in length
CC   targeted to, and which specifically hybridises with, a nucleic acid
CC   molecule encoding 3-hydroxy-3-methylglutaryl-Coenzyme A (HMG-CoA)
CC   reductase, and inhibits the expression of HMG-CoA reductase. The novel
CC   compounds have cardiant, antiarteriosclerotic, and antilipaemic
CC   activities. The compound can be used to treat disorders by antisense gene
CC   therapy. The compounds, compositions and methods are useful for treating
CC   a disease or condition associated with HMG-CoA reductase, such as a
CC   cardiovascular disorder e.g. atherosclerosis, or a disease or condition
CC   involving cholesterol metabolism. They are also useful in research and
CC   diagnostics for modulating the expression of HMG-CoA reductase. This
CC   polynucleotide sequence represents an antisense oligonucleotide of the
CC   invention.
XX
SQ   Sequence 20 BP; 5 A; 7 C; 3 G; 5 T; 0 U; 0 Other;

  Query Match             59.0%;  Score 12.4;  DB 12;  Length 20;
  Best Local Similarity   92.9%;  Pred. No. 1.8e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 ATCTGAAGAGTCTG 21
              |||||| |||||||
Db         18 ATCTGAGGAGTCTG 5


RESULT 19
AAV97669/c
ID   AAV97669 standard; RNA; 17 BP.
XX
AC   AAV97669;
XX
DT   17-MAR-1999  (first entry)
XX
DE   Human EGF-R target sequence nucleotide position 3859.
XX
KW   Human; epidermal growth factor receptor; EGFR; EGF-R; target sequence;
KW   hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;
KW   cancer; genetic drift; detection; mutation; ss.
XX
OS   Homo sapiens.
XX
PN   WO9833893-A2.
XX
PD   06-AUG-1998.
XX
PF   14-JAN-1998;   98WO-US000730.
XX
PR   31-JAN-1997;   97US-0036476P.
PR   04-DEC-1997;   97US-00985162.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (UYAS-) UNIV ASTON.
XX
PI   Akhtar S,  Fell P,  Mcswiggen JA;
XX
DR   WPI; 1998-437449/37.
XX
PT   Enzymatic nucleic acids - which cleave RNA derived from an epidermal
PT   growth factor receptor, useful for inhibiting cell proliferation and for
PT   treating cancers.
XX
PS   Claim 5; Page 77; 109pp; English.
XX
CC   The present invention describes enzymatic nucleic acid molecules (NAMs)
CC   which specifically cleave RNA derived from an epidermal growth factor
CC   receptor (EGF-R) gene. AAV97221 to AAV98043 and AAV98979 to AAV99090
CC   represent specifically claimed target sequence from human EGF-R. AAV98044
CC   to AAV98866 and AAV98867 to V9878 represent hammerhead ribozymes and
CC   hairpin ribozymes respectively for human EGF-R. The NAMs are useful for
CC   cleaving EGF-R RNA in the treatment of a condition associated with EGFR
CC   expression levels e.g. to inhibit cell proliferation in the prevention or
CC   treatment of cancers. The NAMs can also be used as diagnostic tools to
CC   examine genetic drift and mutations within diseased cells or to detect
CC   the presence of EGF-R RNA in a cell
XX
SQ   Sequence 17 BP; 4 A; 6 C; 2 G; 0 T; 5 U; 0 Other;

  Query Match             58.1%;  Score 12.2;  DB 2;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 2.3e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 GCGTATCTGAAGAGTCT 20
              | |||||  ||||||||
Db         17 GGGTATCGAAAGAGTCT 1


RESULT 20
ADB02331/c
ID   ADB02331 standard; DNA; 17 BP.
XX
AC   ADB02331;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human MDZ4 scanning oligonucleotide SEQ ID 3317.
XX
KW   Cytostatic; immunostimulant; gene therapy; vaccine; human;
KW   zinc finger protein; MDZ3; MDZ4; MDZ7; MDZ12; chromosome 7q22.1;
KW   chromosome 6p21.3-22.2; chromosome 16p11.2; chromosome 15q26.1; cancer;
KW   developmental disorder; ss.
XX
OS   Homo sapiens.
XX
PN   EP1281758-A2.
XX
PD   05-FEB-2003.
XX
PF   30-JUL-2002; 2002EP-00016874.
XX
PR   02-AUG-2001; 2001US-00922181.
XX
PA   (AEOM-) AEOMICA INC.
XX
PI   Shannon M,  Gu Y,  Nguyen C;
XX
DR   WPI; 2003-423107/40.
XX
PT   New zinc finger-containing proteins and nucleic acids, useful in
PT   manufacturing a medicament for treating or preventing a disorder
PT   associated with decreased or increased expression or activity of MDZ3,
PT   MDZ4, MDZ7 or MDZ12, e.g. cancer.
XX
PS   Example 8; SEQ ID NO 3317; 103pp; English.
XX
CC   The present invention relates to novel human zinc finger-containing
CC   proteins and their coding sequences: MDZ3, MDZ4, MDZ7, MDZ12. MDZ3 is
CC   encoded at chromosome 7q22.1, MDZ4 is encoded at chromosome 6p21.3-22.2,
CC   MDZ7 is encoded at chromosome 16p11.2 and MDZ12 is encoded at chromosome
CC   15q26.1. The MDZ3, MDZ4, MDZ7, and MDZ12 sequences are useful in therapy,
CC   or in manufacturing a medicament for treating or preventing a disorder
CC   associated with decreased or increased expression or activity of MDZ3,
CC   MDZ4, MDZ7, or MDZ12, e.g. cancer or developmental disorders. The nucleic
CC   acids and proteins are also useful for diagnosing or monitoring a disease
CC   caused by altered expression of MDZ3, MDZ4, MDZ7, or MDZ12. The nucleic
CC   acids can also be used as probes to detect and characterize gross
CC   alterations in MDZ3, MDZ4, MDZ7, or MDZ12 genetic locus. The probes are
CC   useful in constructing microarrays for measuring gene expression. The
CC   proteins are useful as therapeutic agents for gene therapy or as
```

```
CC   vaccines. The present sequence was used to illustrate the invention.
XX
SQ   Sequence 17 BP; 5 A; 6 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             58.1%;  Score 12.2;  DB 8;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 2.3e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CTGGCGTATCTGAAGAG 17
              |||| || | |||||||
Db         17 CTGGAGTCTTTGAAGAG 1


RESULT 21
AAV29903
ID   AAV29903 standard; DNA; 20 BP.
XX
AC   AAV29903;
XX
DT   27-AUG-2003  (revised)
DT   06-AUG-1998  (first entry)
XX
DE   3' PCR primer used to amplify the KSHV ORF 73.
XX
KW   KSHV; body cavity-based lymphoma cell line; Epstein-Barr virus;
KW   characterisation; diagnosis; detection; antibody treatment; PCR primer;
KW   ss.
XX
OS   Synthetic.
OS   Human herpesvirus 8.
XX
PN   WO9812341-A1.
XX
PD   26-MAR-1998.
XX
PF   15-SEP-1997;   97WO-US016282.
XX
PR   20-SEP-1996;   96US-00717291.
XX
PA   (CORR ) CORNELL RES FOUND INC.
XX
PI   Cesarman E,  Arvanitakis L,  Knowles DM,  Mesri E;
XX
DR   WPI; 1998-230320/20.
XX
PT   Kaposi's sarcoma-associated herpes virus positive cell lines - comprising
PT   Kaposi's sarcoma-associated herpes virus, used to study virus and to
PT   develop diagnostic and therapeutic products.
XX
PS   Example 2; Page 18; 46pp; English.
XX
CC   PCR primers AAV29902-03 were used to amplify open reading frame (ORF) 73
CC   of Kaposi's sarcoma-associated herpes virus (KSHV). The specification
CC   describes a cell line comprising KSHV, the cell line preferably being a
CC   body cavity-based lymphoma cell line that does not harbour the Epstein-
CC   Barr virus. The KSHV cell lines can be used for the characterisation of
CC   the properties and functions of the infectious agent KSHV. The purified
CC   virus can be used for diagnostic purposes, e.g. for the detection of
CC   antibodies. The purified virus can also be used for the production of
CC   antibodies which can be used for diagnostic and/or treatment purposes.
CC   (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ   Sequence 20 BP; 5 A; 3 C; 8 G; 4 T; 0 U; 0 Other;

  Query Match             58.1%;  Score 12.2;  DB 2;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 2.3e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 CGTATCTGAAGAGTCTG 21
              || | || |||||||||
Db          1 CGGAGCTAAAGAGTCTG 17


RESULT 22
AAV31711
ID   AAV31711 standard; DNA; 20 BP.
XX
AC   AAV31711;
XX
DT   27-AUG-2003  (revised)
DT   11-SEP-1998  (first entry)
XX
DE   Kaposi's sarcoma associated herpesvirus ORF73 PCR primer.
XX
KW   PCR primer; KSHV; ORF73; Kaposi's sarcoma; ss.
XX
OS   Synthetic.
OS   Human herpesvirus 8.
XX
PN   WO9815289-A1.
XX
PD   16-APR-1998.
XX
PF   09-OCT-1997;   97WO-US018216.
XX
PR   10-OCT-1996;   96US-00728603.
XX
PA   (CORR ) CORNELL RES FOUND INC.
XX
PI   Cesarman E,  Knowles DM;
XX
DR   WPI; 1998-261008/23.
XX
PT   Isolated Kaposi's sarcoma-associated herpesvirus proteins - comprising
PT   antigenic membrane protein, G protein coupled receptor and cyclin protein
PT   used to develop products for diagnosis and therapy.
XX
PS   Example 1; Page 26; 68pp; English.
XX
CC   The sequence is that of a 3' PCR primer P16 which was used to detect
CC   transcripts of ORF73 of Kaposi's sarcoma herpesvirus (KSHV). (Updated on
CC   27-AUG-2003 to correct OS field.)
XX
SQ   Sequence 20 BP; 5 A; 3 C; 8 G; 4 T; 0 U; 0 Other;

  Query Match             58.1%;  Score 12.2;  DB 2;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 2.3e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 CGTATCTGAAGAGTCTG 21
              || | || |||||||||
Db          1 CGGAGCTAAAGAGTCTG 17


RESULT 23
AAD61207/c
ID   AAD61207 standard; DNA; 20 BP.
XX
AC   AAD61207;
XX
DT   15-JAN-2004  (first entry)
XX
DE   Human Ship-1 antisense oligonucleotide ISIS #168288.
XX
KW   Human; Ship-1; SH2-containing phosphatidylinositol phosphatase-1; INPP5D;
KW   insensitivity to apoptotic signal; developmental disorder; inflammation;
KW   immunosuppressive; autoimmune disorder; antisense therapy; antisense;
KW   phosphorothioate backbone; ss.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
```

```
FT                   /note= "Phosphorothioate backbone; All cytidines are 5-
FT                   methyl cytidines"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) nucleotides"
FT   modified_base   16. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) nucleotides"
XX
PN   US2003114401-A1.
XX
PD   19-JUN-2003.
XX
PF   06-DEC-2001; 2001US-00003919.
XX
PR   06-DEC-2001; 2001US-00003919.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Bennett CF,  Freier SM;
XX
DR   WPI; 2003-801302/75.
XX
PT   Antisense compounds targeted to nucleic acid molecule encoding Ship-1,
PT   useful for treating diseases associated with expression of Ship-1, such
PT   as autoimmune and developmental disorders.
XX
PS   Claim 3; Page 25; 0pp; English.
XX
CC   The present invention provides antisense compounds targetted to nucleic
CC   acid molecule encoding Ship-1 (also known as SH2-containing
CC   phosphatidylinositol phosphatase-1 and INPP5D) to modulate/inhibit the
CC   expression of Ship-1. The invention is useful in treatment of diseases
CC   such as insensitivity to apoptotic signals, autoimmune disorders,
CC   developmental disorders and inflammatory disorders. The present sequence
CC   is human Ship-1 antisense oligonucleotide
XX
SQ   Sequence 20 BP; 6 A; 7 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             58.1%;  Score 12.2;  DB 10;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 2.3e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CTGGCGTATCTGAAGAG 17
              |||| || |||| ||||
Db         20 CTGGAGTCTCTGCAGAG 4


RESULT 24
ADH50671/c
ID   ADH50671 standard; DNA; 20 BP.
XX
AC   ADH50671;
XX
DT   25-MAR-2004  (first entry)
XX
DE   Human IRAK-1 DNA, antisense oligonucleotide #65.
XX
KW   Antisense therapy; human; interleukin-1 receptor-associated kinase-1;
KW   IL-1 receptor-associated kinase-1; IRAK-1;
KW   hyperproliferative disorder e.g.; cancer; autoimmune disorder;
KW   altered bone metabolism or inflammation; cytostatic; immunosuppressive;
KW   osteopathic; antiinflammatory; phosphorothioate; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "This oligonucleotide has a phosphorothioate
FT                   backbone and 2'-methyoxyethyl (2'-MOE) wings at the 5'
FT                   and 3' ends, which are 5 nucleotides in length at each
FT                   end. All cytidine residues are 5-methylcytidines"
XX
PN   US2003228690-A1.
XX
PD   11-DEC-2003.
XX
PF   10-JUN-2002; 2002US-00167034.
XX
PR   10-JUN-2002; 2002US-00167034.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Baker BF,  Freier SM,  Dobie KW;
XX
DR   WPI; 2004-052028/05.
XX
PT   New compound having a sequence targeted to a nucleic acid encoding IL-1
PT   receptor-associated kinase-1, useful for preparing a composition for
PT   treating hyperproliferative or autoimmune disorder or inflammation.
XX
PS   Example 15; SEQ ID NO 78; 66pp; English.
XX
CC   The present invention relates to antisense compounds targeted to a
CC   nucleic acid encoding interleukin-1 (IL-1) receptor-associated kinase-1
CC   (IRAK-1). The antisense compound comprises an antisense oligonucleotide
CC   that specifically hybridises with the nucleic acid and inhibits the
CC   expression of IRAK-1. The antisense oligonucleotide is a chimeric
CC   oligonucleotide. The antisense oligonucleotide comprises at least one
CC   modified internucleoside linkage, preferably a phosphorothioate linkage.
CC   It also comprises at least one modified sugar moiety, preferably a 2'-O-
CC   methoxyethyl (2'-MOE) sugar moiety. The antisense oligonucleotide further
CC   comprises at least one modified nucleobase, preferably a 5-
CC   methylcytosine. The antisense oligonucleotides are useful for the
CC   treatment of diseases such as hyperproliferative disorders, e.g. cancer,
CC   autoimmune disorders, altered bone metabolism, and inflammation. The
CC   present sequence represents an antisense oligonucleotide used in the
CC   examples of the present invention.
XX
SQ   Sequence 20 BP; 4 A; 9 C; 4 G; 3 T; 0 U; 0 Other;

  Query Match             58.1%;  Score 12.2;  DB 12;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 2.3e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 GCGTATCTGAAGAGTCT 20
              ||||| ||| || ||||
Db         17 GCGTAGCTGGAGGGTCT 1


RESULT 25
ADI50969/c
ID   ADI50969 standard; DNA; 17 BP.
XX
AC   ADI50969;
XX
DT   15-APR-2004  (first entry)
XX
DE   Human tumour suppression/reversion-related DNA sequence SeqID3472.
XX
KW   tumour suppression; tumour reversion; apoptosis; virus resistance;
KW   cytostatic; virucide; neuroprotective; nootropic; neuroleptic; probe;
KW   primer; PCR; gene chip; antisense; viral disease; tumour;
KW   cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX
OS   Homo sapiens.
XX
PN   WO2003025177-A2.
XX
PD   27-MAR-2003.
XX
PF   17-SEP-2002; 2002WO-IB004523.
```

XX
PR 17-SEP-2001; 2001FR-00011980.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-313354/30.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; SEQ ID NO 3472; 30pp; French.
XX
CC This invention relates to novel isolated nucleic acid sequences involved
CC in the phenomena of tumour suppression, tumour reversion, apoptosis
CC and/or resistance to viruses. The invention may be useful for the
CC development of compounds with a cytostatic, virucide, neuroprotective,
CC nootropic or neuroleptic activity. The DNA sequences may be useful as
CC probes and primers for detecting, indentifying, quantifying and/or
CC amplifying nucleic acid, for example as one component of a gene chip, in
CC vitro as antisense reagents and for production of recombinant
CC polypeptides. The invention may therefore be useful for preparation of
CC pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia. The
CC present sequence is that of a nucleic acid sequence of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/publishedpct_sequences
XX
SQ Sequence 17 BP; 6 A; 4 C; 2 G; 5 T; 0 U; 0 Other;

Query Match 57.1%; Score 12; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.9e+04;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 TATCTGAAGAGT 18
||||||||||||
Db 17 TATCTGAAGAGT 6

RESULT 26
AAC92623/c
ID AAC92623 standard; DNA; 20 BP.
XX
AC AAC92623;
XX
DT 27-MAR-2001 (first entry)
XX
DE Human nucleolin phosphorothioate antisense oligonucleotide, SEQ ID NO:73.
XX
KW Human nucleolin; P92; C23; phosphoprotein; ribosome biogenesis;
KW ribosome transport; cytokinesis; nucleogenesis; cell proliferation;
KW cell growth; transcriptional repression; replication;
KW signal transduction; chromatin decondensation; Ag-NOR family;
KW nucleolin antibody; systemic connective tissue disease; SLE;
KW systemic lupus erythematosus;
KW scleroderma-like chronic graft versus host disease;
KW expression inhibition; tumour formation; cancer; inflammation;
KW immune disorder; phosphorothioate; antisense oligonucleotide; ss.
XX
OS Homo sapiens.
XX
PN US6165786-A.
XX
PD 26-DEC-2000.
XX
PF 03-NOV-1999; 99US-00433699.
XX
PR 03-NOV-1999; 99US-00433699.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Bennett CF, Cowsert LM;
XX
DR WPI; 2001-079848/09.
XX
PT Novel antisense compound targeted to human nucleolin which specifically
PT hybridizes with and inhibits the expression of human nucleolin, useful
PT for modulating the expression of nucleolin in cells.
XX
PS Claim 14; Col 43-44; 41pp; English.
XX
CC Sequences AAC92560-C92639 represent antisense oligonucleotides targetted
CC to the human nucleolin gene, which inhibit its expression. The antisense
CC oligonucleotides were designed to target different regions of the human
CC nucleolin mRNA, and were analysed for their effect on nucleolin mRNA
CC levels by quantitative real-time PCR. Nucleolin (also known as P92 or
CC C23) is the most abundant nucleolar phosphoprotein in actively growing
CC cells. Nucleolin primarily participates in ribosome biogenesis and
CC transport of ribosomal components, being able to transiently bind to pre-
CC ribosomes in the nucleolus via a ribonucleoprotein consensus sequence.
CC However, it has also been shown to be involved in cytokinesis,
CC nucleogenesis, cell proliferation and growth, transcriptional repression,
CC replication, signal transduction, and chromatin decondensation. Nucleolin
CC is a member of the Ag-NOR (active ribosomal gene located in the nucleolar
CC organiser region) family of proteins which are markers of active
CC ribosomal genes, and whose expression is associated with the prediction
CC of tumour growth rate. The presence of antibodies against nucleolin are
CC associated with systemic connective tissue diseases such as systemic
CC lupus erythematosus (SLE) and scleroderma-like chronic graft versus host
CC disease. The oligonucleotides of the invention are useful for diagnosis,
CC prevention and treatment of conditions associated with nucleolin
CC expression, such as tumour formation, immune disorders and inflammation
XX
SQ Sequence 20 BP; 5 A; 6 C; 2 G; 7 T; 0 U; 0 Other;

Query Match 57.1%; Score 12; DB 4; Length 20;
Best Local Similarity 75.0%; Pred. No. 2.9e+04;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 2 TGGCGTATCTGAAGAGTCTG 21
|||| |||| ||| || ||
Db 20 TGGCAAATCTAAAGGGTATG 1

RESULT 27
ADP68593/c
ID ADP68593 standard; DNA; 20 BP.
XX
AC ADP68593;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human PPAR-alpha antisense oligonucleotide seqid 29.
XX
KW cytostatic; gene therapy; PPAR-alpha;
KW peroxisome proliferator-activated receptor-alpha; PPAR-alpha modulator;
KW PPAR-alpha associated disorder; hyperproliferative disorder; human;
KW antisense oligonucleotide; antisense technology; ss.
XX
OS Homo sapiens.
XX
PN US2004115637-A1.
XX
PD 17-JUN-2004.
XX
PF 11-DEC-2002; 2002US-00317500.
XX
PR 11-DEC-2002; 2002US-00317500.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Mckay R, Dobie KW;

```
XX
DR   WPI; 2004-449378/42.
XX
PT   New oligonucleotide compound that inhibits expression of PPAR-alpha,
PT   useful for preparing a composition for treating hyperproliferative
PT   disorders, e.g. cancer.
XX
PS   Example 15; SEQ ID NO 29; 121pp; English.
XX
CC   The invention describes a compound, having a sequence comprising 8-80 bp
CC   targeted to a nucleic acid encoding PPAR-alpha (peroxisome proliferator-
CC   activated receptor-alpha), that specifically hybridises with the nucleic
CC   acid encoding PPAR-alpha comprising 86001-bp sequence and inhibits
CC   expression of PPAR-alpha. Also described are: a method of inhibiting the
CC   expression of PPAR-alpha in cells or tissues; a method of screening for a
CC   modulator of PPAR-alpha; a diagnostic method for identifying a disease
CC   state; a kit or assay device comprising the compound; and a method of
CC   treating an animal having a disease or condition associated with PPAR-
CC   alpha. The oligonucleotide compound is useful for preparing a composition
CC   for treating hyperproliferative disorder e.g. cancer. This sequence
CC   represents a human peroxisome proliferator-activated receptor-alpha (PPAR
CC   -alpha) antisense oligonucleotide.
XX
SQ   Sequence 20 BP; 6 A; 4 C; 4 G; 6 T; 0 U; 0 Other;

  Query Match             57.1%;  Score 12;  DB 12;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 TATCTGAAGAGT 18
              ||||||||||||
Db         20 TATCTGAAGAGT 9


RESULT 28
ADP68748
ID   ADP68748 standard; DNA; 20 BP.
XX
AC   ADP68748;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human PPAR-alpha antisense oligonucleotide seqid 184.
XX
KW   cytostatic; gene therapy; PPAR-alpha;
KW   peroxisome proliferator-activated receptor-alpha; PPAR-alpha modulator;
KW   PPAR-alpha associated disorder; hyperproliferative disorder; human;
KW   antisense oligonucleotide; antisense technology; ss.
XX
OS   Homo sapiens.
XX
PN   US2004115637-A1.
XX
PD   17-JUN-2004.
XX
PF   11-DEC-2002; 2002US-00317500.
XX
PR   11-DEC-2002; 2002US-00317500.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Mckay R,  Dobie KW;
XX
DR   WPI; 2004-449378/42.
XX
PT   New oligonucleotide compound that inhibits expression of PPAR-alpha,
PT   useful for preparing a composition for treating hyperproliferative
PT   disorders, e.g. cancer.
XX
PS   Example 16; SEQ ID NO 184; 121pp; English.
XX
CC   The invention describes a compound, having a sequence comprising 8-80 bp
CC   targeted to a nucleic acid encoding PPAR-alpha (peroxisome proliferator-
CC   activated receptor-alpha), that specifically hybridises with the nucleic
CC   acid encoding PPAR-alpha comprising 86001-bp sequence and inhibits
CC   expression of PPAR-alpha. Also described are: a method of inhibiting the
CC   expression of PPAR-alpha in cells or tissues; a method of screening for a
CC   modulator of PPAR-alpha; a diagnostic method for identifying a disease
CC   state; a kit or assay device comprising the compound; and a method of
CC   treating an animal having a disease or condition associated with PPAR-
CC   alpha. The oligonucleotide compound is useful for preparing a composition
CC   for treating hyperproliferative disorder e.g. cancer. This sequence
CC   represents a human peroxisome proliferator-activated receptor-alpha (PPAR
CC   -alpha) antisense oligonucleotide.
XX
SQ   Sequence 20 BP; 6 A; 4 C; 4 G; 6 T; 0 U; 0 Other;

  Query Match             57.1%;  Score 12;  DB 12;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 2.9e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 TATCTGAAGAGT 18
              ||||||||||||
Db          1 TATCTGAAGAGT 12


RESULT 29
AAA46172/c
ID   AAA46172 standard; DNA; 21 BP.
XX
AC   AAA46172;
XX
DT   06-AUG-2003  (revised)
DT   27-SEP-2000  (first entry)
XX
DE   PCR primer for GST.
XX
KW   GST-GFP fusion construct; circular; green fluorescent protein;
KW   glutathione S-transferase; eukaryotic diploid multicellular parasite;
KW   universal graft; transgenic eukaryotic parasite; acquired deficiency;
KW   genetic deficiency; hormone deficiency; metabolic deficiency;
KW   haematological deficiency; immunological deficiency; immunotherapy;
KW   anti-microbial therapy; anti-cancer therapy; drug addiction;
KW   poisoning condition; geriatric condition; PCR primer; ss.
XX
OS   Schistosoma sp.
XX
PN   WO200032804-A1.
XX
PD   08-JUN-2000.
XX
PF   01-DEC-1999;   99WO-IL000651.
XX
PR   01-DEC-1998;   98US-00201850.
XX
PA   (YISS ) YISSUM RES & DEV CO.
XX
PI   Hamburger J,  Laban A;
XX
DR   WPI; 2000-412348/35.
XX
PT   Eukaryotic diploid multicellular parasite useful as universal grafts for
PT   invivo delivery of beneficial gene products in humans and animals
PT   involves transformation with a transgene.
XX
PS   Example 2; Page 36; 90pp; English.
XX
CC   This sequence represents a PCR primer use to isolate DNA encoding the
CC   Shistosoma glutathion s-transferase protein. The amplified sequence can
CC   be used in a construct to transform the parasite of the invention. The
CC   parasite is a eukaryotic diploid multicellular parasite transformed with
CC   a transgene. Transgenic eukaryotic parasites are useful as universal
CC   grafts for in vivo delivery of beneficial gene product in humans and
CC   animals. The parasites can particularly be used for restoration of
CC   deficiencies whether acquired or genetic, such as hormone deficiencies,
CC   metabolic deficiencies, haematological deficiencies, immunological
```

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CC   deficiencies, immunotherapy, anti-microbial therapy, anti-cancer therapy.
CC   They can also be used for treatment of drug addiction, of poisoning
CC   conditions, and for amelioration of geriatric conditions. Treatment of
CC   humans with in vivo transgenes are universally compatible, readily
CC   available and inexpensive. Genotypic alterations of the patients is
CC   avoided, reducing risks of mutagenesis and malignant transformation.
CC   (Updated on 06-AUG-2003 to correct OS field.)
XX
SQ   Sequence 21 BP; 4 A; 10 C; 3 G; 4 T; 0 U; 0 Other;

  Query Match             57.1%;  Score 12;  DB 3;  Length 21;
  Best Local Similarity   75.0%;  Pred. No. 3e+04;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 TGGCGTATCTGAAGAGTCTG 21
              ||| | || ||| ||| |||
Db         21 TGGAGCATGTGAGGAGGCTG 2


RESULT 30
AAF97151/c
ID   AAF97151 standard; DNA; 21 BP.
XX
AC   AAF97151;
XX
DT   18-NOV-2004  (revised)
DT   06-JUN-2001  (first entry)
XX
DE   Human gene single nucleotide polymorphism #1912.
XX
KW   Human; variant thrombospondin 1; variant thrombospondin 4; SNP;
KW   polymorphism; vascular disease; coronary artery disease; forensics;
KW   myocardial infarction; atherosclerosis; stroke; venous thromboembolism;
KW   pulmonary embolism; paternity test; ds.
XX
OS   Homo sapiens.
OS   Unidentified.
XX
FH   Key             Location/Qualifiers
FT   variation       11
FT                   /*tag=  a
FT                   /standard_name= "Single nucleotide polymorphism"
XX
PN   WO200118250-A2.
XX
PD   15-MAR-2001.
XX
PF   07-SEP-2000; 2000WO-US024503.
XX
PR   10-SEP-1999;   99US-0153357P.
PR   26-JUL-2000; 2000US-0220947P.
PR   16-AUG-2000; 2000US-0225724P.
XX
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
PA   (MILL-) MILLENNIUM PHARM INC.
XX
PI   Lander ES,  Gargill M,  Ireland JS,  Bolk S,  Daley GQ,  Mccarthy JJ;
XX
DR   WPI; 2001-226749/23.
XX
PT   Nucleic acids comprising single nucleotide polymorphisms, useful in
PT   applications such as forensics, paternity testing, medicine, genetic
PT   analysis and phenotype correlations to diseases such as diabetes and
PT   atherosclerosis.
XX
PS   Example; Page 178; 242pp; English.
XX
CC   The present invention provides a method of diagnosing a vascular disease
CC   in an individual, involving determining the sequence at various
CC   polymorphic sites within the human thrombospondin 1 and thrombospondin 4
CC   genes. The sequences at a number of polymorphic sites are also provided
CC   in the specification. In particular, the method can be used in the
CC   diagnosis of atherosclerosis, myocardial infarction, coronary heart
CC   disease, stroke, peripheral vascular diseases, venous thromboembolism and
CC   pulmonary embolism. Single nucleotide polymorphisms (SNPs) are also
CC   useful in forensics, paternity testing, genetic analysis and phenotype
CC   correlations to diseases. The present sequence is an example of one of
CC   the human gene SNPS shown in the specification
CC
CC   Revised record issued on 18-NOV-2004 : The variantion feature was
CC   incorrectly given a captial V
XX
SQ   Sequence 21 BP; 5 A; 5 C; 6 G; 5 T; 0 U; 0 Other;

  Query Match             57.1%;  Score 12;  DB 4;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 3e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 CTGAAGAGTCTG 21
              ||||||||||||
Db         16 CTGAAGAGTCTG 5


RESULT 31
AAQ51964
ID   AAQ51964 standard; RNA; 17 BP.
XX
AC   AAQ51964;
XX
DT   25-MAR-2003  (revised)
DT   26-MAY-1994  (first entry)
XX
DE   BCL-2 mRNA ribozyme cleavable nucleotide (2100).
XX
KW   Multiple drug resistance; mdr-1; ribozyme; membrane protein; liver;
KW   resistance; chemotherapeutic agent; colchicine; doxorubicin; colon;
KW   actinomycin D; vinblastine; small intestine; kidney; adrenal gland;
KW   adenocarcinoma; bowel; transformed phenotype; promyelocytic leukemia;
KW   human; chronic myelogenous leukemia; CML; follicular lymphoma;
KW   B-cell acute lymphocytic leukemia; breast cancer; colon carcinoma;
KW   neuroblastoma; lung cancer; genetic drift; mutation; hammerhead motif;
KW   hairpin; hepatitis delta virus; group I intron; RNaseP; ss.
XX
OS   Homo sapiens.
XX
PN   WO9323057-A1.
XX
PD   25-NOV-1993.
XX
PF   13-MAY-1993;   93WO-US004573.
XX
PR   14-MAY-1992;   92US-00882822.
PR   14-MAY-1992;   92US-00882885.
PR   26-AUG-1992;   92US-00936110.
PR   26-AUG-1992;   92US-00936421.
PR   26-AUG-1992;   92US-00936422.
PR   26-AUG-1992;   92US-00936531.
PR   26-AUG-1992;   92US-00936532.
PR   07-DEC-1992;   92US-00987131.
PR   19-JAN-1993;   93US-00006122.
PR   19-JAN-1993;   93US-00008910.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
XX
PI   Thompson JD,  Draper KG;
XX
DR   WPI; 1993-386203/48.
XX
PT   New enzymatic RNA molecules (ribozymes) - which cleave mRNA associated
PT   with tumours or mRNA expressed from gene encoding multiple drug
PT   resistance.
XX
PS   Claim 3; Fig 6; 69pp; English.
XX
CC   The sequences given in AAQ51825-2266 represent areas of mRNAs which are
CC   associated with development or maintenance of chronic myelogenous
```

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CC   leukemia (CML), promyelocytic leukemia, Burkitt's lymphoma, or acute
CC   lymphocytic leukemia, follicular lymphoma, B-cell acute lymphocytic
CC   leukemia, breast cancer, colon carcinoma, neuroblastoma and lung cancer.
CC   The full length mRNAs containing these target sequences, encode aberant
CC   cellular proteins which are able to control cellular proliferation and
CC   are directly linked to a leukemic phenotype. These target sequences are
CC   identified by the ribozyme of the invention. The ribozymes is formed in a
CC   hammerhead motif, but may also be formed in the motif of a hairpin,
CC   hepatitis delta virus, group I intron or RNaseP-like RNA. These ribozymes
CC   may be used to inhibit the development or expression of a transformed
CC   phenotype in man and other animals by modulating expression of the
CC   corresponding gene. Cleavage of target mRNAs expressed in pre-neoplastic
CC   and transformed cells elicits inhibition of the transformed state.
CC   Multiple drug resistance (mdr-1) mRNA specific ribozymes remove the
CC   mechanism of drug resistance used by transformed cells and thus enhances
CC   drug therapies for tumours. The ribozymes may also be used to study
CC   genetic drift and mutations within cells. (Updated on 25-MAR-2003 to
CC   correct PN field.)
XX
SQ   Sequence 17 BP; 3 A; 5 C; 3 G; 0 T; 6 U; 0 Other;

  Query Match             56.2%;  Score 11.8;  DB 2;  Length 17;
  Best Local Similarity   53.3%;  Pred. No. 3.6e+04;
  Matches    8;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 GTATCTGAAGAGTCT 20
              |: :|:||||| :|:
Db          3 GUCUCUGAAGACUCU 17


RESULT 32
AAV97667/c
ID   AAV97667 standard; RNA; 17 BP.
XX
AC   AAV97667;
XX
DT   17-MAR-1999  (first entry)
XX
DE   Human EGF-R target sequence nucleotide position 3856.
XX
KW   Human; epidermal growth factor receptor; EGFR; EGF-R; target sequence;
KW   hammerhead ribozyme; hairpin ribozyme; inhibition; cell proliferation;
KW   cancer; genetic drift; detection; mutation; ss.
XX
OS   Homo sapiens.
XX
PN   WO9833893-A2.
XX
PD   06-AUG-1998.
XX
PF   14-JAN-1998;   98WO-US000730.
XX
PR   31-JAN-1997;   97US-0036476P.
PR   04-DEC-1997;   97US-00985162.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (UYAS-) UNIV ASTON.
XX
PI   Akhtar S,  Fell P,  Mcswiggen JA;
XX
DR   WPI; 1998-437449/37.
XX
PT   Enzymatic nucleic acids - which cleave RNA derived from an epidermal
PT   growth factor receptor, useful for inhibiting cell proliferation and for
PT   treating cancers.
XX
PS   Claim 5; Page 77; 109pp; English.
XX
CC   The present invention describes enzymatic nucleic acid molecules (NAMs)
CC   which specifically cleave RNA derived from an epidermal growth factor
CC   receptor (EGF-R) gene. AAV97221 to AAV98043 and AAV98979 to AAV99090
CC   represent specifically claimed target sequence from human EGF-R. AAV98044
CC   to AAV98866 and AAV98867 to V9878 represent hammerhead ribozymes and
CC   hairpin ribozymes respectively for human EGF-R. The NAMs are useful for
CC   cleaving EGF-R RNA in the treatment of a condition associated with EGFR
CC   expression levels e.g. to inhibit cell proliferation in the prevention or
CC   treatment of cancers. The NAMs can also be used as diagnostic tools to
CC   examine genetic drift and mutations within diseased cells or to detect
CC   the presence of EGF-R RNA in a cell
XX
SQ   Sequence 17 BP; 4 A; 5 C; 2 G; 0 T; 6 U; 0 Other;

  Query Match             56.2%;  Score 11.8;  DB 2;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 3.6e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 TATCTGAAGAGTCTG 21
              ||||  |||||||||
Db         17 TATCGAAAGAGTCTG 3


RESULT 33
ABK03278/c
ID   ABK03278 standard; RNA; 17 BP.
XX
AC   ABK03278;
XX
DT   12-MAR-2002  (first entry)
XX
DE   Human CD20 Inozyme #229.
XX
KW   Human; ss; antisense therapy; cytostatic; antiinflammatory; haemostatic;
KW   cerebroprotective; nootropic; neuroprotective; antiparkinsonian;
KW   muscular; CD20; neurite growth inhibitor gene; NOGO; hammerhead ribozyme;
KW   DNAzyme; inozyme; G-cleaver; amberzyme; zinzyme; lymphoma; leukaemia;
KW   B-cell lymphoma; non-Hodgkin's lymphoma; NHL; lymphocytic leukaemia;
KW   human immunodeficiency virus; HIV associated NHL; mantle-cell lymphoma;
KW   MCL; immunocytoma; IMC; immune thrombocytopaenia; stroke; dementia;
KW   inflammatory arthropathy; central nervous system injury;
KW   cerebrovascular accident; CVA; Alzheimer's disease; multiple sclerosis;
KW   chemotherapy-induced neuropathy; amyotrophic lateral sclerosis; ALS;
KW   Parkinson's disease; ataxia; Huntington's disease;
KW   Creutzfeldt-Jakob disease; muscular dystrophy; neurodegenerative disease.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200159103-A2.
XX
PD   16-AUG-2001.
XX
PF   09-FEB-2001; 2001WO-US004273.
XX
PR   11-FEB-2000; 2000US-0181797P.
PR   28-FEB-2000; 2000US-0185516P.
PR   06-MAR-2000; 2000US-0187128P.
XX
PA   (RIBO-) RIBOZYME PHARM INC.
PA   (BLAT/) BLATT L.
PA   (MCSW/) MCSWIGGEN J.
PA   (CHOW/) CHOWRIRA B M.
XX
PI   Blatt L,  Mcswiggen J,  Chowrira BM;
XX
DR   WPI; 2001-607195/69.
XX
PT   Nucleic acid molecules, e.g., enzymatic nucleic acids and antisense
PT   constructs, which down regulate expression of a CD20 gene or neurite
PT   growth inhibitor gene useful for treating, e.g., lymphoma, leukemia, and
PT   central nervous system injury.
XX
PS   Claim 30; Page 149; 200pp; English.
XX
CC   The invention relates to a nucleic acid molecule which down regulates
CC   expression of a CD20 gene and a nucleic acid molecule which down
CC   regulates expression of a neurite growth inhibitor gene (NOGO). The
```

CC nucleic acids may be enzymatic nucleic acids (e.g. a ribozyme or a
CC DNAzyme) an Inozyme (an endolytic nucleic acid cleaving a an RNA molecule
CC possessing an NCH motif), a G-cleaver (cleaving RNA with a NYN motif) pr
CC an amberzyme (cleaving RNA with an NGN triplet), a zinzyme (cleaving RNA
CC with a YGY motif). The CD20-targetting nucleic acid is used to cleave RNA
CC of CD20 in the presence of a divalent cation that is preferably Mg^2^+.
CC Furthermore, it may be contacted with a cell to reduce CD20 activity of
CC the cell and treat a patient having a condition associated with the level
CC of CD20. The treatment may further comprise the use of one or more
CC therapies. In particular, the CD20 targetting nucleic acid may be used to
CC treat lymphoma, leukaemia, B-cell lymphoma, low-grade or follicular non-
CC Hodgkin's lymphoma (NHL), bulky low-grade or follicular NHL, lymphocytic
CC leukaemia, HIV (human immunodeficiency virus) associated NHL, mantle-cell
CC lymphoma (MCL), immunocytoma (IMC), small B-cell lymphocytic lymphoma,
CC immune thrombocytopaenia, and inflammatory arthropathy. The NOGO-
CC targetting nucleic acid is used to cleave RNA of the NOGO gene in the
CC presence of a divalent cation that is preferably Mg^2^+. Furthermore, the
CC nucleic acid may be contacted with a cell to reduce NOGO activity of the
CC cell and treat a patient having a condition associated with the level of
CC NOGO. The treatment may further comprise the use of one or more
CC therapies. In particular, the NOGO-targetting nucleic acid may be used to
CC treat central nervous system (CNS) injury and cerebrovascular accident
CC (CVA, stroke), Alzheimer's disease, dementia, multiple sclerosis (MS),
CC chemotherapy-induced neuropathy, amyotrophic lateral sclerosis (ALS),
CC Parkinson's disease, ataxia, Huntington's disease, Creutzfeldt-Jakob
CC disease, muscular dystrophy, and/or other neurodegenerative disease
CC states which respond to the modulation of NOGO expression. The present
CC sequence is an inozyme of the invention
XX
SQ Sequence 17 BP; 5 A; 6 C; 2 G; 0 T; 4 U; 0 Other;

Query Match 56.2%; Score 11.8; DB 4; Length 17;
Best Local Similarity 86.7%; Pred. No. 3.6e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GCGTATCTGAAGAGT 18
|||||| || |||||
Db 16 GCGTATGTGCAGAGT 2

RESULT 34
ADF92273
ID ADF92273 standard; DNA; 17 BP.
XX
AC ADF92273;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human cytokeratin 19-derived F3 PCR primer - SEQ ID 361.
XX
KW human; cytokeratin; CK; LAMP; loop mediated isothermal amplification;
KW tumour metastasis; prostate cancer; lymphoma; human; CK19; ss; primer;
KW PCR; F3.
XX
OS Homo sapiens.
XX
PN WO2003097878-A1.
XX
PD 27-NOV-2003.
XX
PF 20-MAY-2003; 2003WO-JP006256.
XX
PR 21-MAY-2002; 2002JP-00145689.
PR 17-JUN-2002; 2002JP-00175271.
PR 09-JUL-2002; 2002JP-00199759.
XX
PA (SYSM-) SYSMEX CORP.
XX
PI Tada S, Akai Y, Imura Y, Abe S, Minekawa H;
XX
DR WPI; 2004-012543/01.
XX
PT LAMP nucleic acid amplification primers for detection of cytokeratin
PT expression as indicator in diagnosis of tumour metastasis.
XX
PS Claim 19; SEQ ID NO 361; 266pp; Japanese.
XX
CC The invention relates to novel nucleic acid amplification primers for the
CC detection of human cytokeratin (CK) 18, 19 or 20 expression by the LAMP
CC (loop mediated isothermal amplification) method. The primers of the
CC invention may be useful for the detecting cytokeratin 18-20 expression as
CC an indicator for the diagnosis of tumour metastasis, particularly
CC prostate cancer and lymphoma. The amplification using the primers is
CC highly efficient and allows very sensitive detection of tumour
CC metastasis. The current sequence is that of the human CK19-related PCR
CC primer of the invention.
XX
SQ Sequence 17 BP; 4 A; 5 C; 5 G; 3 T; 0 U; 0 Other;

Query Match 56.2%; Score 11.8; DB 12; Length 17;
Best Local Similarity 86.7%; Pred. No. 3.6e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGGCGTATCTGAAG 15
||||| || ||||||
Db 3 CTGGCCTACCTGAAG 17

RESULT 35
ADQ61034
ID ADQ61034 standard; RNA; 19 BP.
XX
AC ADQ61034;
XX
DT 09-SEP-2004 (first entry)
XX
DE Anti-FLT1 siRNA related DNA sequence SEQ ID NO:736.
XX
KW ss; siRNA; gene silencing; Bcl-2; optimised; short interfering RNA;
KW RNA interference.
XX
OS Synthetic.
XX
PN WO2004045543-A2.
XX
PD 03-JUN-2004.
XX
PF 14-NOV-2003; 2003WO-US036787.
XX
PR 14-NOV-2002; 2002US-0426137P.
PR 10-SEP-2003; 2003US-0502050P.
XX
PA (DHAR-) DHARMACON INC.
XX
PI Anastasia K, Angela R, Devin L, William M, Stephen S;
XX
DR WPI; 2004-420527/39.
XX
PT Selecting siRNA by selecting an siRNA molecule of 19-25 nucleoside bases
PT by selecting a target gene and measuring the functionality of the
PT nucleotide sequences that are complementary to a stretch of nucleotides
PT of the target sequence.
XX
PS Example 12; SEQ ID NO 736; 199pp; English.
XX
CC The invention relates to a novel method for selecting siRNA (short
CC interfering RNA) comprising selecting an siRNA molecule of 19-25
CC nucleoside bases by selecting a target gene and measuring the
CC functionality of sequences of 19-25 nucleotides in length that are
CC substantially complementary to a stretch of nucleotides of the target
CC sequence, where the functionality is dependent upon non-target specific
CC criteria. Also claimed are methods for gene-silencing, developing an
CC siRNA algorithm for selecting siRNA, selecting an siRNA with improved
CC functionality, selecting hyperfunctional siRNA, an siRNA molecule
CC effective at silencing Bcl-2, and a kit for gene silencing comprising the
CC siRNA. The siRNA molecule comprises a sequence substantially similar to a

```
CC   sequence consisting of GGGAGAUAGUGAUGAAGUA; GAAGUACAUCCAUUAUAAG;
CC   GUACGACAACCGGGAGAUA; AGAUAGUGAUGAAGUACAU; UGAAGACUCUGCUCAGUUU;
CC   CAUGCGGCCUCUGUUUGA; UGCGGCCUCUGUUUGAUUU; GAGAUAGUGAUGAAGUACA;
CC   GGAGAUAGUGAUGAAGUAC; and GAAGACUCUGCUCAGUUUG. The siRNA molecule
CC   comprises a sense strand and an anti-sense strand. The siRNA molecule
CC   comprises a hairpin. The siRNA molecule comprises between 18 and 30 base
CC   pairs. The kit comprises at least two siRNA, comprising a first optimised
CC   siRNA and a second optimised siRNA. The method is useful in selecting
CC   siRNA for generating a gene silencing reagent. The present sequence is
CC   used in the exemplification of the invention. The sequence is shown in
CC   the specification as DNA, but described as siRNA.
XX
SQ   Sequence 19 BP; 7 A; 2 C; 7 G; 3 T; 0 U; 0 Other;

  Query Match             56.2%;  Score 11.8;  DB 12;  Length 19;
  Best Local Similarity   86.7%;  Pred. No. 3.7e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GGCGTATCTGAAGAG 17
              | ||||  ||||||||
Db          2 GACGTAACTGAAGAG 16


RESULT 36
ADR79337/c
ID   ADR79337 standard; DNA; 19 BP.
XX
AC   ADR79337;
XX
DT   16-DEC-2004  (first entry)
XX
DE   Human apolipoprotein B (ApoB) oligonucleotide seqid 3822.
XX
KW   antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic;
KW   cytostatic; anticonvulsant; nootropic; muscula; anti-HIV;
KW   RNA interference; iRNA; antisense technology; lipid metabolism;
KW   cholesterol imbalance; dyslipidaemia hypercholesterolaemia;
KW   coronary artery disease; CAD; coronary heart disease; CHD;
KW   atherosclerosis; hepatic glucose production;
KW   glucose-metabolism-related disorder; diabetes; cancer; breast cancer;
KW   colon cancer; lung cancer; neurological disease; Huntington disease;
KW   spinocerebellar ataxia; viral disease; AIDS; apolipoprotein B; apoB; ss.
XX
OS   Homo sapiens.
XX
PN   WO2004080406-A2.
XX
PD   23-SEP-2004.
XX
PF   08-MAR-2004; 2004WO-US007070.
XX
PR   07-MAR-2003; 2003US-0452682P.
PR   12-MAR-2003; 2003US-0454265P.
PR   13-MAR-2003; 2003US-0454962P.
PR   13-MAR-2003; 2003US-0455050P.
PR   14-APR-2003; 2003US-0462894P.
PR   17-APR-2003; 2003US-0463772P.
PR   25-APR-2003; 2003US-0465665P.
PR   25-APR-2003; 2003US-0465802P.
PR   09-MAY-2003; 2003US-0469612P.
PR   08-AUG-2003; 2003US-0493986P.
PR   11-AUG-2003; 2003US-0494597P.
PR   26-SEP-2003; 2003US-0506341P.
PR   09-OCT-2003; 2003US-0510246P.
PR   10-OCT-2003; 2003US-0510318P.
PR   07-NOV-2003; 2003US-0518453P.
XX
PA   (ALNY-) ALNYLAM PHARM.
XX
PI   Manoharan M,  Bumcrot D;
XX
DR   WPI; 2004-677362/66.
XX
PT   Interference RNA agent useful for treating dyslipidemias, coronary artery
PT   disease, diabetes, cancer or neurological disease, comprises sense
PT   sequence and antisense sequence which has specific modifications.
XX
PS   Example 5; SEQ ID NO 3822; 378pp; English.
XX
CC   The invention describes a RNA interference (iRNA) agent (I) comprising a
CC   sense sequence and an antisense sequence, where the sense sequences have
CC   one or more asymmetrical 2'-O alkyl modifications, the antisense
CC   sequences have one or more asymmetrical phosphorothioate modifications
CC   and the antisense sequence targets a human gene sequence. Also described
CC   are: a pharmaceutical preparation comprising (I); reducing (M1) apoB-100
CC   levels or glucose-6-phosphatase levels in a subject; producing (I);
CC   stabilising (I), involves selecting a sequence with activity and
CC   introducing one or more asymmetrical modification in the sequence, where
CC   the modification decreases nuclease sensitivity while not decreasing its
CC   activity; a kit comprising (I) and instruction for its use; and a device
CC   that can be dispense or administer a composition comprising (I). (I) is
CC   useful for reducing apoB-100 levels or glucose-6-phosphatase levels. (M1)
CC   is useful for reducing apoB-100 levels or glucose-6-phosphatase levels.
CC   The subject is suffering from a disorder characterised by elevated or
CC   otherwise unwanted expression of apoB-100, elevated or otherwise unwanted
CC   levels of cholesterol, and/or disregulation of lipid metabolism. The
CC   disorder is chosen from the HDL/LDL cholesterol imbalance,
CC   dyslipidaemias, hypercholestorolaemia, statin-resistant
CC   hypercholesterolaemia, coronary artery disease (CAD), coronary heart
CC   disease (CHD) and atherosclerosis. (I) is administered to a subject to
CC   inhibit hepatic glucose production or for treating glucose-metabolism-
CC   related disorder e.g. diabetes or type-2 diabetes. (I) is useful for
CC   treating the diseases as mentioned above, cancer (e.g. breast, colon or
CC   lung cancer), neurological disease (e.g., Huntington disease or
CC   spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence
CC   represents a human apolipoprotein B (ApoB) antisense oligonucleotide that
CC   can be used to control ApoB gene expression.
XX
SQ   Sequence 19 BP; 5 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             56.2%;  Score 11.8;  DB 13;  Length 19;
  Best Local Similarity   86.7%;  Pred. No. 3.7e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 TATCTGAAGAGTCTG 21
              | |||||||||  |||
Db         17 TTTCTGAAGAGCCTG 3


RESULT 37
ADR80012/c
ID   ADR80012 standard; DNA; 19 BP.
XX
AC   ADR80012;
XX
DT   16-DEC-2004  (first entry)
XX
DE   Human apolipoprotein B (ApoB) oligonucleotide seqid 4508.
XX
KW   antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic;
KW   cytostatic; anticonvulsant; nootropic; muscula; anti-HIV;
KW   RNA interference; iRNA; antisense technology; lipid metabolism;
KW   cholesterol imbalance; dyslipidaemia hypercholesterolaemia;
KW   coronary artery disease; CAD; coronary heart disease; CHD;
KW   atherosclerosis; hepatic glucose production;
KW   glucose-metabolism-related disorder; diabetes; cancer; breast cancer;
KW   colon cancer; lung cancer; neurological disease; Huntington disease;
KW   spinocerebellar ataxia; viral disease; AIDS; apolipoprotein B; apoB; ss.
XX
OS   Homo sapiens.
XX
PN   WO2004080406-A2.
XX
PD   23-SEP-2004.
XX
PF   08-MAR-2004; 2004WO-US007070.
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XX
PR   07-MAR-2003; 2003US-0452682P.
PR   12-MAR-2003; 2003US-0454265P.
PR   13-MAR-2003; 2003US-0454962P.
PR   13-MAR-2003; 2003US-0455050P.
PR   14-APR-2003; 2003US-0462894P.
PR   17-APR-2003; 2003US-0463772P.
PR   25-APR-2003; 2003US-0465665P.
PR   25-APR-2003; 2003US-0465802P.
PR   09-MAY-2003; 2003US-0469612P.
PR   08-AUG-2003; 2003US-0493986P.
PR   11-AUG-2003; 2003US-0494597P.
PR   26-SEP-2003; 2003US-0506341P.
PR   09-OCT-2003; 2003US-0510246P.
PR   10-OCT-2003; 2003US-0510318P.
PR   07-NOV-2003; 2003US-0518453P.
XX
PA   (ALNY-) ALNYLAM PHARM.
XX
PI   Manoharan M,  Bumcrot D;
XX
DR   WPI; 2004-677362/66.
XX
PT   Interference RNA agent useful for treating dyslipidemias, coronary artery
PT   disease, diabetes, cancer or neurological disease, comprises sense
PT   sequence and antisense sequence which has specific modifications.
XX
PS   Example 5; SEQ ID NO 4508; 378pp; English.
XX
CC   The invention describes a RNA interference (iRNA) agent (I) comprising a
CC   sense sequence and an antisense sequence, where the sense sequences have
CC   one or more asymmetrical 2'-O alkyl modifications, the antisense
CC   sequences have one or more asymmetrical phosphorothioate modifications
CC   and the antisense sequence targets a human gene sequence. Also described
CC   are: a pharmaceutical preparation comprising (I); reducing (M1) apoB-100
CC   levels or glucose-6-phosphatase levels in a subject; producing (I);
CC   stabilising (I), involves selecting a sequence with activity and
CC   introducing one or more asymmetrical modification in the sequence, where
CC   the modification decreases nuclease sensitivity while not decreasing its
CC   activity; a kit comprising (I) and instruction for its use; and a device
CC   that can be dispense or administer a composition comprising (I). (I) is
CC   useful for reducing apoB-100 levels or glucose-6-phosphatase levels. (M1)
CC   is useful for reducing apoB-100 levels or glucose-6-phosphatase levels.
CC   The subject is suffering from a disorder characterised by elevated or
CC   otherwise unwanted expression of apoB-100, elevated or otherwise unwanted
CC   levels of cholesterol, and/or disregulation of lipid metabolism. The
CC   disorder is chosen from the HDL/LDL cholesterol imbalance,
CC   dyslipidaemias, hypercholestorolaemia, statin-resistant
CC   hypercholesterolaemia, coronary artery disease (CAD), coronary heart
CC   disease (CHD) and atherosclerosis. (I) is administered to a subject to
CC   inhibit hepatic glucose production or for treating glucose-metabolism-
CC   related disorder e.g. diabetes or type-2 diabetes. (I) is useful for
CC   treating the diseases as mentioned above, cancer (e.g. breast, colon or
CC   lung cancer), neurological disease (e.g., Huntington disease or
CC   spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence
CC   represents a human apolipoprotein B (ApoB) antisense oligonucleotide that
CC   can be used to control ApoB gene expression.
XX
SQ   Sequence 19 BP; 5 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             56.2%;  Score 11.8;  DB 13;  Length 19;
  Best Local Similarity   86.7%;  Pred. No. 3.7e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 TATCTGAAGAGTCTG 21
              | ||||||||| |||
Db         16 TTTCTGAAGAGCCTG 2


RESULT 38
ADR75873/c
ID   ADR75873 standard; DNA; 19 BP.
XX
AC   ADR75873;
XX
DT   16-DEC-2004  (first entry)
XX
DE   Human apolipoprotein B (ApoB) oligonucleotide seqid 358.
XX
KW   antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic;
KW   cytostatic; anticonvulsant; nootropic; muscula; anti-HIV;
KW   RNA interference; iRNA; antisense technology; lipid metabolism;
KW   cholesterol imbalance; dyslipidaemia hypercholesterolaemia;
KW   coronary artery disease; CAD; coronary heart disease; CHD;
KW   atherosclerosis; hepatic glucose production;
KW   glucose-metabolism-related disorder; diabetes; cancer; breast cancer;
KW   colon cancer; lung cancer; neurological disease; Huntington disease;
KW   spinocerebellar ataxia; viral disease; AIDS; apolipoprotein B; apoB; ss.
XX
OS   Homo sapiens.
XX
PN   WO2004080406-A2.
XX
PD   23-SEP-2004.
XX
PF   08-MAR-2004; 2004WO-US007070.
XX
PR   07-MAR-2003; 2003US-0452682P.
PR   12-MAR-2003; 2003US-0454265P.
PR   13-MAR-2003; 2003US-0454962P.
PR   13-MAR-2003; 2003US-0455050P.
PR   14-APR-2003; 2003US-0462894P.
PR   17-APR-2003; 2003US-0463772P.
PR   25-APR-2003; 2003US-0465665P.
PR   25-APR-2003; 2003US-0465802P.
PR   09-MAY-2003; 2003US-0469612P.
PR   08-AUG-2003; 2003US-0493986P.
PR   11-AUG-2003; 2003US-0494597P.
PR   26-SEP-2003; 2003US-0506341P.
PR   09-OCT-2003; 2003US-0510246P.
PR   10-OCT-2003; 2003US-0510318P.
PR   07-NOV-2003; 2003US-0518453P.
XX
PA   (ALNY-) ALNYLAM PHARM.
XX
PI   Manoharan M,  Bumcrot D;
XX
DR   WPI; 2004-677362/66.
XX
PT   Interference RNA agent useful for treating dyslipidemias, coronary artery
PT   disease, diabetes, cancer or neurological disease, comprises sense
PT   sequence and antisense sequence which has specific modifications.
XX
PS   Example 5; SEQ ID NO 358; 378pp; English.
XX
CC   The invention describes a RNA interference (iRNA) agent (I) comprising a
CC   sense sequence and an antisense sequence, where the sense sequences have
CC   one or more asymmetrical 2'-O alkyl modifications, the antisense
CC   sequences have one or more asymmetrical phosphorothioate modifications
CC   and the antisense sequence targets a human gene sequence. Also described
CC   are: a pharmaceutical preparation comprising (I); reducing (M1) apoB-100
CC   levels or glucose-6-phosphatase levels in a subject; producing (I);
CC   stabilising (I), involves selecting a sequence with activity and
CC   introducing one or more asymmetrical modification in the sequence, where
CC   the modification decreases nuclease sensitivity while not decreasing its
CC   activity; a kit comprising (I) and instruction for its use; and a device
CC   that can be dispense or administer a composition comprising (I). (I) is
CC   useful for reducing apoB-100 levels or glucose-6-phosphatase levels. (M1)
CC   is useful for reducing apoB-100 levels or glucose-6-phosphatase levels.
CC   The subject is suffering from a disorder characterised by elevated or
CC   otherwise unwanted expression of apoB-100, elevated or otherwise unwanted
CC   levels of cholesterol, and/or disregulation of lipid metabolism. The
CC   disorder is chosen from the HDL/LDL cholesterol imbalance,
CC   dyslipidaemias, hypercholestorolaemia, statin-resistant
CC   hypercholesterolaemia, coronary artery disease (CAD), coronary heart
CC   disease (CHD) and atherosclerosis. (I) is administered to a subject to
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CC   inhibit hepatic glucose production or for treating glucose-metabolism-
CC   related disorder e.g. diabetes or type-2 diabetes. (I) is useful for
CC   treating the diseases as mentioned above, cancer (e.g. breast, colon or
CC   lung cancer), neurological disease (e.g., Huntington disease or
CC   spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence
CC   represents a human apolipoprotein B (ApoB) antisense oligonucleotide that
CC   can be used to control ApoB gene expression.
XX
SQ   Sequence 19 BP; 5 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             56.2%;  Score 11.8;  DB 13;  Length 19;
  Best Local Similarity   86.7%;  Pred. No. 3.7e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 TATCTGAAGAGTCTG 21
              | ||||||||| |||
Db         17 TTTCTGAAGAGCCTG 3


RESULT 39
ADR77702/c
ID   ADR77702 standard; DNA; 19 BP.
XX
AC   ADR77702;
XX
DT   16-DEC-2004  (first entry)
XX
DE   Human apolipoprotein B (ApoB) oligonucleotide seqid 2187.
XX
KW   antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic;
KW   cytostatic; anticonvulsant; nootropic; muscula; anti-HIV;
KW   RNA interference; iRNA; antisense technology; lipid metabolism;
KW   cholesterol imbalance; dyslipidaemia hypercholesterolaemia;
KW   coronary artery disease; CAD; coronary heart disease; CHD;
KW   atherosclerosis; hepatic glucose production;
KW   glucose-metabolism-related disorder; diabetes; cancer; breast cancer;
KW   colon cancer; lung cancer; neurological disease; Huntington disease;
KW   spinocerebellar ataxia; viral disease; AIDS; apolipoprotein B; apoB; ss.
XX
OS   Homo sapiens.
XX
PN   WO2004080406-A2.
XX
PD   23-SEP-2004.
XX
PF   08-MAR-2004; 2004WO-US007070.
XX
PR   07-MAR-2003; 2003US-0452682P.
PR   12-MAR-2003; 2003US-0454265P.
PR   13-MAR-2003; 2003US-0454962P.
PR   13-MAR-2003; 2003US-0455050P.
PR   14-APR-2003; 2003US-0462894P.
PR   17-APR-2003; 2003US-0463772P.
PR   25-APR-2003; 2003US-0465665P.
PR   25-APR-2003; 2003US-0465802P.
PR   09-MAY-2003; 2003US-0469612P.
PR   08-AUG-2003; 2003US-0493986P.
PR   11-AUG-2003; 2003US-0494597P.
PR   26-SEP-2003; 2003US-0506341P.
PR   09-OCT-2003; 2003US-0510246P.
PR   10-OCT-2003; 2003US-0510318P.
PR   07-NOV-2003; 2003US-0518453P.
XX
PA   (ALNY-) ALNYLAM PHARM.
XX
PI   Manoharan M,  Bumcrot D;
XX
DR   WPI; 2004-677362/66.
XX
PT   Interference RNA agent useful for treating dyslipidemias, coronary artery
PT   disease, diabetes, cancer or neurological disease, comprises sense
PT   sequence and antisense sequence which has specific modifications.
XX
PS   Example 5; SEQ ID NO 2187; 378pp; English.
XX
CC   The invention describes a RNA interference (iRNA) agent (I) comprising a
CC   sense sequence and an antisense sequence, where the sense sequences have
CC   one or more asymmetrical 2'-O alkyl modifications, the antisense
CC   sequences have one or more asymmetrical phosphorothioate modifications
CC   and the antisense sequence targets a human gene sequence. Also described
CC   are: a pharmaceutical preparation comprising (I); reducing (M1) apoB-100
CC   levels or glucose-6-phosphatase levels in a subject; producing (I);
CC   stabilising (I), involves selecting a sequence with activity and
CC   introducing one or more asymmetrical modification in the sequence, where
CC   the modification decreases nuclease sensitivity while not decreasing its
CC   activity; a kit comprising (I) and instruction for its use; and a device
CC   that can be dispense or administer a composition comprising (I). (I) is
CC   useful for reducing apoB-100 levels or glucose-6-phosphatase levels. (M1)
CC   is useful for reducing apoB-100 levels or glucose-6-phosphatase levels.
CC   The subject is suffering from a disorder characterised by elevated or
CC   otherwise unwanted expression of apoB-100, elevated or otherwise unwanted
CC   levels of cholesterol, and/or disregulation of lipid metabolism. The
CC   disorder is chosen from the HDL/LDL cholesterol imbalance,
CC   dyslipidaemias, hypercholestorolaemia, statin-resistant
CC   hypercholesterolaemia, coronary artery disease (CAD), coronary heart
CC   disease (CHD) and atherosclerosis. (I) is administered to a subject to
CC   inhibit hepatic glucose production or for treating glucose-metabolism-
CC   related disorder e.g. diabetes or type-2 diabetes. (I) is useful for
CC   treating the diseases as mentioned above, cancer (e.g. breast, colon or
CC   lung cancer), neurological disease (e.g., Huntington disease or
CC   spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence
CC   represents a human apolipoprotein B (ApoB) antisense oligonucleotide that
CC   can be used to control ApoB gene expression.
XX
SQ   Sequence 19 BP; 5 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

  Query Match             56.2%;  Score 11.8;  DB 13;  Length 19;
  Best Local Similarity   86.7%;  Pred. No. 3.7e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 TATCTGAAGAGTCTG 21
              | ||||||||| |||
Db         17 TTTCTGAAGAGCCTG 3


RESULT 40
ADR78491/c
ID   ADR78491 standard; DNA; 19 BP.
XX
AC   ADR78491;
XX
DT   16-DEC-2004  (first entry)
XX
DE   Human apolipoprotein B (ApoB) oligonucleotide seqid 2976.
XX
KW   antilipemic; cardiant; vasotropic; antiarteriosclerotic; antidiabetic;
KW   cytostatic; anticonvulsant; nootropic; muscula; anti-HIV;
KW   RNA interference; iRNA; antisense technology; lipid metabolism;
KW   cholesterol imbalance; dyslipidaemia hypercholesterolaemia;
KW   coronary artery disease; CAD; coronary heart disease; CHD;
KW   atherosclerosis; hepatic glucose production;
KW   glucose-metabolism-related disorder; diabetes; cancer; breast cancer;
KW   colon cancer; lung cancer; neurological disease; Huntington disease;
KW   spinocerebellar ataxia; viral disease; AIDS; apolipoprotein B; apoB; ss.
XX
OS   Homo sapiens.
XX
PN   WO2004080406-A2.
XX
PD   23-SEP-2004.
XX
PF   08-MAR-2004; 2004WO-US007070.
XX
PR   07-MAR-2003; 2003US-0452682P.
PR   12-MAR-2003; 2003US-0454265P.
PR   13-MAR-2003; 2003US-0454962P.
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PR 13-MAR-2003; 2003US-0455050P.
PR 14-APR-2003; 2003US-0462894P.
PR 17-APR-2003; 2003US-0463772P.
PR 25-APR-2003; 2003US-0465665P.
PR 25-APR-2003; 2003US-0465802P.
PR 09-MAY-2003; 2003US-0469612P.
PR 08-AUG-2003; 2003US-0493986P.
PR 11-AUG-2003; 2003US-0494597P.
PR 26-SEP-2003; 2003US-0506341P.
PR 09-OCT-2003; 2003US-0510246P.
PR 10-OCT-2003; 2003US-0510318P.
PR 07-NOV-2003; 2003US-0518453P.
XX
PA (ALNY-) ALNYLAM PHARM.
XX
PI Manoharan M, Bumcrot D;
XX
DR WPI; 2004-677362/66.
XX
PT Interference RNA agent useful for treating dyslipidemias, coronary artery
PT disease, diabetes, cancer or neurological disease, comprises sense
PT sequence and antisense sequence which has specific modifications.
XX
PS Example 5; SEQ ID NO 2976; 378pp; English.
XX
CC The invention describes a RNA interference (iRNA) agent (I) comprising a
CC sense sequence and an antisense sequence, where the sense sequences have
CC one or more asymmetrical 2'-O alkyl modifications, the antisense
CC sequences have one or more asymmetrical phosphorothioate modifications
CC and the antisense sequence targets a human gene sequence. Also described
CC are: a pharmaceutical preparation comprising (I); reducing (M1) apoB-100
CC levels or glucose-6-phosphatase levels in a subject; producing (I);
CC stabilising (I), involves selecting a sequence with activity and
CC introducing one or more asymmetrical modification in the sequence, where
CC the modification decreases nuclease sensitivity while not decreasing its
CC activity; a kit comprising (I) and instruction for its use; and a device
CC that can be dispense or administer a composition comprising (I). (I) is
CC useful for reducing apoB-100 levels or glucose-6-phosphatase levels. (M1)
CC is useful for reducing apoB-100 levels or glucose-6-phosphatase levels.
CC The subject is suffering from a disorder characterised by elevated or
CC otherwise unwanted expression of apoB-100, elevated or otherwise unwanted
CC levels of cholesterol, and/or disregulation of lipid metabolism. The
CC disorder is chosen from the HDL/LDL cholesterol imbalance,
CC dyslipidaemias, hypercholestorolaemia, statin-resistant
CC hypercholesterolaemia, coronary artery disease (CAD), coronary heart
CC disease (CHD) and atherosclerosis. (I) is administered to a subject to
CC inhibit hepatic glucose production or for treating glucose-metabolism-
CC related disorder e.g. diabetes or type-2 diabetes. (I) is useful for
CC treating the diseases as mentioned above, cancer (e.g. breast, colon or
CC lung cancer), neurological disease (e.g., Huntington disease or
CC spinocerebellar ataxia) or viral disease (e.g., AIDS). This sequence
CC represents a human apolipoprotein B (ApoB) antisense oligonucleotide that
CC can be used to control ApoB gene expression.
XX
SQ Sequence 19 BP; 5 A; 5 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 56.2%; Score 11.8; DB 13; Length 19;
Best Local Similarity 86.7%; Pred. No. 3.7e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          7 TATCTGAAGAGTCTG 21
              | ||||||||| |||
Db         17 TTTCTGAAGAGCCTG 3
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Job time : 244 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 12, 2005, 09:56:43 ; Search time 95 Seconds
(without alignments)
361.703 Million cell updates/sec

Title: US-09-743-825-8
Perfect score: 21
Sequence: 1 ctggcgtatctgaagagtctg 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 457068

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	13	61.9	20	3	US-08-842-079-3	Sequence 3, Appli
	2	13	61.9	20	4	US-09-638-857-3	Sequence 3, Appli
c	3	12.8	61.0	17	3	US-08-985-162-448	Sequence 448, App
c	4	12.8	61.0	17	4	US-09-401-063-448	Sequence 448, App
c	5	12.8	61.0	20	2	US-08-450-905B-134	Sequence 134, App
c	6	12.8	61.0	20	3	US-07-982-759F-134	Sequence 134, App
c	7	12.2	58.1	17	3	US-08-985-162-449	Sequence 449, App
c	8	12.2	58.1	17	4	US-09-401-063-449	Sequence 449, App
	9	12.2	58.1	20	2	US-08-717-291-8	Sequence 8, Appli
	10	12.2	58.1	20	3	US-08-728-603-8	Sequence 8, Appli
c	11	12	57.1	20	3	US-09-433-699-73	Sequence 73, Appl
	12	11.8	56.2	16	4	US-09-371-772B-5737	Sequence 5737, Ap
	13	11.8	56.2	17	1	US-07-852-260-4	Sequence 4, Appli
	14	11.8	56.2	17	1	US-07-936-421-18	Sequence 18, Appl
	15	11.8	56.2	17	2	US-08-461-503-4	Sequence 4, Appli
c	16	11.8	56.2	17	3	US-08-985-162-447	Sequence 447, App
	17	11.8	56.2	17	3	US-08-465-250-4	Sequence 4, Appli
	18	11.8	56.2	17	4	US-09-371-772B-4438	Sequence 4438, Ap
c	19	11.8	56.2	17	4	US-09-401-063-447	Sequence 447, App
c	20	11.8	56.2	20	3	US-09-488-857B-38	Sequence 38, Appl
	21	11.8	56.2	20	4	US-09-198-452A-1366	Sequence 1366, Ap
c	22	11.8	56.2	21	4	US-09-478-189-118	Sequence 118, App
	23	11.6	55.2	20	3	US-09-280-805-129	Sequence 129, App
	24	11.6	55.2	20	3	US-09-517-467B-30	Sequence 30, Appl
c	25	11.6	55.2	20	4	US-09-198-452A-2767	Sequence 2767, Ap
c	26	11.6	55.2	20	4	US-09-657-289A-12	Sequence 12, Appl
c	27	11.6	55.2	21	4	US-09-657-472-1916	Sequence 1916, Ap
c	28	11.4	54.3	19	4	US-09-422-978-6486	Sequence 6486, Ap
c	29	11.4	54.3	20	2	US-08-602-093-12	Sequence 12, Appl
c	30	11.2	53.3	17	3	US-08-985-162-450	Sequence 450, App
c	31	11.2	53.3	17	4	US-09-401-063-450	Sequence 450, App
	32	11.2	53.3	18	4	US-09-422-978-5682	Sequence 5682, Ap
	33	11.2	53.3	19	1	US-08-555-678-57	Sequence 57, Appl
c	34	11.2	53.3	19	4	US-09-422-978-4659	Sequence 4659, Ap
c	35	11.2	53.3	19	4	US-09-696-791-466	Sequence 466, App
c	36	11.2	53.3	19	4	US-09-696-791-467	Sequence 467, App
	37	11.2	53.3	20	3	US-09-488-671-22	Sequence 22, Appl
	38	11.2	53.3	20	3	US-09-488-671-23	Sequence 23, Appl
	39	11.2	53.3	20	3	US-09-488-671-24	Sequence 24, Appl
c	40	11.2	53.3	20	3	US-09-517-584A-86	Sequence 86, Appl
	41	11.2	53.3	20	4	US-09-198-452A-2499	Sequence 2499, Ap
	42	11.2	53.3	21	4	US-09-422-978-11644	Sequence 11644, A
	43	11.2	53.3	21	4	US-09-636-728-44	Sequence 44, Appl
	44	11	52.4	12	3	US-09-281-418-154	Sequence 154, App
	45	11	52.4	18	1	US-08-599-252-1	Sequence 1, Appli
	46	11	52.4	18	1	US-08-436-074-1	Sequence 1, Appli
	47	11	52.4	18	3	US-08-849-488-12	Sequence 12, Appl
	48	11	52.4	18	5	PCT-US96-06352-1	Sequence 1, Appli
	49	11	52.4	18	5	PCT-US96-06583-1	Sequence 1, Appli
c	50	11	52.4	20	3	US-09-484-617-76	Sequence 76, Appl
c	51	11	52.4	20	4	US-09-198-452A-4507	Sequence 4507, Ap
c	52	11	52.4	20	4	US-09-601-144-33	Sequence 33, Appl
	53	11	52.4	21	4	US-09-657-472-2486	Sequence 2486, Ap
c	54	10.8	51.4	15	2	US-08-585-684B-1266	Sequence 1266, Ap
c	55	10.8	51.4	15	3	US-09-038-073-1266	Sequence 1266, Ap
	56	10.8	51.4	17	3	US-08-584-040-1681	Sequence 1681, Ap
	57	10.8	51.4	17	4	US-09-371-772B-226	Sequence 226, App
	58	10.8	51.4	17	4	US-09-685-664B-226	Sequence 226, App
c	59	10.8	51.4	18	2	US-08-505-617-13	Sequence 13, Appl
c	60	10.8	51.4	18	2	US-08-928-692-67	Sequence 67, Appl
c	61	10.8	51.4	18	2	US-09-018-170-13	Sequence 13, Appl
c	62	10.8	51.4	18	3	US-09-339-972-67	Sequence 67, Appl
c	63	10.8	51.4	19	4	US-09-422-978-9661	Sequence 9661, Ap
c	64	10.8	51.4	19	4	US-09-575-081B-14	Sequence 14, Appl
c	65	10.8	51.4	20	1	US-08-474-542A-109	Sequence 109, App
	66	10.8	51.4	20	1	US-08-474-542A-115	Sequence 115, App
c	67	10.8	51.4	20	1	US-08-457-648-109	Sequence 109, App
	68	10.8	51.4	20	1	US-08-457-648-115	Sequence 115, App
	69	10.8	51.4	20	3	US-09-289-267-74	Sequence 74, Appl
	70	10.8	51.4	20	3	US-09-326-186B-185	Sequence 185, App
	71	10.8	51.4	20	4	US-09-198-452A-1961	Sequence 1961, Ap
	72	10.8	51.4	21	1	US-08-588-821-6	Sequence 6, Appli
	73	10.8	51.4	21	1	US-08-915-214-6	Sequence 6, Appli
	74	10.8	51.4	21	2	US-09-005-532-6	Sequence 6, Appli
	75	10.8	51.4	21	2	US-09-001-826-16	Sequence 16, Appl
	76	10.8	51.4	21	3	US-09-091-952A-169	Sequence 169, App
	77	10.8	51.4	21	4	US-09-264-854-16	Sequence 16, Appl
c	78	10.8	51.4	21	4	US-09-657-472-1398	Sequence 1398, Ap
c	79	10.6	50.5	17	4	US-09-866-108A-9827	Sequence 9827, Ap
c	80	10.6	50.5	18	3	US-09-632-580A-87	Sequence 87, Appl
c	81	10.6	50.5	20	1	US-08-525-697-6	Sequence 6, Appli
c	82	10.6	50.5	20	3	US-09-489-868A-39	Sequence 39, Appl
c	83	10.6	50.5	20	3	US-09-851-520-30	Sequence 30, Appl
c	84	10.6	50.5	20	4	US-09-198-452A-2221	Sequence 2221, Ap
	85	10.6	50.5	21	3	US-08-276-968A-25	Sequence 25, Appl
	86	10.4	49.5	17	4	US-09-404-912-381	Sequence 381, App
	87	10.4	49.5	18	2	US-08-432-871C-28	Sequence 28, Appl
	88	10.4	49.5	18	3	US-09-474-922A-69	Sequence 69, Appl
	89	10.4	49.5	18	3	US-09-270-956-28	Sequence 28, Appl
	90	10.4	49.5	19	2	US-08-860-882A-52	Sequence 52, Appl
	91	10.4	49.5	19	3	US-09-171-945-110	Sequence 110, App
	92	10.4	49.5	19	3	US-09-011-769A-34	Sequence 34, Appl
	93	10.4	49.5	20	1	US-08-588-821-54	Sequence 54, Appl
	94	10.4	49.5	20	1	US-08-915-214-54	Sequence 54, Appl
	95	10.4	49.5	20	2	US-09-005-532-54	Sequence 54, Appl
c	96	10.4	49.5	20	3	US-09-288-461-92	Sequence 92, Appl
c	97	10.4	49.5	20	3	US-09-487-368A-228	Sequence 228, App
c	98	10.4	49.5	20	3	US-09-791-211-84	Sequence 84, Appl
	99	10.4	49.5	20	3	US-09-485-077A-2	Sequence 2, Appli
c	100	10.4	49.5	20	4	US-09-629-644A-228	Sequence 228, App

ALIGNMENTS

RESULT 1
US-08-842-079-3
; Sequence 3, Application US/08842079
; Patent No. 6133434
; GENERAL INFORMATION:
; APPLICANT: BUELL, GARY N.
; APPLICANT: SURPRENANT, ANNMARIE
; APPLICANT: KAWASHIMA, ERIC
; TITLE OF INVENTION: A PURINERGIC RECEPTOR
; FILE REFERENCE: 1430-160
; CURRENT APPLICATION NUMBER: US/08/842,079
; CURRENT FILING DATE: 1997-04-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-08-842-079-3

Query Match 61.9%; Score 13; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGCGTATCTGAAG 15
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Db 1 GGCGTATCTGAAG 13

RESULT 2
US-09-638-857-3
; Sequence 3, Application US/09638857
; Patent No. 6509163
; GENERAL INFORMATION:
; APPLICANT: BUELL, GARY N.
; APPLICANT: SURPRENANT, ANNMARIE
; APPLICANT: KAWASHIMA, ERIC
; TITLE OF INVENTION: A PURINERGIC RECEPTOR
; FILE REFERENCE: 1430-160
; CURRENT APPLICATION NUMBER: US/09/638,857
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: 08/842,079
; PRIOR FILING DATE: 1997-04-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Synthetic
US-09-638-857-3

Query Match 61.9%; Score 13; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GGCGTATCTGAAG 15
||||||||||||| |
Db 1 GGCGTATCTGAAG 13

RESULT 3
US-08-985-162-448/c
; Sequence 448, Application US/08985162
; Patent No. 6057156
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; MEDIUM TYPE: storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: IBM P.C. DOS 5.0
; SOFTWARE: FastSEQ for Windows 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/985,162
; FILING DATE: 04 December 1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/036,476
; FILING DATE: 31 January 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 230/107
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 448:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-985-162-448

Query Match 61.0%; Score 12.8; DB 3; Length 17;
Best Local Similarity 87.5%; Pred. No. 3.6e+03;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GTATCTGAAGAGTCTG 21
||||| |||||||||
Db 16 GTATCGAAAGAGTCTG 1

RESULT 4
US-09-401-063-448/c
; Sequence 448, Application US/09401063
; Patent No. 6623962
; GENERAL INFORMATION:
; APPLICANT: Akhtar, Saghir
; APPLICANT: Fell, Patricia
; APPLICANT: McSwiggen, James
; TITLE OF INVENTION: ENZYMATIC NUCLEIC ACID TREATMENT
; TITLE OF INVENTION: OF DISEASES OR CONDITIONS RELATED
; TITLE OF INVENTION: TO LEVELS OF EPIDERMAL GROWTH
; TITLE OF INVENTION: FACTOR RECEPTORS
; NUMBER OF SEQUENCES: 1877
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles

```
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/401,063
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/985,162
;      FILING DATE:  04 December 1997
;      APPLICATION NUMBER:  60/036,476
;      FILING DATE:  31 January 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  230/107
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213)  955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  448:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-401-063-448

  Query Match             61.0%;  Score 12.8;  DB 4;  Length 17;
  Best Local Similarity   87.5%;  Pred. No. 3.6e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 GTATCTGAAGAGTCTG 21
              ||||| |||||||||
Db         16 GTATCGAAAGAGTCTG 1


RESULT 5
US-08-450-905B-134/c
; Sequence 134, Application US/08450905B
; Patent No. 5856301
;  GENERAL INFORMATION:
;    APPLICANT:
;    TITLE OF INVENTION:  Stem Cell Inhibiting Proteins
;    NUMBER OF SEQUENCES:  178
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HALE and DORR
;      STREET:  60 State Street
;      CITY:  Boston
;      STATE:  MA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/450,905B
;      FILING DATE:  26-MAR-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  07/982,759
;      FILING DATE:  08-MAR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9127319.3
;      FILING DATE:  23-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9221587.0
;      FILING DATE:  14-OCT-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BAKER, HOLLIE L.
;      REGISTRATION NUMBER:  31,321
;      REFERENCE/DOCKET NUMBER:  102.378.120DV-2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-526-6110
;      TELEFAX:  617-526-5000
;  INFORMATION FOR SEQ ID NO:  134:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20  base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..20
;      OTHER INFORMATION:  /product= "BB9513 oligomer"
US-08-450-905B-134

  Query Match             61.0%;  Score 12.8;  DB 2;  Length 20;
  Best Local Similarity   87.5%;  Pred. No. 3.6e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CTGGCGTATCTGAAGA 16
              ||| || |||||||||
Db         17 CTGACGCATCTGAAGA 2


RESULT 6
US-07-982-759F-134/c
; Sequence 134, Application US/07982759F
; Patent No. 6057123
;  GENERAL INFORMATION:
;    APPLICANT:  CRAIG, Stewart
;    APPLICANT:  GEORGE, Michael
;    APPLICANT:  EDWARDS, Richard Mark
;    APPLICANT:  CZAPLEWSKI, Lloyd George
;    APPLICANT:  GILBERT, Richard
;    TITLE OF INVENTION:  Stem Cell Inhibiting Proteins
;    NUMBER OF SEQUENCES:  178
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  HALE and DORR LLP
;      STREET:  60 State Street
;      CITY:  Boston
;      STATE:  MA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/982,759F
;      FILING DATE:  08-MAR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9127319.3
;      FILING DATE:  23-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  GB 9221587.0
;      FILING DATE:  14-OCT-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BAKER, HOLLIE L.
;      REGISTRATION NUMBER:  31,321
;      REFERENCE/DOCKET NUMBER:  102378.120
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-526-6000
;      TELEFAX:  617-526-5000
;  INFORMATION FOR SEQ ID NO:  134:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20  base pairs
;      TYPE:  nucleic acid
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;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
;    FEATURE:
;      NAME/KEY:  misc_feature
;      LOCATION:  1..20
;      OTHER INFORMATION:  /product= "BB9513 oligomer"
US-07-982-759F-134

  Query Match             61.0%;  Score 12.8;  DB 3;  Length 20;
  Best Local Similarity   87.5%;  Pred. No. 3.6e+03;
  Matches   14;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CTGGCGTATCTGAAGA 16
              ||| || |||||||||
Db         17 CTGACGCATCTGAAGA 2


RESULT 7
US-08-985-162-449/c
; Sequence 449, Application US/08985162
; Patent No. 6057156
;  GENERAL INFORMATION:
;    APPLICANT:  Akhtar, Saghir
;    APPLICANT:  Fell, Patricia
;    APPLICANT:  McSwiggen, James
;    TITLE OF INVENTION:  ENZYMATIC NUCLEIC ACID TREATMENT
;    TITLE OF INVENTION:  OF DISEASES OR CONDITIONS RELATED
;    TITLE OF INVENTION:  TO LEVELS OF EPIDERMAL GROWTH
;    TITLE OF INVENTION:  FACTOR RECEPTORS
;    NUMBER OF SEQUENCES:  1877
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/985,162
;      FILING DATE:  04 December 1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/036,476
;      FILING DATE:  31 January 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  230/107
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213)  955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  449:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-985-162-449

  Query Match             58.1%;  Score 12.2;  DB 3;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 7.2e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 GCGTATCTGAAGAGTCT 20
              | |||||  ||||||||
Db         17 GGGTATCGAAAGAGTCT 1


RESULT 8
US-09-401-063-449/c
; Sequence 449, Application US/09401063
; Patent No. 6623962
;  GENERAL INFORMATION:
;    APPLICANT:  Akhtar, Saghir
;    APPLICANT:  Fell, Patricia
;    APPLICANT:  McSwiggen, James
;    TITLE OF INVENTION:  ENZYMATIC NUCLEIC ACID TREATMENT
;    TITLE OF INVENTION:  OF DISEASES OR CONDITIONS RELATED
;    TITLE OF INVENTION:  TO LEVELS OF EPIDERMAL GROWTH
;    TITLE OF INVENTION:  FACTOR RECEPTORS
;    NUMBER OF SEQUENCES:  1877
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/401,063
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/985,162
;      FILING DATE:  04 December 1997
;      APPLICATION NUMBER:  60/036,476
;      FILING DATE:  31 January 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  230/107
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213)  955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  449:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-401-063-449

  Query Match             58.1%;  Score 12.2;  DB 4;  Length 17;
  Best Local Similarity   82.4%;  Pred. No. 7.2e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 GCGTATCTGAAGAGTCT 20
              | |||||  ||||||||
Db         17 GGGTATCGAAAGAGTCT 1


RESULT 9
US-08-717-291-8
; Sequence 8, Application US/08717291
; Patent No. 5908773
;  GENERAL INFORMATION:
;    APPLICANT:  Cesarman, Ethel
;    APPLICANT:  Arvanitakis, Leandros
;    APPLICANT:  Knowles, Daniel M.
```

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;    APPLICANT:  Mesri, Enrique
;    TITLE OF INVENTION:  KSHV POSITIVE CELL LINES
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON, HARGRAVE, DEVANS & DOYLE LLP
;      STREET:  Clinton Square, P.O. Box 1051
;      CITY:  Rochester
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  14603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/717,291
;      FILING DATE:
;      CLASSIFICATION:  530
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BRAMAN, SUSAN J.
;      REGISTRATION NUMBER:  34,103
;      REFERENCE/DOCKET NUMBER:  19603/1360
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  716-263-1636
;      TELEFAX:  716-263-1600
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-717-291-8

  Query Match             58.1%;  Score 12.2;  DB 2;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 7.3e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 CGTATCTGAAGAGTCTG 21
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Db          1 CGGAGCTAAAGAGTCTG 17


RESULT 10
US-08-728-603-8
; Sequence 8, Application US/08728603
; Patent No. 6093806
;  GENERAL INFORMATION:
;    APPLICANT:  Cesarman, Ethel
;    APPLICANT:  Knowles, Daniel M.
;    TITLE OF INVENTION:  PROTEINS OF KAPOSI'S SARCOMA ASSOCIATED
;    TITLE OF INVENTION:  HERPESVIRUS
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON, HARGRAVE, DEVANS & DOYLE LLP
;      STREET:  Clinton Square, P.O. Box 1051
;      CITY:  Rochester
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  14603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/728,603
;      FILING DATE:  10-OCT-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BRAMAN, SUSAN J.
;      REGISTRATION NUMBER:  34,103
;      REFERENCE/DOCKET NUMBER:  19603/720
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  716-263-1636
;      TELEFAX:  716-263-1600
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-08-728-603-8

  Query Match             58.1%;  Score 12.2;  DB 3;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 7.3e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 CGTATCTGAAGAGTCTG 21
              || | || |||||||||
Db          1 CGGAGCTAAAGAGTCTG 17


RESULT 11
US-09-433-699-73/c
; Sequence 73, Application US/09433699B
; Patent No. 6165786
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT: Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF NUCLEOLIN EXPRESSION
;  FILE REFERENCE: RTS-0109
;  CURRENT APPLICATION NUMBER: US/09/433,699B
;  CURRENT FILING DATE: 1999-11-03
;  NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 73
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-433-699-73

  Query Match             57.1%;  Score 12;  DB 3;  Length 20;
  Best Local Similarity   75.0%;  Pred. No. 9.3e+03;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 TGGCGTATCTGAAGAGTCTG 21
              |||| |||| ||| || ||
Db         20 TGGCAAATCTAAAGGGTATG 1


RESULT 12
US-09-371-772B-5737
; Sequence 5737, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5737
```

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;   LENGTH: 16
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-371-772B-5737

  Query Match             56.2%;  Score 11.8;  DB 4;  Length 16;
  Best Local Similarity   73.3%;  Pred. No. 1.1e+04;
  Matches   11;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GGCGTATCTGAAGAG 17
              | ||:| |:||||||
Db          2 GACGUAACUGAAGAG 16


RESULT 13
US-07-852-260-4
; Sequence 4, Application US/07852260
; Patent No. 5525715
;  GENERAL INFORMATION:
;    APPLICANT:  Racaniello, Vincent
;    APPLICANT:  Tatem, Joanne M.
;    APPLICANT:  Weeks-Levy, Carolyn L.
;    TITLE OF INVENTION:  METHODS FOR PRODUCING RNA VIRUSES FROM
;    TITLE OF INVENTION:  cDNA
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham
;      STREET:  30 Rockefeller Plaza
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10112
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/852,260
;      FILING DATE:  19920619
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  36607-B-PCT-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 977-9550
;      TELEFAX:  (212) 664-0525
;      TELEX:  422523 COOP UI
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-07-852-260-4

  Query Match             56.2%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 1.1e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GGCGTATCTGAAGAG 17
              |||||||||||  ||
Db          1 GGCGTATCTGACAAG 15


RESULT 14
US-07-936-421-18
; Sequence 18, Application US/07936421
; Patent No. 5750390
;  GENERAL INFORMATION:
;    APPLICANT:  James D. Thompson
;    APPLICANT:  Kenneth G. Draper
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR
;    TITLE OF INVENTION:  TREATMENT OF DISEASES CAUSED
;    TITLE OF INVENTION:  BY EXPRESSION OF THE BCL-2
;    TITLE OF INVENTION:  GENE
;    NUMBER OF SEQUENCES:  22
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  611 West Sixth Street
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  90017
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS (Version 5.0)
;      SOFTWARE:  WordPerfect (Version 5.1)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/936,421
;      FILING DATE:  19920826
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;    PRIOR APPLICATION DATA:  including application
;    PRIOR APPLICATION DATA:  described below:                    none
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  197/243
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-07-936-421-18

  Query Match             56.2%;  Score 11.8;  DB 1;  Length 17;
  Best Local Similarity   53.3%;  Pred. No. 1.1e+04;
  Matches    8;  Conservative    5;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 GTATCTGAAGAGTCT 20
              |: :|:||||| :|:
Db          3 GUCUCUGAAGACUCU 17


RESULT 15
US-08-461-503-4
; Sequence 4, Application US/08461503
; Patent No. 5834302
;  GENERAL INFORMATION:
;    APPLICANT:  Racaniello, Vincent
;    APPLICANT:  Tatem, Joanne M.
;    APPLICANT:  Weeks-Levy, Carolyn L.
;    TITLE OF INVENTION:  METHODS FOR PRODUCING RNA VIRUSES
;    TITLE OF INVENTION:  FROM cDNA
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10112
;    COMPUTER READABLE FORM:
```

```
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/461,503
;      FILING DATE:  5-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  36607-D-PCT-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 278-0400
;      TELEFAX:  (212) 391-0525
;      TELEX:  422523 COOP UI
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-461-503-4

  Query Match             56.2%;  Score 11.8;  DB 2;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 1.1e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GGCGTATCTGAAGAG 17
              ||||||||||| ||
Db          1 GGCGTATCTGACAAG 15


RESULT 16
US-08-985-162-447/c
; Sequence 447, Application US/08985162
; Patent No. 6057156
;  GENERAL INFORMATION:
;    APPLICANT:  Akhtar, Saghir
;    APPLICANT:  Fell, Patricia
;    APPLICANT:  McSwiggen, James
;    TITLE OF INVENTION:  ENZYMATIC NUCLEIC ACID TREATMENT
;    TITLE OF INVENTION:  OF DISEASES OR CONDITIONS RELATED
;    TITLE OF INVENTION:  TO LEVELS OF EPIDERMAL GROWTH
;    TITLE OF INVENTION:  FACTOR RECEPTORS
;    NUMBER OF SEQUENCES:  1877
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/985,162
;      FILING DATE:  04 December 1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/036,476
;      FILING DATE:  31 January 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  230/107
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213)  955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  447:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-985-162-447

  Query Match             56.2%;  Score 11.8;  DB 3;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 1.1e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 TATCTGAAGAGTCTG 21
              ||||  |||||||||
Db         17 TATCGAAAGAGTCTG 3


RESULT 17
US-08-465-250-4
; Sequence 4, Application US/08465250
; Patent No. 6136570
;  GENERAL INFORMATION:
;    APPLICANT:  Racaniello, Vincent
;    APPLICANT:  Tatem, Joanne M.
;    APPLICANT:  Weeks-Levy, Carolyn L.
;    TITLE OF INVENTION:  METHODS FOR PRODUCING RNA VIRUSES FROM
;    TITLE OF INVENTION:  cDNA
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Cooper & Dunham LLP
;      STREET:  1185 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release 1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/465,250
;      FILING DATE:  6-JUN-1995
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  White, John P.
;      REGISTRATION NUMBER:  28,678
;      REFERENCE/DOCKET NUMBER:  36607-E-PCT-US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 278-0400
;      TELEFAX:  (212) 391-0525
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
US-08-465-250-4

  Query Match             56.2%;  Score 11.8;  DB 3;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 1.1e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GGCGTATCTGAAGAG 17
```

```
              ||||||||||| ||
Db          1 GGCGTATCTGACAAG 15


RESULT 18
US-09-371-772B-4438
; Sequence 4438, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4438
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-371-772B-4438

  Query Match             56.2%;  Score 11.8;  DB 4;  Length 17;
  Best Local Similarity   73.3%;  Pred. No. 1.1e+04;
  Matches   11;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GGCGTATCTGAAGAG 17
              | ||:| |:||||||
Db          1 GACGUAACUGAAGAG 15


RESULT 19
US-09-401-063-447/c
; Sequence 447, Application US/09401063
; Patent No. 6623962
;  GENERAL INFORMATION:
;    APPLICANT:  Akhtar, Saghir
;    APPLICANT:  Fell, Patricia
;    APPLICANT:  McSwiggen, James
;    TITLE OF INVENTION:  ENZYMATIC NUCLEIC ACID TREATMENT
;    TITLE OF INVENTION:  OF DISEASES OR CONDITIONS RELATED
;    TITLE OF INVENTION:  TO LEVELS OF EPIDERMAL GROWTH
;    TITLE OF INVENTION:  FACTOR RECEPTORS
;    NUMBER OF SEQUENCES:  1877
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/401,063
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/985,162
;      FILING DATE:  04 December 1997
;      APPLICATION NUMBER:  60/036,476
;      FILING DATE:  31 January 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  230/107
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213)  955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  447:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-401-063-447

  Query Match             56.2%;  Score 11.8;  DB 4;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 1.1e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 TATCTGAAGAGTCTG 21
              |||| |||||||||
Db         17 TATCGAAAGAGTCTG 3


RESULT 20
US-09-488-857B-38/c
; Sequence 38, Application US/09488857B
; Patent No. 6255110
; GENERAL INFORMATION:
;  APPLICANT:      Lex M. Cowsert
;  APPLICANT:  Jacqueline Wyatt
;  TITLE OF INVENTION:      ANTISENSE MODULATION OF ARA70 EXPRESSION
;  FILE REFERENCE:      RTS-0117
;  CURRENT APPLICATION NUMBER: US/09/488,857B
;  CURRENT FILING DATE:  2000-01-21
;  NUMBER OF SEQ ID NOS:      90
; SEQ ID NO 38
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-488-857B-38

  Query Match             56.2%;  Score 11.8;  DB 3;  Length 20;
  Best Local Similarity   86.7%;  Pred. No. 1.2e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CTGGCGTATCTGAAG 15
              ||||| ||||||||
Db         16 CTGGCCAATCTGAAG 2


RESULT 21
US-09-198-452A-1366
; Sequence 1366, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, prever
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/09/198,452A
;  CURRENT FILING DATE:  1998-11-24
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1366
;   LENGTH: 20
;   TYPE: DNA
```

```
;   ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1366

  Query Match             56.2%;  Score 11.8;  DB 4;  Length 20;
  Best Local Similarity   86.7%;  Pred. No. 1.2e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 GCGTATCTGAAGAGT 18
              ||| |||||| ||||
Db          1 GCGGATCTGAGGAGT 15


RESULT 22
US-09-478-189-118/c
; Sequence 118, Application US/09478189
; Patent No. 6534293
; GENERAL INFORMATION:
;  APPLICANT:  Barany, Francis
;  APPLICANT:  Liu, Jianzhao
;  APPLICANT:  Kirk, Brian W.
;  APPLICANT:  Zirvi, Monib
;  APPLICANT:  Gerry, No. 6534293man P.
;  APPLICANT:  Paty, Philip B.
;  TITLE OF INVENTION:  ACCELERATING IDENTIFICATION OF SINGLE NUCLEOTIDE
;  TITLE OF INVENTION:  POLYMORPHISMS AND ALIGNMENT OF CLONES IN GENOMIC
;  TITLE OF INVENTION:  SEQUENCING
;  FILE REFERENCE:  19603/2621
;  CURRENT APPLICATION NUMBER: US/09/478,189
;  CURRENT FILING DATE:  2000-01-05
;  PRIOR APPLICATION NUMBER:  60/114,881
;  PRIOR FILING DATE:  1999-01-06
;  NUMBER OF SEQ ID NOS:  181
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 118
;    LENGTH: 21
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Description of Artificial Sequence:  probe/primer
US-09-478-189-118

  Query Match             56.2%;  Score 11.8;  DB 4;  Length 21;
  Best Local Similarity   86.7%;  Pred. No. 1.2e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CTGGCGTATCTGAAG 15
              |||| || |||||||
Db         17 CTGGTGTGTCTGAAG 3


RESULT 23
US-09-280-805-129
; Sequence 129, Application US/09280805
; Patent No. 6184212
;  GENERAL INFORMATION:
;    APPLICANT:  Loren J. Miraglia, Pamela Nero, Mark J.
;    APPLICANT:  Graham, Brett P. Monia
;    TITLE OF INVENTION:  ANTISENSE MODULATION OF HUMAN MDM2
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  271
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Law Offices of Jane Massey Licata
;      STREET:  66 East Main Street
;      CITY:  Marlton
;      STATE:  NJ
;      COUNTRY:  U.S.A.
;      ZIP:  08053
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;      COMPUTER:  IBM PC
;      OPERATING SYSTEM:  WINDOWS 95
;      SOFTWARE:  WORDPERFECT 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/280,805
;      FILING DATE:  herewith
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/048,810
;      FILING DATE:  March 26, 1998
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Licata, Jane Massey
;      REGISTRATION NUMBER:  32,257
;      REFERENCE/DOCKET NUMBER:  ISPH-0346
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-810-1515
;      TELEFAX:  609-810-1454
;  INFORMATION FOR SEQ ID NO:  129:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
;    ANTI-SENSE:  Yes
US-09-280-805-129

  Query Match             55.2%;  Score 11.6;  DB 3;  Length 20;
  Best Local Similarity   77.8%;  Pred. No. 1.5e+04;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 TGGCGTATCTGAAGAGTC 19
              ||||||  ||| ||| ||
Db          1 TGGCGTCCCTGTAGATTC 18


RESULT 24
US-09-517-467B-30
; Sequence 30, Application US/09517467B
; Patent No. 6451602
; GENERAL INFORMATION:
;  APPLICANT: Ian Popoff
;  APPLICANT:  Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PARP EXPRESSION
;  FILE REFERENCE: RTS-0150
;  CURRENT APPLICATION NUMBER: US/09/517,467B
;  CURRENT FILING DATE:  2001-03-02
;  PRIOR APPLICATION NUMBER: 09/517,467
;  PRIOR FILING DATE: 2000-03-02
;  NUMBER OF SEQ ID NOS: 345
; SEQ ID NO 30
;    LENGTH: 20
;    TYPE: DNA
;    ORGANISM: Artificial Sequence
;    FEATURE:
;    OTHER INFORMATION: Antisense Oligonucleotide
US-09-517-467B-30

  Query Match             55.2%;  Score 11.6;  DB 3;  Length 20;
  Best Local Similarity   77.8%;  Pred. No. 1.5e+04;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 GCGTATCTGAAGAGTCTG 21
              || |||| ||||| || |
Db          1 GCTTATCCGAAGACTCCG 18


RESULT 25
US-09-198-452A-2767/c
; Sequence 2767, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, preve
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/09/198,452A
```

```
;  CURRENT FILING DATE:  1998-11-24
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 2767
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
US-09-198-452A-2767

  Query Match             55.2%;  Score 11.6;  DB 4;  Length 20;
  Best Local Similarity   77.8%;  Pred. No. 1.5e+04;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 GCGTATCTGAAGAGTCTG 21
              || | |||||| || |||
Db         20 GCTTCTCTGAACAGACTG 3


RESULT 26
US-09-657-289A-12/c
; Sequence 12, Application US/09657289A
; Patent No. 6737245
; GENERAL INFORMATION:
;  APPLICANT: Francis, Kevin P.
;  APPLICANT:  Contag, Pamela R.
;  APPLICANT:  Joh, Danny J.
;  TITLE OF INVENTION: LUCIFERASE EXPRESSION CASSETTES AND METHODS OF USE
;  FILE REFERENCE: 9400-0006
;  CURRENT APPLICATION NUMBER: US/09/657,289A
;  CURRENT FILING DATE:  2000-09-07
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: LUXA-REV
US-09-657-289A-12

  Query Match             55.2%;  Score 11.6;  DB 4;  Length 20;
  Best Local Similarity   77.8%;  Pred. No. 1.5e+04;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 GCGTATCTGAAGAGTCTG 21
              || | ||||| |||| ||
Db         19 GCATCTCTGAGGAGTGTG 2


RESULT 27
US-09-657-472-1916/c
; Sequence 1916, Application US/09657472
; Patent No. 6727063
; GENERAL INFORMATION:
;  APPLICANT: Lander, Eric S.
;  APPLICANT:  Cargill, Michele
;  APPLICANT:  Ireland, James S.
;  APPLICANT:  Bolk, Stacey
;  APPLICANT:  Daley, George Q.
;  APPLICANT:  McCarthy, Jeanette J.
;  TITLE OF INVENTION: SINGLE NUCLEOTIDE POLYMORPHISMS IN GENES
;  FILE REFERENCE: 2825.1027-001
;  CURRENT APPLICATION NUMBER: US/09/657,472
;  CURRENT FILING DATE:  2000-09-07
;  PRIOR APPLICATION NUMBER: US 60/153,357
;  PRIOR FILING DATE: 1999-09-10
;  PRIOR APPLICATION NUMBER: US 60/220,947
;  PRIOR FILING DATE: 2000-07-26
;  PRIOR APPLICATION NUMBER: US 60/225,724
;  PRIOR FILING DATE: 2000-08-16
;  NUMBER OF SEQ ID NOS: 2551
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1916
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-657-472-1916

  Query Match             55.2%;  Score 11.6;  DB 4;  Length 21;
  Best Local Similarity   91.7%;  Pred. No. 1.5e+04;
  Matches   11;  Conservative    1;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 CTGAAGAGTCTG 21
              |||||:||||||
Db         16 CTGAARAGTCTG 5


RESULT 28
US-09-422-978-6486/c
; Sequence 6486, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT: Blumenfeld, Marta
;  APPLICANT: Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/09/422,978
;  CURRENT FILING DATE: 1999-10-20
;  EARLIER APPLICATION NUMBER: US 09/298,850
;  EARLIER FILING DATE: 1999-04-21
;  EARLIER APPLICATION NUMBER: US 60/109,732
;  EARLIER FILING DATE: 1998-11-23
;  EARLIER APPLICATION NUMBER: US 60/082,614
;  EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 6486
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..19
;   OTHER INFORMATION: upstream amplification primer 99-11786 for SEQ 2552,
US-09-422-978-6486

  Query Match             54.3%;  Score 11.4;  DB 4;  Length 19;
  Best Local Similarity   92.3%;  Pred. No. 1.9e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CTGGCGTATCTGA 13
              ||||| |||||||
Db         17 CTGGCTTATCTGA 5


RESULT 29
US-08-602-093-12/c
; Sequence 12, Application US/08602093
; Patent No. 5837535
;  GENERAL INFORMATION:
;    APPLICANT:  Joseph, Rajiv
;    APPLICANT:  Dou, Dexian
;    TITLE OF INVENTION:  A NOVEL NEURONAL-NEONATAL GENE:
;    TITLE OF INVENTION:  NEURONATIN
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Kohn & Associates
;      STREET:  30500 No. 5837535thwestern Hwy.
;      CITY:  Farmington Hills
;      STATE:  Michigan
;      COUNTRY:  US
;      ZIP:  48334
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
```

```
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/602,093
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Kohn, Kenneth I.
;      REGISTRATION NUMBER:  30,995
;      REFERENCE/DOCKET NUMBER:  1059.00015
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (810) 539-5050
;      TELEFAX:  (810) 539-5055
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-602-093-12

  Query Match             54.3%;  Score 11.4;  DB 2;  Length 20;
  Best Local Similarity   92.3%;  Pred. No. 1.9e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 GTATCTGAAGAGT 18
              ||| |||||||||
Db         19 GTACCTGAAGAGT 7


RESULT 30
US-08-985-162-450/c
; Sequence 450, Application US/08985162
; Patent No. 6057156
;  GENERAL INFORMATION:
;    APPLICANT:  Akhtar, Saghir
;    APPLICANT:  Fell, Patricia
;    APPLICANT:  McSwiggen, James
;    TITLE OF INVENTION:  ENZYMATIC NUCLEIC ACID TREATMENT
;    TITLE OF INVENTION:  OF DISEASES OR CONDITIONS RELATED
;    TITLE OF INVENTION:  TO LEVELS OF EPIDERMAL GROWTH
;    TITLE OF INVENTION:  FACTOR RECEPTORS
;    NUMBER OF SEQUENCES:  1877
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/985,162
;      FILING DATE:  04 December 1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/036,476
;      FILING DATE:  31 January 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  230/107
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213)  955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  450:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-985-162-450

  Query Match             53.3%;  Score 11.2;  DB 3;  Length 17;
  Best Local Similarity   81.2%;  Pred. No. 2.3e+04;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 GCGTATCTGAAGAGTC 19
              | |||||  |||||||
Db         16 GGGTATCGAAAGAGTC 1


RESULT 31
US-09-401-063-450/c
; Sequence 450, Application US/09401063
; Patent No. 6623962
;  GENERAL INFORMATION:
;    APPLICANT:  Akhtar, Saghir
;    APPLICANT:  Fell, Patricia
;    APPLICANT:  McSwiggen, James
;    TITLE OF INVENTION:  ENZYMATIC NUCLEIC ACID TREATMENT
;    TITLE OF INVENTION:  OF DISEASES OR CONDITIONS RELATED
;    TITLE OF INVENTION:  TO LEVELS OF EPIDERMAL GROWTH
;    TITLE OF INVENTION:  FACTOR RECEPTORS
;    NUMBER OF SEQUENCES:  1877
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/401,063
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/985,162
;      FILING DATE:  04 December 1997
;      APPLICATION NUMBER:  60/036,476
;      FILING DATE:  31 January 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  230/107
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213)  955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  450:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-401-063-450

  Query Match             53.3%;  Score 11.2;  DB 4;  Length 17;
  Best Local Similarity   81.2%;  Pred. No. 2.3e+04;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 GCGTATCTGAAGAGTC 19
              | |||||  |||||||
Db         16 GGGTATCGAAAGAGTC 1
```

```
RESULT 32
US-09-422-978-5682
; Sequence 5682, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT: Blumenfeld, Marta
;  APPLICANT: Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/09/422,978
;  CURRENT FILING DATE: 1999-10-20
;  EARLIER APPLICATION NUMBER: US 09/298,850
;  EARLIER FILING DATE: 1999-04-21
;  EARLIER APPLICATION NUMBER: US 60/109,732
;  EARLIER FILING DATE: 1998-11-23
;  EARLIER APPLICATION NUMBER: US 60/082,614
;  EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 5682
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..18
;   OTHER INFORMATION: upstream amplification primer 99-6097 for SEQ 1748,
US-09-422-978-5682

  Query Match             53.3%;  Score 11.2;  DB 4;  Length 18;
  Best Local Similarity   81.2%;  Pred. No. 2.3e+04;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          6 GTATCTGAAGAGTCTG 21
              ||  ||||| ||||||
Db          3 GTCCCTGAAAAGTCTG 18


RESULT 33
US-08-555-678-57
; Sequence 57, Application US/08555678
; Patent No. 5763174
;  GENERAL INFORMATION:
;    APPLICANT:  Nishikura, Kazuko
;    TITLE OF INVENTION:  RNA Editing Enzyme and Methods
;    TITLE OF INVENTION:  of Use Thereof
;    NUMBER OF SEQUENCES:  67
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Cntr, P.O. Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/555,678
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/197,794
;      FILING DATE:  17-FEB-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/280,443
;      FILING DATE:  25-JUL-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/457,459
;      FILING DATE:  01-JUN-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST49DUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  57:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  19 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  other nucleic acid
;      DESCRIPTION:  /desc = "primer"
US-08-555-678-57

  Query Match             53.3%;  Score 11.2;  DB 1;  Length 19;
  Best Local Similarity   81.2%;  Pred. No. 2.4e+04;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          6 GTATCTGAAGAGTCTG 21
              ||||||||   |||||
Db          4 GTATCTGAGCTGTCTG 19


RESULT 34
US-09-422-978-4659/c
; Sequence 4659, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT: Blumenfeld, Marta
;  APPLICANT: Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/09/422,978
;  CURRENT FILING DATE: 1999-10-20
;  EARLIER APPLICATION NUMBER: US 09/298,850
;  EARLIER FILING DATE: 1999-04-21
;  EARLIER APPLICATION NUMBER: US 60/109,732
;  EARLIER FILING DATE: 1998-11-23
;  EARLIER APPLICATION NUMBER: US 60/082,614
;  EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4659
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..19
;   OTHER INFORMATION: upstream amplification primer 99-16867 for SEQ 725,
US-09-422-978-4659

  Query Match             53.3%;  Score 11.2;  DB 4;  Length 19;
  Best Local Similarity   81.2%;  Pred. No. 2.4e+04;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CTGGCGTATCTGAAGA 16
              ||||| |  |||||||
Db         16 CTGGCATTGCTGAAGA 1


RESULT 35
US-09-696-791-466/c
; Sequence 466, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
;  APPLICANT:  Robbins, Joan M.
;  APPLICANT:  Tritz, Richard
;  TITLE OF INVENTION:  RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
```

```
;  TITLE OF INVENTION:  SKIN AND EYE DISEASES
;  FILE REFERENCE:  480124.407
;  CURRENT APPLICATION NUMBER: US/09/696,791
;  CURRENT FILING DATE:  2000-10-25
;  NUMBER OF SEQ ID NOS:  4523
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 466
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Cdk4 ribozyme binding site
US-09-696-791-466

  Query Match             53.3%;  Score 11.2;  DB 4;  Length 19;
  Best Local Similarity   81.2%;  Pred. No. 2.4e+04;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          6 GTATCTGAAGAGTCTG 21
              ||| ||| ||| ||||
Db         19 GTAGCTGTAGATTCTG 4


RESULT 36
US-09-696-791-467/c
; Sequence 467, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
;  APPLICANT:  Robbins, Joan M.
;  APPLICANT:  Tritz, Richard
;  TITLE OF INVENTION:  RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
;  TITLE OF INVENTION:  SKIN AND EYE DISEASES
;  FILE REFERENCE:  480124.407
;  CURRENT APPLICATION NUMBER: US/09/696,791
;  CURRENT FILING DATE:  2000-10-25
;  NUMBER OF SEQ ID NOS:  4523
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 467
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Cdk4 ribozyme binding site
US-09-696-791-467

  Query Match             53.3%;  Score 11.2;  DB 4;  Length 19;
  Best Local Similarity   81.2%;  Pred. No. 2.4e+04;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          6 GTATCTGAAGAGTCTG 21
              ||| ||| ||| ||||
Db         17 GTAGCTGTAGATTCTG 2


RESULT 37
US-09-488-671-22
; Sequence 22, Application US/09488671A
; Patent No. 6187545
; GENERAL INFORMATION:
;  APPLICANT: Robert McKay
;  APPLICANT: Madeline M. Butler
;  APPLICANT: Jacqueline Wyatt
;  APPLICANT: Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PEPCK-CYTOSOLIC EXPRESSION
;  FILE REFERENCE: RTS-0123
;  CURRENT APPLICATION NUMBER: US/09/488,671A
;  CURRENT FILING DATE: 2000-01-21
;  NUMBER OF SEQ ID NOS: 177
; SEQ ID NO 22
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-488-671-22

  Query Match             53.3%;  Score 11.2;  DB 3;  Length 20;
  Best Local Similarity   81.2%;  Pred. No. 2.4e+04;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 GGCGTATCTGAAGAGT 18
              ||| | |||| |||||
Db          1 GGCATTTCTGCAGAGT 16


RESULT 38
US-09-488-671-23
; Sequence 23, Application US/09488671A
; Patent No. 6187545
; GENERAL INFORMATION:
;  APPLICANT: Robert McKay
;  APPLICANT: Madeline M. Butler
;  APPLICANT: Jacqueline Wyatt
;  APPLICANT: Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PEPCK-CYTOSOLIC EXPRESSION
;  FILE REFERENCE: RTS-0123
;  CURRENT APPLICATION NUMBER: US/09/488,671A
;  CURRENT FILING DATE: 2000-01-21
;  NUMBER OF SEQ ID NOS: 177
; SEQ ID NO 23
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-488-671-23

  Query Match             53.3%;  Score 11.2;  DB 3;  Length 20;
  Best Local Similarity   81.2%;  Pred. No. 2.4e+04;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 GGCGTATCTGAAGAGT 18
              ||| | |||| |||||
Db          3 GGCATTTCTGCAGAGT 18


RESULT 39
US-09-488-671-24
; Sequence 24, Application US/09488671A
; Patent No. 6187545
; GENERAL INFORMATION:
;  APPLICANT: Robert McKay
;  APPLICANT: Madeline M. Butler
;  APPLICANT: Jacqueline Wyatt
;  APPLICANT: Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF PEPCK-CYTOSOLIC EXPRESSION
;  FILE REFERENCE: RTS-0123
;  CURRENT APPLICATION NUMBER: US/09/488,671A
;  CURRENT FILING DATE: 2000-01-21
;  NUMBER OF SEQ ID NOS: 177
; SEQ ID NO 24
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-488-671-24

  Query Match             53.3%;  Score 11.2;  DB 3;  Length 20;
  Best Local Similarity   81.2%;  Pred. No. 2.4e+04;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 GGCGTATCTGAAGAGT 18
              ||| | |||| |||||
Db          5 GGCATTTCTGCAGAGT 20
```

RESULT 40
US-09-517-584A-86/c
; Sequence 86, Application US/09517584A
; Patent No. 6187587
; GENERAL INFORMATION:
; APPLICANT: Ian Popoff
; APPLICANT: Vickie L. Brown-Driver
; APPLICANT: Lex M. Cowsert
; TITLE OF INVENTION: ANTISENSE MODULATION OF E2F TRANSCRIPTION FACTOR 1 EXPRESSIO
; FILE REFERENCE: RTS-0121
; CURRENT APPLICATION NUMBER: US/09/517,584A
; CURRENT FILING DATE: 2000-03-22
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 86
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-517-584A-86

Query Match 53.3%; Score 11.2; DB 3; Length 20;
Best Local Similarity 81.2%; Pred. No. 2.4e+04;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          6 GTATCTGAAGAGTCTG 21
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Db         17 GTGTCTGAAGCGCCTG 2
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Search completed: August 12, 2005, 11:05:05
Job time : 97 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 12, 2005, 10:02:58 ; Search time 371 Seconds
(without alignments)
367.253 Million cell updates/sec

Title: US-09-743-825-8
Perfect score: 21
Sequence: 1 ctggcgtatctgaagagtctg 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7305758 seqs, 3244068913 residues

Total number of hits satisfying chosen parameters: 2019958

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published_Applications_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c	1	13.8	65.7	20	19	US-10-619-739-1019	Sequence 1019, Ap
c	2	12.8	61.0	17	10	US-09-848-754A-448	Sequence 448, App
c	3	12.8	61.0	17	10	US-09-848-754A-1754	Sequence 1754, Ap
c	4	12.8	61.0	20	19	US-10-619-739-630	Sequence 630, App
	5	12.4	59.0	20	17	US-10-190-366-64	Sequence 64, Appl
c	6	12.4	59.0	20	17	US-10-190-366-261	Sequence 261, App
c	7	12.4	59.0	21	21	US-10-847-918-10748	Sequence 10748, A
c	8	12.4	59.0	21	21	US-10-847-918-10750	Sequence 10750, A
c	9	12.4	59.0	21	21	US-10-847-918-10921	Sequence 10921, A
c	10	12.4	59.0	21	21	US-10-847-918-10922	Sequence 10922, A
	11	12.4	59.0	21	21	US-10-847-918-10923	Sequence 10923, A
c	12	12.2	58.1	17	10	US-09-848-754A-449	Sequence 449, App
c	13	12.2	58.1	20	15	US-10-003-919-31	Sequence 31, Appl
c	14	12.2	58.1	20	17	US-10-167-034-78	Sequence 78, Appl
c	15	12	57.1	20	19	US-10-317-500-29	Sequence 29, Appl
	16	12	57.1	20	19	US-10-317-500-184	Sequence 184, App
	17	12	57.1	21	19	US-10-786-720-13349	Sequence 13349, A
c	18	12	57.1	21	20	US-10-751-736-46408	Sequence 46408, A
c	19	12	57.1	21	20	US-10-751-736-46777	Sequence 46777, A
	20	11.8	56.2	16	18	US-10-138-674-5737	Sequence 5737, Ap
	21	11.8	56.2	16	19	US-10-287-949A-5737	Sequence 5737, Ap
c	22	11.8	56.2	17	10	US-09-848-754A-447	Sequence 447, App
c	23	11.8	56.2	17	10	US-09-780-164-577	Sequence 577, App
	24	11.8	56.2	17	18	US-10-138-674-4438	Sequence 4438, Ap
	25	11.8	56.2	17	18	US-10-138-674-7389	Sequence 7389, Ap
	26	11.8	56.2	17	19	US-10-287-949A-4438	Sequence 4438, Ap
	27	11.8	56.2	17	19	US-10-287-949A-7389	Sequence 7389, Ap
	28	11.8	56.2	17	20	US-10-712-633-339	Sequence 339, App
c	29	11.8	56.2	20	17	US-10-181-991-38	Sequence 38, Appl
c	30	11.8	56.2	20	17	US-10-174-319-24	Sequence 24, Appl
	31	11.8	56.2	20	17	US-10-174-319-94	Sequence 94, Appl
	32	11.8	56.2	20	17	US-10-289-762-1366	Sequence 1366, Ap
	33	11.8	56.2	20	19	US-10-766-185-87	Sequence 87, Appl
	34	11.8	56.2	20	20	US-10-719-370A-166	Sequence 166, App
c	35	11.8	56.2	21	16	US-10-198-235-118	Sequence 118, App
c	36	11.8	56.2	21	21	US-10-643-775-862	Sequence 862, App
	37	11.6	55.2	20	9	US-09-752-983-129	Sequence 129, App
c	38	11.6	55.2	20	9	US-09-888-049-15	Sequence 15, Appl
c	39	11.6	55.2	20	13	US-10-094-146-4	Sequence 4, Appli
c	40	11.6	55.2	20	14	US-10-093-365-20	Sequence 20, Appl
	41	11.6	55.2	20	17	US-10-005-344-129	Sequence 129, App
	42	11.6	55.2	20	17	US-10-148-835-44	Sequence 44, Appl
c	43	11.6	55.2	20	17	US-10-289-762-2767	Sequence 2767, Ap
	44	11.6	55.2	20	19	US-10-304-105-46	Sequence 46, Appl
c	45	11.6	55.2	20	19	US-10-316-232-15	Sequence 15, Appl
c	46	11.6	55.2	20	21	US-10-831-901A-1979	Sequence 1979, Ap
c	47	11.6	55.2	20	21	US-10-831-901A-1980	Sequence 1980, Ap
c	48	11.6	55.2	20	21	US-10-831-901A-1981	Sequence 1981, Ap
c	49	11.6	55.2	20	22	US-10-889-351-12	Sequence 12, Appl
	50	11.6	55.2	21	20	US-10-792-280-349	Sequence 349, App
	51	11.6	55.2	21	20	US-10-792-280-1372	Sequence 1372, Ap
	52	11.6	55.2	21	20	US-10-751-736-22299	Sequence 22299, A
	53	11.4	54.3	18	9	US-09-969-373-1686	Sequence 1686, Ap
	54	11.4	54.3	18	9	US-09-969-373-1688	Sequence 1688, Ap
	55	11.4	54.3	18	21	US-10-852-797-227	Sequence 227, App
c	56	11.4	54.3	19	17	US-10-349-143-6486	Sequence 6486, Ap
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	61	11.4	54.3	20	17	US-10-190-366-196	Sequence 196, App
c	62	11.4	54.3	20	17	US-10-190-366-389	Sequence 389, App
	63	11.4	54.3	20	17	US-10-211-179-56	Sequence 56, Appl
	64	11.4	54.3	20	19	US-10-648-593-321	Sequence 321, App
	65	11.4	54.3	20	19	US-10-671-395-421	Sequence 421, App
	66	11.4	54.3	20	19	US-10-671-395-477	Sequence 477, App
	67	11.4	54.3	20	19	US-10-671-395-528	Sequence 528, App
	68	11.4	54.3	20	19	US-10-671-395-552	Sequence 552, App
	69	11.4	54.3	20	19	US-10-671-395-694	Sequence 694, App
	70	11.4	54.3	20	19	US-10-671-395-844	Sequence 844, App
	71	11.4	54.3	20	19	US-10-671-395-955	Sequence 955, App
	72	11.4	54.3	20	19	US-10-671-395-1110	Sequence 1110, Ap
c	73	11.4	54.3	21	19	US-10-699-557-128	Sequence 128, App
c	74	11.4	54.3	21	19	US-10-786-720-20845	Sequence 20845, A
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	78	11.4	54.3	21	20	US-10-751-736-29994	Sequence 29994, A
	79	11.4	54.3	21	21	US-10-847-918-3289	Sequence 3289, Ap
	80	11.4	54.3	21	21	US-10-847-918-3290	Sequence 3290, Ap

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	82	11.4	54.3	21	21	US-10-847-918-4033	Sequence 4033, Ap
	83	11.4	54.3	21	21	US-10-847-918-4034	Sequence 4034, Ap
c	84	11.4	54.3	21	21	US-10-847-918-4035	Sequence 4035, Ap
	85	11.4	54.3	21	21	US-10-847-918-5116	Sequence 5116, Ap
	86	11.4	54.3	21	21	US-10-847-918-5117	Sequence 5117, Ap
c	87	11.4	54.3	21	21	US-10-847-918-5118	Sequence 5118, Ap
	88	11.4	54.3	21	21	US-10-847-918-5260	Sequence 5260, Ap
	89	11.4	54.3	21	21	US-10-847-918-5261	Sequence 5261, Ap
c	90	11.4	54.3	21	21	US-10-847-918-5262	Sequence 5262, Ap
c	91	11.4	54.3	21	21	US-10-847-918-10747	Sequence 10747, A
	92	11.4	54.3	21	21	US-10-847-918-10749	Sequence 10749, A
	93	11.4	54.3	21	21	US-10-847-918-10752	Sequence 10752, A
	94	11.2	53.3	17	10	US-09-927-046-156	Sequence 156, App
	95	11.2	53.3	17	10	US-09-927-046-157	Sequence 157, App
c	96	11.2	53.3	17	10	US-09-848-754A-450	Sequence 450, App
	97	11.2	53.3	17	15	US-10-156-306-4879	Sequence 4879, Ap
	98	11.2	53.3	18	17	US-10-349-143-5682	Sequence 5682, Ap
	99	11.2	53.3	19	10	US-09-864-636A-1817	Sequence 1817, Ap
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ALIGNMENTS

RESULT 1
US-10-619-739-1019/c
; Sequence 1019, Application US/10619739
; Publication No. US20040175719A1
; GENERAL INFORMATION:
; APPLICANT: Christians, Frederick C.
; TITLE OF INVENTION: Synthetic Tag Genes
; FILE REFERENCE: 3502.1
; CURRENT APPLICATION NUMBER: US/10/619,739
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: 60/395,530
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 2068
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1019
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-619-739-1019

Query Match 65.7%; Score 13.8; DB 19; Length 20;
Best Local Similarity 88.2%; Pred. No. 5.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CGTATCTGAAGAGTCTG 21
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Db 20 CATATCTGGAGAGTCTG 4

RESULT 2
US-09-848-754A-448/c
; Sequence 448, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MBHB00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 448
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-448

Query Match 61.0%; Score 12.8; DB 10; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GTATCTGAAGAGTCTG 21
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Db 16 GTATCGAAAGAGTCTG 1

RESULT 3
US-09-848-754A-1754/c
; Sequence 1754, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
; TITLE OF INVENTION: Levels of Epidermal Growth Factor Receptors
; FILE REFERENCE: MBHB00-958-I (400/018)
; CURRENT APPLICATION NUMBER: US/09/848,754A
; CURRENT FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 9645
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1754
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-09-848-754A-1754

Query Match 61.0%; Score 12.8; DB 10; Length 17;
Best Local Similarity 87.5%; Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 GTATCTGAAGAGTCTG 21
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Db 17 GTATCGAAAGAGTCTG 2

RESULT 4
US-10-619-739-630/c
; Sequence 630, Application US/10619739
; Publication No. US20040175719A1
; GENERAL INFORMATION:
; APPLICANT: Christians, Frederick C.
; TITLE OF INVENTION: Synthetic Tag Genes
; FILE REFERENCE: 3502.1
; CURRENT APPLICATION NUMBER: US/10/619,739
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: 60/395,530
; PRIOR FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 2068
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 630
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide
US-10-619-739-630

Query Match 61.0%; Score 12.8; DB 19; Length 20;
Best Local Similarity 87.5%; Pred. No. 1.7e+04;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 GCGTATCTGAAGAGTC 19
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Db 17 GCGTATCTGCATAGTC 2

RESULT 5
US-10-190-366-64
; Sequence 64, Application US/10190366

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; Publication No. US20040006031A1
; GENERAL INFORMATION:
;  APPLICANT: Nicholas M. Dean
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF HMG-COA REDUCTASE EXPRESSION
;  FILE REFERENCE: PTS-0023
;  CURRENT APPLICATION NUMBER: US/10/190,366
;  CURRENT FILING DATE:  2002-07-02
;  NUMBER OF SEQ ID NOS: 409
; SEQ ID NO 64
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-190-366-64

  Query Match             59.0%;  Score 12.4;  DB 17;  Length 20;
  Best Local Similarity   92.9%;  Pred. No. 2.8e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 ATCTGAAGAGTCTG 21
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Db          3 ATCTGAGGAGTCTG 16


RESULT 6
US-10-190-366-261/c
; Sequence 261, Application US/10190366
; Publication No. US20040006031A1
; GENERAL INFORMATION:
;  APPLICANT: Nicholas M. Dean
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF HMG-COA REDUCTASE EXPRESSION
;  FILE REFERENCE: PTS-0023
;  CURRENT APPLICATION NUMBER: US/10/190,366
;  CURRENT FILING DATE:  2002-07-02
;  NUMBER OF SEQ ID NOS: 409
; SEQ ID NO 261
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-190-366-261

  Query Match             59.0%;  Score 12.4;  DB 17;  Length 20;
  Best Local Similarity   92.9%;  Pred. No. 2.8e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 ATCTGAAGAGTCTG 21
              |||||| |||||||
Db         18 ATCTGAGGAGTCTG 5


RESULT 7
US-10-847-918-10748/c
; Sequence 10748, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Be, Xiaobing
;  APPLICANT:  Liu, Wei
;  APPLICANT:  Slonim, Donna
;  APPLICANT:  Howes, Steve
;  TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
;  FILE REFERENCE: 031896-026000 (AM101264)
;  CURRENT APPLICATION NUMBER: US/10/847,918
;  CURRENT FILING DATE:  2004-05-19
;  PRIOR APPLICATION NUMBER: US 60/471,729
;  PRIOR FILING DATE: 2003-05-20
;  NUMBER OF SEQ ID NOS: 14937
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10748
;   LENGTH: 21
;   TYPE: RNA
;   ORGANISM: RNAi-sense strand
US-10-847-918-10748

  Query Match             59.0%;  Score 12.4;  DB 21;  Length 21;
  Best Local Similarity   92.9%;  Pred. No. 2.8e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 ATCTGAAGAGTCTG 21
              ||||||||| ||||
Db         20 ATCTGAAGACTCTG 7


RESULT 8
US-10-847-918-10750/c
; Sequence 10750, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Be, Xiaobing
;  APPLICANT:  Liu, Wei
;  APPLICANT:  Slonim, Donna
;  APPLICANT:  Howes, Steve
;  TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
;  FILE REFERENCE: 031896-026000 (AM101264)
;  CURRENT APPLICATION NUMBER: US/10/847,918
;  CURRENT FILING DATE:  2004-05-19
;  PRIOR APPLICATION NUMBER: US 60/471,729
;  PRIOR FILING DATE: 2003-05-20
;  NUMBER OF SEQ ID NOS: 14937
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10750
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-847-918-10750

  Query Match             59.0%;  Score 12.4;  DB 21;  Length 21;
  Best Local Similarity   92.9%;  Pred. No. 2.8e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 ATCTGAAGAGTCTG 21
              ||||||||| ||||
Db         14 ATCTGAAGACTCTG 1


RESULT 9
US-10-847-918-10921/c
; Sequence 10921, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Be, Xiaobing
;  APPLICANT:  Liu, Wei
;  APPLICANT:  Slonim, Donna
;  APPLICANT:  Howes, Steve
;  TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
;  FILE REFERENCE: 031896-026000 (AM101264)
;  CURRENT APPLICATION NUMBER: US/10/847,918
;  CURRENT FILING DATE:  2004-05-19
;  PRIOR APPLICATION NUMBER: US 60/471,729
;  PRIOR FILING DATE: 2003-05-20
;  NUMBER OF SEQ ID NOS: 14937
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10921
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-847-918-10921
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  Query Match            59.0%;  Score 12.4;  DB 21;  Length 21;
  Best Local Similarity  92.9%;  Pred. No. 2.8e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 ATCTGAAGAGTCTG 21
              ||||||||| ||||
Db         16 ATCTGAAGACTCTG 3


RESULT 10
US-10-847-918-10922/c
; Sequence 10922, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Be, Xiaobing
;  APPLICANT:  Liu, Wei
;  APPLICANT:  Slonim, Donna
;  APPLICANT:  Howes, Steve
;  TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
;  FILE REFERENCE: 031896-026000 (AM101264)
;  CURRENT APPLICATION NUMBER: US/10/847,918
;  CURRENT FILING DATE:  2004-05-19
;  PRIOR APPLICATION NUMBER: US 60/471,729
;  PRIOR FILING DATE: 2003-05-20
;  NUMBER OF SEQ ID NOS: 14937
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10922
;   LENGTH: 21
;   TYPE: RNA
;   ORGANISM: RNAi-sense strand
US-10-847-918-10922

  Query Match            59.0%;  Score 12.4;  DB 21;  Length 21;
  Best Local Similarity  92.9%;  Pred. No. 2.8e+04;
  Matches   13;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 ATCTGAAGAGTCTG 21
              ||||||||| ||||
Db         14 ATCTGAAGACTCTG 1


RESULT 11
US-10-847-918-10923
; Sequence 10923, Application US/10847918
; Publication No. US20050119210A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Be, Xiaobing
;  APPLICANT:  Liu, Wei
;  APPLICANT:  Slonim, Donna
;  APPLICANT:  Howes, Steve
;  TITLE OF INVENTION: Compositions and Methods for Diagnosing and Treating Cancers
;  FILE REFERENCE: 031896-026000 (AM101264)
;  CURRENT APPLICATION NUMBER: US/10/847,918
;  CURRENT FILING DATE:  2004-05-19
;  PRIOR APPLICATION NUMBER: US 60/471,729
;  PRIOR FILING DATE: 2003-05-20
;  NUMBER OF SEQ ID NOS: 14937
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10923
;   LENGTH: 21
;   TYPE: RNA
;   ORGANISM: RNAi-antisense strand
US-10-847-918-10923

  Query Match            59.0%;  Score 12.4;  DB 21;  Length 21;
  Best Local Similarity  64.3%;  Pred. No. 2.8e+04;
  Matches    9;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 ATCTGAAGAGTCTG 21
              |:|:|||||  :|:|
Db          6 AUCUGAAGACUCUG 19


RESULT 12
US-09-848-754A-449/c
; Sequence 449, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Levels of Epidermal Growth Factor Receptors
;  FILE REFERENCE: MBHB00-958-I (400/018)
;  CURRENT APPLICATION NUMBER: US/09/848,754A
;  CURRENT FILING DATE:  2001-05-03
;  NUMBER OF SEQ ID NOS: 9645
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 449
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-848-754A-449

  Query Match            58.1%;  Score 12.2;  DB 10;  Length 17;
  Best Local Similarity  82.4%;  Pred. No. 3.5e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 GCGTATCTGAAGAGTCT 20
              | |||||  ||||||||
Db         17 GGGTATCGAAAGAGTCT 1


RESULT 13
US-10-003-919-31/c
; Sequence 31, Application US/10003919
; Publication No. US20030114401A1
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF SHIP-1 EXPRESSION
;  FILE REFERENCE: RTS-0256
;  CURRENT APPLICATION NUMBER: US/10/003,919
;  CURRENT FILING DATE:  2001-12-06
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 31
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-003-919-31

  Query Match            58.1%;  Score 12.2;  DB 15;  Length 20;
  Best Local Similarity  82.4%;  Pred. No. 3.5e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CTGGCGTATCTGAAGAG 17
              |||| || |||| ||||
Db         20 CTGGAGTCTCTGCAGAG 4


RESULT 14
US-10-167-034-78/c
; Sequence 78, Application US/10167034
; Publication No. US20030228690A1
; GENERAL INFORMATION:
;  APPLICANT: Brenda F. Baker
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF IL-1 RECEPTOR-ASSOCIATED KINASE-1 EXPRESS
;  FILE REFERENCE: PTS-0003
;  CURRENT APPLICATION NUMBER: US/10/167,034
;  CURRENT FILING DATE:  2002-06-10
;  NUMBER OF SEQ ID NOS: 142
; SEQ ID NO 78
```

```
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-167-034-78

  Query Match             58.1%;  Score 12.2;  DB 17;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 3.5e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 GCGTATCTGAAGAGTCT 20
              ||||| ||| || ||||
Db         17 GCGTAGCTGGAGGGTCT 1


RESULT 15
US-10-317-500-29/c
; Sequence 29, Application US/10317500
; Publication No. US20040115637A1
; GENERAL INFORMATION:
;  APPLICANT: Robert McKay
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF PPAR-ALPHA EXPRESSION
;  FILE REFERENCE: RTS-0380
;  CURRENT APPLICATION NUMBER: US/10/317,500
;  CURRENT FILING DATE:  2002-12-11
;  NUMBER OF SEQ ID NOS: 276
; SEQ ID NO 29
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-317-500-29

  Query Match             57.1%;  Score 12;  DB 19;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 TATCTGAAGAGT 18
              ||||||||||||
Db         20 TATCTGAAGAGT 9


RESULT 16
US-10-317-500-184
; Sequence 184, Application US/10317500
; Publication No. US20040115637A1
; GENERAL INFORMATION:
;  APPLICANT: Robert McKay
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF PPAR-ALPHA EXPRESSION
;  FILE REFERENCE: RTS-0380
;  CURRENT APPLICATION NUMBER: US/10/317,500
;  CURRENT FILING DATE:  2002-12-11
;  NUMBER OF SEQ ID NOS: 276
; SEQ ID NO 184
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-317-500-184

  Query Match             57.1%;  Score 12;  DB 19;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 4.4e+04;
  Matches   12;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 TATCTGAAGAGT 18
              ||||||||||||
Db          1 TATCTGAAGAGT 12


RESULT 17
US-10-786-720-13349
; Sequence 13349, Application US/10786720
; Publication No. US20040191818A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  O'Toole, Margot
;  APPLICANT:  Liu, Wei
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING AUTOIMMUNE
;  TITLE OF INVENTION:  DISEASES
;  FILE REFERENCE: 031896-023000 (AM101331L)
;  CURRENT APPLICATION NUMBER: US/10/786,720
;  CURRENT FILING DATE:  2004-02-26
;  NUMBER OF SEQ ID NOS: 21135
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13349
;   LENGTH: 21
;   TYPE: RNA
;   ORGANISM: RNAi-sense strand
US-10-786-720-13349

  Query Match             57.1%;  Score 12;  DB 19;  Length 21;
  Best Local Similarity   50.0%;  Pred. No. 4.4e+04;
  Matches   10;  Conservative    5;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 CTGGCGTATCTGAAGAGTCT 20
              |:|  | |:|: |||| :|:
Db          1 CUGAGGCAUCUCAAGACUCU 20


RESULT 18
US-10-751-736-46408/c
; Sequence 46408, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Martinez, Robert
;  APPLICANT:  Brown, Eugene
;  APPLICANT:  Liu, Wei
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
;  TITLE OF INVENTION:  CANCERS
;  FILE REFERENCE: AM100927 (031896-002000)
;  CURRENT APPLICATION NUMBER: US/10/751,736
;  CURRENT FILING DATE:  2003-01-06
;  PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
;  PRIOR FILING DATE: 2003-01-06
;  NUMBER OF SEQ ID NOS: 54873
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46408
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-751-736-46408

  Query Match             57.1%;  Score 12;  DB 20;  Length 21;
  Best Local Similarity   75.0%;  Pred. No. 4.4e+04;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 TGGCGTATCTGAAGAGTCTG 21
              || | | ||||| ||| |||
Db         20 TGTCCTCTCTGATGAGGCTG 1


RESULT 19
US-10-751-736-46777/c
; Sequence 46777, Application US/10751736
; Publication No. US20040265230A1
; GENERAL INFORMATION:
;  APPLICANT: Wyeth
;  APPLICANT:  Martinez, Robert
;  APPLICANT:  Brown, Eugene
;  APPLICANT:  Liu, Wei
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING AND TREATING COLON
```

```
;  TITLE OF INVENTION:  CANCERS
;  FILE REFERENCE: AM100927 (031896-002000)
;  CURRENT APPLICATION NUMBER: US/10/751,736
;  CURRENT FILING DATE:  2003-01-06
;  PRIOR APPLICATION NUMBER: US Provisional Application 60/438,000
;  PRIOR FILING DATE: 2003-01-06
;  NUMBER OF SEQ ID NOS: 54873
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46777
;   LENGTH: 21
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-751-736-46777

  Query Match            57.1%;  Score 12;  DB 20;  Length 21;
  Best Local Similarity  75.0%;  Pred. No. 4.4e+04;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 TGGCGTATCTGAAGAGTCTG 21
              || | | ||||| ||| |||
Db         20 TGTCCTCTCTGATGAGGCTG 1


RESULT 20
US-10-138-674-5737
; Sequence 5737, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/138,674
;  CURRENT FILING DATE:  2002-05-03
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5737
;   LENGTH: 16
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-138-674-5737

  Query Match            56.2%;  Score 11.8;  DB 18;  Length 16;
  Best Local Similarity  73.3%;  Pred. No. 5.5e+04;
  Matches   11;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GGCGTATCTGAAGAG 17
              | ||:| |:||||||
Db          2 GACGUAACUGAAGAG 16


RESULT 21
US-10-287-949A-5737
; Sequence 5737, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00-876-N (400/049)
;  CURRENT APPLICATION NUMBER: US/10/287,949A
;  CURRENT FILING DATE:  2003-04-11
;  NUMBER OF SEQ ID NOS: 20822
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5737
;   LENGTH: 16
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-10-287-949A-5737

  Query Match            56.2%;  Score 11.8;  DB 19;  Length 16;
  Best Local Similarity  73.3%;  Pred. No. 5.5e+04;
  Matches   11;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GGCGTATCTGAAGAG 17
              | ||:| |:||||||
Db          2 GACGUAACUGAAGAG 16


RESULT 22
US-09-848-754A-447/c
; Sequence 447, Application US/09848754A
; Publication No. US20030073207A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Levels of Epidermal Growth Factor Receptors
;  FILE REFERENCE: MBHB00-958-I (400/018)
;  CURRENT APPLICATION NUMBER: US/09/848,754A
;  CURRENT FILING DATE:  2001-05-03
;  NUMBER OF SEQ ID NOS: 9645
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 447
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-848-754A-447

  Query Match            56.2%;  Score 11.8;  DB 10;  Length 17;
  Best Local Similarity  86.7%;  Pred. No. 5.5e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 TATCTGAAGAGTCTG 21
              ||||  |||||||||
Db         17 TATCGAAAGAGTCTG 3


RESULT 23
US-09-780-164-577/c
; Sequence 577, Application US/09780164
; Publication No. US20030092646A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Blatt, Larry
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: Method and Reagent for the Inhibition of CD20
;  FILE REFERENCE: 400/010
;  CURRENT APPLICATION NUMBER: US/09/780,164
;  CURRENT FILING DATE:  2001-02-09
;  PRIOR APPLICATION NUMBER: 60/185,516
;  PRIOR FILING DATE: 2000-02-28
;  NUMBER OF SEQ ID NOS: 2603
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 577
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo sapiens
US-09-780-164-577

  Query Match            56.2%;  Score 11.8;  DB 10;  Length 17;
  Best Local Similarity  86.7%;  Pred. No. 5.5e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 GCGTATCTGAAGAGT 18
              |||||| || |||||
Db         16 GCGTATGTGCAGAGT 2
```

RESULT 24
US-10-138-674-4438
; Sequence 4438, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4438
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-4438

Query Match 56.2%; Score 11.8; DB 18; Length 17;
Best Local Similarity 73.3%; Pred. No. 5.5e+04;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGCGTATCTGAAGAG 17
| ||:| |:||||||
Db 1 GACGUAACUGAAGAG 15

RESULT 25
US-10-138-674-7389
; Sequence 7389, Application US/10138674
; Publication No. US20040077565A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/138,674
; CURRENT FILING DATE: 2002-05-03
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7389
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-138-674-7389

Query Match 56.2%; Score 11.8; DB 18; Length 17;
Best Local Similarity 73.3%; Pred. No. 5.5e+04;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGCGTATCTGAAGAG 17
| ||:| |:||||||
Db 3 GACGUAACUGAAGAG 17

RESULT 26
US-10-287-949A-4438
; Sequence 4438, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Rel
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4438
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-4438

Query Match 56.2%; Score 11.8; DB 19; Length 17;
Best Local Similarity 73.3%; Pred. No. 5.5e+04;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGCGTATCTGAAGAG 17
| ||:| |:||||||
Db 1 GACGUAACUGAAGAG 15

RESULT 27
US-10-287-949A-7389
; Sequence 7389, Application US/10287949A
; Publication No. US20040102389A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pam
; APPLICANT: McSwiggen, Jim
; APPLICANT: Stinchcomb, Dan
; APPLICANT: Escobedo, Jaime
; TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
; TITLE OF INVENTION: Levels of Vascular Endothelial Growth Factor Receptor
; FILE REFERENCE: MBHB00-876-N (400/049)
; CURRENT APPLICATION NUMBER: US/10/287,949A
; CURRENT FILING DATE: 2003-04-11
; NUMBER OF SEQ ID NOS: 20822
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7389
; LENGTH: 17
; TYPE: RNA
; ORGANISM: Homo sapiens
US-10-287-949A-7389

Query Match 56.2%; Score 11.8; DB 19; Length 17;
Best Local Similarity 73.3%; Pred. No. 5.5e+04;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGCGTATCTGAAGAG 17
| ||:| |:||||||
Db 3 GACGUAACUGAAGAG 17

RESULT 28
US-10-712-633-339
; Sequence 339, Application US/10712633
; Publication No. US20040220128A1
; GENERAL INFORMATION:
; APPLICANT: Ribozyme Pharmaceuticals, Inc.
; APPLICANT: Pavco, Pamela
; APPLICANT: Sandberg, Jennifer
; APPLICANT: Gordon, Gilad
; APPLICANT: McSwiggen, James
; APPLICANT: Stinchcomb, Dan
; TITLE OF INVENTION: NUCLEIC ACID BASED MODULATION OF VASCULAR ENDOTHELIAL GROWTH FACT
; TITLE OF INVENTION: RECEPTOR FOR THE TREATMENT OF ANGIOGENESIS RELATED DISEASES AND
; FILE REFERENCE: MBHB02-325PCT (400/047)
; CURRENT APPLICATION NUMBER: US/10/712,633
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/005,974
; PRIOR FILING DATE: 1995-10-26

```
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  PRIOR APPLICATION NUMBER: US 09/371,772
;  PRIOR FILING DATE: 1999-08-10
;  PRIOR APPLICATION NUMBER: US 09/708,690
;  PRIOR FILING DATE: 2000-11-07
;  PRIOR APPLICATION NUMBER: US 09/870,161
;  PRIOR FILING DATE: 2001-05-29
;  PRIOR APPLICATION NUMBER: US 60/334,461
;  PRIOR FILING DATE: 2001-11-30
;  PRIOR APPLICATION NUMBER: US 10/138,674
;  PRIOR FILING DATE: 2002-05-03
;  NUMBER OF SEQ ID NOS: 5989
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 339
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Homo Sapiens
US-10-712-633-339

  Query Match             56.2%;  Score 11.8;  DB 20;  Length 17;
  Best Local Similarity   73.3%;  Pred. No. 5.5e+04;
  Matches   11;  Conservative    2;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GGCGTATCTGAAGAG 17
              | ||:| |:||||||
Db          3 GACGUAACUGAAGAG 17


RESULT 29
US-10-181-991-38/c
; Sequence 38, Application US/10181991
; Publication No. US20030211609A1
; GENERAL INFORMATION:
;  APPLICANT: Isis Pharmaceuticals, Inc.
;  APPLICANT:  Lex M. Cowsert
;  APPLICANT:  Jacqueline Wyatt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF ARA70 EXPRESSION
;  FILE REFERENCE: RTSP-0357
;  CURRENT APPLICATION NUMBER: US/10/181,991
;  CURRENT FILING DATE:  2002-07-25
;  PRIOR APPLICATION NUMBER: 09/488,857
;  PRIOR FILING DATE: 2000-01-21
;  NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 38
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-181-991-38

  Query Match             56.2%;  Score 11.8;  DB 17;  Length 20;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CTGGCGTATCTGAAG 15
              |||||  ||||||||
Db         16 CTGGCCAATCTGAAG 2


RESULT 30
US-10-174-319-24/c
; Sequence 24, Application US/10174319
; Publication No. US20030232771A1
; GENERAL INFORMATION:
;  APPLICANT: Donna T. Ward
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF MARK3 EXPRESSION
;  FILE REFERENCE: PTS-0018
;  CURRENT APPLICATION NUMBER: US/10/174,319
;  CURRENT FILING DATE:  2002-06-17
;  NUMBER OF SEQ ID NOS: 121
; SEQ ID NO 24
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-174-319-24

  Query Match             56.2%;  Score 11.8;  DB 17;  Length 20;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GGCGTATCTGAAGAG 17
              |||||||| ||| ||
Db         20 GGCGTATCCGAAAAG 6


RESULT 31
US-10-174-319-94
; Sequence 94, Application US/10174319
; Publication No. US20030232771A1
; GENERAL INFORMATION:
;  APPLICANT: Donna T. Ward
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF MARK3 EXPRESSION
;  FILE REFERENCE: PTS-0018
;  CURRENT APPLICATION NUMBER: US/10/174,319
;  CURRENT FILING DATE:  2002-06-17
;  NUMBER OF SEQ ID NOS: 121
; SEQ ID NO 94
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-174-319-94

  Query Match             56.2%;  Score 11.8;  DB 17;  Length 20;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 GGCGTATCTGAAGAG 17
              |||||||| ||| ||
Db          1 GGCGTATCCGAAAAG 15


RESULT 32
US-10-289-762-1366
; Sequence 1366, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, prever
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/10/289,762
;  CURRENT FILING DATE:  2003-03-27
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1366
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
US-10-289-762-1366

  Query Match             56.2%;  Score 11.8;  DB 17;  Length 20;
  Best Local Similarity   86.7%;  Pred. No. 5.6e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          4 GCGTATCTGAAGAGT 18
              ||| |||||| ||||
Db          1 GCGGATCTGAGGAGT 15
```

RESULT 33
US-10-766-185-87
; Sequence 87, Application US/10766185
; Publication No. US20040152655A1
; GENERAL INFORMATION:
; APPLICANT: Yoon, Heejeong
; APPLICANT: Ahn, Chang Ho
; APPLICANT: Lee, Young Bok
; APPLICANT: Mao, Lingjun
; APPLICANT: Jiang, Xiaoming
; TITLE OF INVENTION: Antisense Oligonucleotides that inhibit expression of HIF-1
; FILE REFERENCE: REX 7034
; CURRENT APPLICATION NUMBER: US/10/766,185
; CURRENT FILING DATE: 2004-01-28
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 87
; LENGTH: 20
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: antisense oligonucleotide
US-10-766-185-87

Query Match 56.2%; Score 11.8; DB 19; Length 20;
Best Local Similarity 86.7%; Pred. No. 5.6e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CGTATCTGAAGAGTC 19
| |||||||||| ||
Db 3 CATATCTGAAGATTC 17

RESULT 34
US-10-719-370A-166
; Sequence 166, Application US/10719370A
; Publication No. US20040220393A1
; GENERAL INFORMATION:
; APPLICANT: Ward, Donna T.
; APPLICANT: Dobie, Kenneth W.
; APPLICANT: Marcusson, Eric G.
; APPLICANT: Freier, Susan M.
; TITLE OF INVENTION: MODULATION OF HIF1a AND HIF2a EXPRESSION
; FILE REFERENCE: ISPT-1010
; CURRENT APPLICATION NUMBER: US/10/719,370A
; CURRENT FILING DATE: 2003-11-21
; PRIOR APPLICATION NUMBER: US 10/304,126
; PRIOR FILING DATE: 2002-11-23
; NUMBER OF SEQ ID NOS: 458
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 166
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-719-370A-166

Query Match 56.2%; Score 11.8; DB 20; Length 20;
Best Local Similarity 86.7%; Pred. No. 5.6e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 CGTATCTGAAGAGTC 19
| |||||||||| ||
Db 3 CATATCTGAAGATTC 17

RESULT 35
US-10-198-235-118/c
; Sequence 118, Application US/10198235
; Publication No. US20030190634A1
; GENERAL INFORMATION:
; APPLICANT: Barany, Francis
; APPLICANT: Liu, Jianzhao
; APPLICANT: Kirk, Brian W.
; APPLICANT: Zirvi, Monib
; APPLICANT: Gerry, No. US20030190634A1man P.
; APPLICANT: Paty, Philip B.
; TITLE OF INVENTION: ACCELERATING IDENTIFICATION OF SINGLE NUCLEOTIDE
; TITLE OF INVENTION: POLYMORPHISMS AND ALIGNMENT OF CLONES IN GENOMIC
; TITLE OF INVENTION: SEQUENCING
; FILE REFERENCE: 19603/2621
; CURRENT APPLICATION NUMBER: US/10/198,235
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: US/09/478,189
; PRIOR FILING DATE: 2000-01-05
; PRIOR APPLICATION NUMBER: 60/114,881
; PRIOR FILING DATE: 1999-01-06
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 118
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: probe/primer
US-10-198-235-118

Query Match 56.2%; Score 11.8; DB 16; Length 21;
Best Local Similarity 86.7%; Pred. No. 5.6e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CTGGCGTATCTGAAG 15
|||| || |||||||
Db 17 CTGGTGTGTCTGAAG 3

RESULT 36
US-10-643-775-862/c
; Sequence 862, Application US/10643775
; Publication No. US20050026156A1
; GENERAL INFORMATION:
; APPLICANT: Lie, Oystein
; APPLICANT: Slettan, Audun
; APPLICANT: Hoyum, Morten
; APPLICANT: Lingaas, Frode
; TITLE OF INVENTION: Verification of Food Origin Based on
; TITLE OF INVENTION: Nucleic Acid Pattern Recognition
; FILE REFERENCE: 66849-019
; CURRENT APPLICATION NUMBER: US/10/643,775
; CURRENT FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US 60/404,200
; PRIOR FILING DATE: 2002-08-16
; NUMBER OF SEQ ID NOS: 1377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 862
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Oreochromis niloticus
US-10-643-775-862

Query Match 56.2%; Score 11.8; DB 21; Length 21;
Best Local Similarity 86.7%; Pred. No. 5.6e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GGCGTATCTGAAGAG 17
||||||| || ||||
Db 15 GGCGTATTTGGAGAG 1

RESULT 37
US-09-752-983-129
; Sequence 129, Application US/09752983
; Patent No. US20010016575A1

```
;  GENERAL INFORMATION:
;    APPLICANT:  Loren J. Miraglia, Pamela Nero, Mark J.
;    APPLICANT:  Graham, Brett P. Monia
;    TITLE OF INVENTION:  ANTISENSE MODULATION OF HUMAN MDM2
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  271
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Law Offices of Jane Massey Licata
;      STREET:  66 East Main Street
;      CITY:  Marlton
;      STATE:  NJ
;      COUNTRY:  U.S.A.
;      ZIP:  08053
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
;      COMPUTER:  IBM PC
;      OPERATING SYSTEM:  WINDOWS 95
;      SOFTWARE:  WORDPERFECT 6.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/752,983
;      FILING DATE:  02-Jan-2001
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/280,805
;      FILING DATE:  <Unknown>
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Licata, Jane Massey
;      REGISTRATION NUMBER:  32,257
;      REFERENCE/DOCKET NUMBER:  ISPH-0346
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  609-810-1515
;      TELEFAX:  609-810-1454
;  INFORMATION FOR SEQ ID NO:  129:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  Nucleic Acid
;      STRANDEDNESS:  Single
;      TOPOLOGY:  Linear
;    ANTI-SENSE:  Yes
US-09-752-983-129

  Query Match             55.2%;  Score 11.6;  DB 9;  Length 20;
  Best Local Similarity   77.8%;  Pred. No. 7e+04;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 TGGCGTATCTGAAGAGTC 19
              ||||||  ||| ||| ||
Db          1 TGGCGTCCCTGTAGATTC 18


RESULT 38
US-09-888-049-15/c
; Sequence 15, Application US/09888049
; Patent No. US20020137215A1
; GENERAL INFORMATION:
;  APPLICANT: Francis, Kevin P.
;  APPLICANT:  Purchio, Anthony F.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE THEREOF IN MODIFYING
;  TITLE OF INVENTION:  THE GENOMES OF MICROORGANISMS
;  FILE REFERENCE: PXE-013.USP / 9400-0013
;  CURRENT APPLICATION NUMBER: US/09/888,049
;  CURRENT FILING DATE:  2001-06-21
;  PRIOR APPLICATION NUMBER: 60/216,257
;  PRIOR FILING DATE: 2000-07-06
;  PRIOR APPLICATION NUMBER: 60/274,105
;  PRIOR FILING DATE: 2001-03-07
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Primer
;   OTHER INFORMATION: LuxA-Rev
US-09-888-049-15

  Query Match             55.2%;  Score 11.6;  DB 9;  Length 20;
  Best Local Similarity   77.8%;  Pred. No. 7e+04;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 GCGTATCTGAAGAGTCTG 21
              || | ||||| |||| ||
Db         19 GCATCTCTGAGGAGTGTG 2


RESULT 39
US-10-094-146-4/c
; Sequence 4, Application US/10094146
; Publication No. US20020192755A1
; GENERAL INFORMATION:
;  APPLICANT: FRANCIS, Kevin P.
;  APPLICANT:  DOYLE, Timothy C.
;  APPLICANT:  NAWOTKA, Kevin A.
;  TITLE OF INVENTION: METHODS OF SCREENING FOR INTRODUCTION OF DNA INTO A
;  TITLE OF INVENTION:  TARGET CELL
;  FILE REFERENCE: 9400-0015 / PXE-015.US
;  CURRENT APPLICATION NUMBER: US/10/094,146
;  CURRENT FILING DATE:  2002-06-10
;  PRIOR APPLICATION NUMBER: 60/274,094
;  PRIOR FILING DATE: 2001-03-07
;  PRIOR APPLICATION NUMBER: 60/292,828
;  PRIOR FILING DATE: 2001-05-22
;  NUMBER OF SEQ ID NOS: 35
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: primer LuxA-Rev
US-10-094-146-4

  Query Match             55.2%;  Score 11.6;  DB 13;  Length 20;
  Best Local Similarity   77.8%;  Pred. No. 7e+04;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 GCGTATCTGAAGAGTCTG 21
              || | ||||| |||| ||
Db         19 GCATCTCTGAGGAGTGTG 2


RESULT 40
US-10-093-365-20/c
; Sequence 20, Application US/10093365
; Publication No. US20030099962A1
; GENERAL INFORMATION:
;  APPLICANT: Schernthaner, Johann
;  APPLICANT:  Piche, Caroline
;  APPLICANT:  Robert, Laurian
;  TITLE OF INVENTION: Methods to Isolate Gene Coding and Flanking DNA
;  FILE REFERENCE: 0811.1200001
;  CURRENT APPLICATION NUMBER: US/10/093,365
;  CURRENT FILING DATE:  2002-03-08
;  PRIOR APPLICATION NUMBER: US 60/274,239
;  PRIOR FILING DATE: 2001-03-09
;  NUMBER OF SEQ ID NOS: 47
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Artificial DNA Sequence
US-10-093-365-20
```

Query Match 55.2%; Score 11.6; DB 14; Length 20;
Best Local Similarity 77.8%; Pred. No. 7e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          3 GGCGTATCTGAAGAGTCT 20
              ||||| | ||||||  ||
Db         19 GGCGTTTATGAAGACGCT 2
```

Search completed: August 12, 2005, 11:11:23
Job time : 373 secs

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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 12, 2005, 09:55:08 ; Search time 1806 Seconds
(without alignments)
442.608 Million cell updates/sec

Title: US-09-743-825-8
Perfect score: 21
Sequence: 1 ctggcgtatctgaagagtctg 21

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 15386

Minimum DB seq length: 0
Maximum DB seq length: 21

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	10.4	49.5	20	8	AZ784664	AZ784664 2M0027I10
c	2	10.2	48.6	15	9	AJ592729	AJ592729 Arabidops
c	3	10	47.6	21	6	CA851013	CA851013 D09B11_C1
c	4	9.8	46.7	19	8	AZ495849	AZ495849 1M0331N22
	5	9.8	46.7	19	8	AZ875769	AZ875769 2M0190A02
	6	9.6	45.7	20	8	AZ489135	AZ489135 1M0319H15
	7	9.4	44.8	17	9	CL681189	CL681189 PRI0130b_
	8	9.2	43.8	20	8	AZ308384	AZ308384 1M0011K17
c	9	9.2	43.8	20	8	AZ316351	AZ316351 1M0034A11
c	10	9.2	43.8	20	8	AZ328275	AZ328275 1M0052A01
c	11	9	42.9	10	9	AJ587417	AJ587417 Arabidops
	12	9	42.9	16	1	AJ684587	AJ684587 AJ684587
	13	9	42.9	20	8	AZ625776	AZ625776 1M0465C08
c	14	9	42.9	21	4	BG924548	BG924548 HNC27-1-G
c	15	8.8	41.9	17	9	AJ587168	AJ587168 Arabidops
	16	8.8	41.9	20	6	C00979	C00979 HUMGS000336
c	17	8.8	41.9	20	7	CF325351	CF325351 JMT1--03-
	18	8.8	41.9	20	7	D20709	D20709 HUMGS01685
c	19	8.6	41.0	19	1	AJ671616	AJ671616 AJ671616
c	20	8.6	41.0	19	7	CO778852	CO778852 BL004D_H0
c	21	8.6	41.0	20	8	AZ480596	AZ480596 1M0302D18
c	22	8.6	41.0	20	8	AZ658035	AZ658035 1M0534P03
c	23	8.6	41.0	21	9	AG194535	AG194535 Pan trogl
c	24	8.4	40.0	19	8	AZ623493	AZ623493 1M0461M13
	25	8.4	40.0	20	8	AZ818271	AZ818271 2M0088M08
c	26	8.4	40.0	20	9	AG199044	AG199044 Pan trogl
	27	8.4	40.0	20	9	AG203835	AG203835 Pan trogl
c	28	8.4	40.0	21	8	AZ787920	AZ787920 2M0034M09
	29	8.2	39.0	13	9	CL694050	CL694050 PRI0163a_
	30	8.2	39.0	17	9	CL423467	CL423467 01S0557-0
	31	8.2	39.0	18	1	AJ662026	AJ662026 AJ662026
	32	8.2	39.0	18	9	AJ588865	AJ588865 Arabidops
c	33	8.2	39.0	19	8	AZ358656	AZ358656 1M0101K12
	34	8.2	39.0	20	5	BQ595520	BQ595520 E012693-0
	35	8.2	39.0	20	8	AZ320114	AZ320114 1M0040D05
	36	8.2	39.0	20	8	AZ436082	AZ436082 1M0233A10
c	37	8.2	39.0	20	8	AZ772787	AZ772787 1M0583M24
	38	8.2	39.0	20	8	AZ807038	AZ807038 2M0069C06
	39	8.2	39.0	21	9	CL436802	CL436802 PST3869-N
c	40	8	38.1	11	4	BG927412	BG927412 HNC1-1-G1
c	41	8	38.1	14	4	BG924475	BG924475 HNC27-1-D
c	42	8	38.1	15	7	D11800	D11800 HUMHM01G12
c	43	8	38.1	15	7	D11801	D11801 HUMHM01H01
c	44	8	38.1	15	7	D11803	D11803 HUMHM01H05
c	45	8	38.1	15	7	D11818	D11818 HUMHM02B04
c	46	8	38.1	16	4	BG928185	BG928185 HNC65-1-D
c	47	8	38.1	17	4	BG929060	BG929060 HNC11-1-G
c	48	8	38.1	18	4	BG900971	BG900971 HOA52-1-C
c	49	8	38.1	18	4	BG924473	BG924473 HNC27-1-D
c	50	8	38.1	19	4	BG928126	BG928126 HNC65-1-B
	51	8	38.1	20	6	CD532195	CD532195 26A8 Arab
	52	8	38.1	20	7	CO779101	CO779101 BL005C_F0
	53	8	38.1	20	8	AZ316351	AZ316351 1M0034A11
c	54	8	38.1	20	8	AZ619410	AZ619410 1M0451F11
	55	8	38.1	20	8	AZ649987	AZ649987 1M0519J21
	56	8	38.1	20	8	AZ817897	AZ817897 2M0087D09
c	57	8	38.1	20	8	AZ835078	AZ835078 2M0129E07
	58	8	38.1	21	7	CO792195	CO792195 NT014B_H0
c	59	8	38.1	21	8	AZ511294	AZ511294 1M0356G16
c	60	8	38.1	21	8	AZ607204	AZ607204 1M0429H03
c	61	8	38.1	21	8	AZ623540	AZ623540 1M0461G23
	62	8	38.1	21	8	AZ875020	AZ875020 2M0189B24
	63	8	38.1	21	9	AG203054	AG203054 Pan trogl
c	64	7.8	37.1	15	1	AJ649143	AJ649143 AJ649143
c	65	7.8	37.1	18	9	AJ587324	AJ587324 Arabidops
c	66	7.8	37.1	18	9	AJ592301	AJ592301 Arabidops
	67	7.8	37.1	19	7	CF317235	CF317235 HD--06-N1
c	68	7.8	37.1	19	7	CO792214	CO792214 NT014C_A1
	69	7.8	37.1	19	8	AZ490612	AZ490612 1M0323L11
	70	7.8	37.1	19	8	AZ508355	AZ508355 1M0350O13
	71	7.8	37.1	19	8	AZ795136	AZ795136 2M0049A16
c	72	7.8	37.1	19	8	AZ834391	AZ834391 2M0117N04
	73	7.8	37.1	19	9	CL668704	CL668704 PRI0158b_
	74	7.8	37.1	20	5	BQ593485	BQ593485 S015529-0
	75	7.8	37.1	20	8	AZ475341	AZ475341 1M0293H11
	76	7.8	37.1	20	8	AZ610524	AZ610524 1M0435B21
c	77	7.8	37.1	20	8	AZ832001	AZ832001 2M0112O01
	78	7.8	37.1	20	9	AG190598	AG190598 Pan trogl
c	79	7.8	37.1	20	9	AJ587844	AJ587844 Arabidops
c	80	7.8	37.1	21	1	AU256271	AU256271 AU256271
c	81	7.8	37.1	21	8	AZ331625	AZ331625 1M0059M07
c	82	7.8	37.1	21	8	AZ346766	AZ346766 1M0082H08
c	83	7.8	37.1	21	8	AZ510119	AZ510119 1M0354I23
	84	7.8	37.1	21	8	AZ628010	AZ628010 1M0476K09
	85	7.8	37.1	21	8	AZ819244	AZ819244 2M0089F14
	86	7.8	37.1	21	8	AZ820567	AZ820567 2M0092B19
	87	7.8	37.1	21	8	AZ875300	AZ875300 2M0189D22
c	88	7.6	36.2	18	9	AJ598221	AJ598221 Arabidops
	89	7.6	36.2	19	4	BG927923	BG927923 HNC45-1-E
	90	7.6	36.2	19	6	C01992	C01992 HUMGS000401
	91	7.6	36.2	19	9	CL678657	CL678657 PRI0123c_
	92	7.6	36.2	20	1	AB088509	AB088509 AB088509
c	93	7.6	36.2	20	7	CO794844	CO794844 NT144D_B0
	94	7.6	36.2	20	8	AZ646291	AZ646291 1M0512D07
	95	7.6	36.2	20	8	AZ774829	AZ774829 2M0004D10
	96	7.6	36.2	20	9	AJ587945	AJ587945 Arabidops
c	97	7.6	36.2	21	1	AU257572	AU257572 AU257572

c 98	7.6	36.2	21	7	CO788185	CO788185	NT003C_A1
99	7.6	36.2	21	8	AZ393342	AZ393342	1M0156C21
100	7.6	36.2	21	8	AZ441394	AZ441394	1M0233P05

ALIGNMENTS

RESULT 1
AZ784664
LOCUS AZ784664 20 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0027I10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0027I10 R, genomic survey sequence.
ACCESSION AZ784664
VERSION AZ784664.1 GI:12920631
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0027 row: I column: 10
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0027I10"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
ORIGIN

Query Match 49.5%; Score 10.4; DB 8; Length 20;
Best Local Similarity 91.7%; Pred. No. 1.8e+06;
Matches 11; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy         10 CTGAAGAGTCTG 21
              |||||| |||||
Db          1 CTGAAGGGTCTG 12
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RESULT 2
AJ592729/c
LOCUS AJ592729 15 bp DNA linear GSS 15-JAN-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, right border, clone 631B09, genomic survey sequence.
ACCESSION AJ592729
VERSION AJ592729.1 GI:37942353
KEYWORDS GSS; right border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G., Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE 22363535
PUBMED 12446565
REFERENCE 2 (bases 1 to 15)
AUTHORS Balzergue,S.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
FEATURES Location/Qualifiers
source 1. .15
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassillewskija"
/db_xref="taxon:3702"
/clone="631B09"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
misc_feature 1. .15
/note="T-DNA flanking sequence
right border"
ORIGIN

Query Match 48.6%; Score 10.2; DB 9; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.2e+06;
Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy          2 TGGCGTATCTGAAGA 16
              ||| | ||||| |||
Db         15 TGGAGAATCTGGAGA 1
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RESULT 3
CA851013/c
LOCUS CA851013 21 bp mRNA linear EST 01-AUG-2003
DEFINITION D09B11_C11_04.ab1 cDNA Peking library 2, 4 day SCN3 Glycine max cDNA clone D09B11 5', mRNA sequence.

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ACCESSION   CA851013
VERSION     CA851013.1  GI:33387806
KEYWORDS    EST.
SOURCE      Glycine max (soybean)
  ORGANISM  Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
            Glycine.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Alkharouf,N.W., Khan,R. and Matthews,B.F.
  TITLE     Analysis of expressed sequence tags from roots of resistant soybean
            infected by the soybean cyst nematode
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Alkharouf, N.W.
            Soybean Genomics and Improvement Laboratory (SGIL)
            US Department of Agriculture (USDA), ARS, PSI
            Bldg.006, Rm 118, 10300 Baltimore Ave., Beltsville, MD 20705-2350,
            USA
            Tel: 301 504 5750
            Fax: 301 504 5728
            Email: alkharon@ba.ars.usda.gov.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Glycine max"
                     /mol_type="mRNA"
                     /cultivar="Peking"
                     /db_xref="taxon:3847"
                     /clone="D09B11"
                     /tissue_type="Roots"
                     /dev_stage="Seedlings"
                     /clone_lib="cDNA Peking library 2, 4 day SCN3"
                     /note="Vector: pBluescript SK-; cDNA clones from mRNA
                     extracted from Peking roots 2 and 4 days past invasion."
ORIGIN

  Query Match             47.6%;  Score 10;  DB 6;  Length 21;
  Best Local Similarity   72.2%;  Pred. No. 2.9e+06;
  Matches   13;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          4 GCGTATCTGAAGAGTCTG 21
              |||||| || | | | ||
Db         20 GCGTATGTGTATATTATG 3


RESULT 4
AZ495849/c
LOCUS       AZ495849                 19 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0331N22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0331N22 R, genomic survey sequence.
ACCESSION   AZ495849
VERSION     AZ495849.1  GI:10671571
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0331  row: N  column: 22
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0331N22"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             46.7%;  Score 9.8;  DB 8;  Length 19;
  Best Local Similarity   84.6%;  Pred. No. 3.6e+06;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          9 TCTGAAGAGTCTG 21
              |||| |||| |||
Db         15 TCTGCAGAGCCTG 3


RESULT 5
AZ875769
LOCUS       AZ875769                 19 bp    DNA     linear   GSS 21-FEB-2001
DEFINITION  2M0190A02R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0190A02 R, genomic survey sequence.
ACCESSION   AZ875769
VERSION     AZ875769.1  GI:13086107
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
```

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          Insert Length: 10000   Std Error: 0.00
          Plate: 0190  row: A  column: 02
          Seq primer: CACACAGGAAACAGCTATGACC
          Class: plasmid ends
          High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0190A02"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match            46.7%;  Score 9.8;  DB 8;  Length 19;
  Best Local Similarity  84.6%;  Pred. No. 3.6e+06;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CTGGCGTATCTGA 13
              |||| || |||||
Db          7 CTGGAGTGTCTGA 19


RESULT 6
AZ489135
LOCUS       AZ489135                 20 bp    DNA     linear   GSS 05-OCT-2000
DEFINITION  1M0319H15R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0319H15 R, genomic survey sequence.
ACCESSION   AZ489135
VERSION     AZ489135.1  GI:10658589
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
```

```
          Insert Length: 10000   Std Error: 0.00
          Plate: 0319  row: H  column: 15
          Seq primer: CACACAGGAAACAGCTATGACC
          Class: plasmid ends
          High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0319H15"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match            45.7%;  Score 9.6;  DB 8;  Length 20;
  Best Local Similarity  75.0%;  Pred. No. 4.6e+06;
  Matches   12;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 TGGCGTATCTGAAGAG 17
              |||| | ||||| | |
Db          3 TGGCTTTTCTGAGGGG 18


RESULT 7
CL681189
LOCUS       CL681189                 17 bp    DNA     linear   GSS 09-JUL-2004
DEFINITION  PRI0130b_G06_2 - PRI0130b.BR (17) Mixed stage fosmid library of P.
            pacificus var. California Pristionchus pacificus genomic, genomic
            survey sequence.
ACCESSION   CL681189
VERSION     CL681189.1  GI:50188197
KEYWORDS    GSS.
SOURCE      Pristionchus pacificus
  ORGANISM  Pristionchus pacificus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
            Neodiplogasteridae; Pristionchus.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
  TITLE     AppaDB: an AcedB database for the nematode satellite organism
            Pristionchus pacificus
  JOURNAL   Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT     Contact: Sommer RJ
            Evolutionary Biology
            Max-Planck-Institute for Developmental Biology
            Spemannstr. 37-39, Tuebingen D-72076, Germany
            Tel: 00497071601371
            Fax: 00497071601498
            Email: ralf.sommer@tuebingen.mpg.de
            This library was generated at Caltech, Pasadena, USA and end
            sequenced at Vancouver, Canada.
            Seq primer: T7
```

```
          Class: fosmid ends.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Pristionchus pacificus"
                     /mol_type="genomic DNA"
                     /strain="California"
                     /db_xref="taxon:54126"
                     /clone_lib="Mixed stage fosmid library of P. pacificus
                     var. California"
                     /note="Vector: pEpifos-5 Fosmid vector"
ORIGIN

  Query Match             44.8%;  Score 9.4;  DB 9;  Length 17;
  Best Local Similarity   90.9%;  Pred. No. 5.7e+06;
  Matches   10;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 GTATCTGAAGA 16
              ||||||| |||
Db          6 GTATCTGCAGA 16


RESULT 8
AZ308384
LOCUS       AZ308384                 20 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0011K17F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0011K17 F, genomic survey sequence.
ACCESSION   AZ308384
VERSION     AZ308384.1  GI:10348326
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000  Std Error: 0.00
            Plate: 0011  row: K  column: 17
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0011K17"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             43.8%;  Score 9.2;  DB 8;  Length 20;
  Best Local Similarity   78.6%;  Pred. No. 7.4e+06;
  Matches   11;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          8 ATCTGAAGAGTCTG 21
              |||||||| | | |
Db          4 ATCTGAAGTGACCG 17


RESULT 9
AZ316351/c
LOCUS       AZ316351                 20 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0034A11F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0034A11 F, genomic survey sequence.
ACCESSION   AZ316351
VERSION     AZ316351.1  GI:10364090
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000  Std Error: 0.00
            Plate: 0034  row: A  column: 11
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0034A11"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
```

adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

```
  Query Match             43.8%;  Score 9.2;  DB 8;  Length 20;
  Best Local Similarity   78.6%;  Pred. No. 7.4e+06;
  Matches   11;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          8 ATCTGAAGAGTCTG 21
              |||| ||||  |||
Db         20 ATCTCAAGATACTG 7
```

RESULT 10
AZ328275/c
LOCUS AZ328275 20 bp DNA linear GSS 29-SEP-2000
DEFINITION 1M0052A01F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0052A01 F, genomic survey sequence.
ACCESSION AZ328275
VERSION AZ328275.1 GI:10387840
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 20)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0052 row: A column: 01
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 20.
FEATURES Location/Qualifiers
source 1. .20
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0052A01"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The

adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 43.8%; Score 9.2; DB 8; Length 20;
Best Local Similarity 78.6%; Pred. No. 7.4e+06;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 GCGTATCTGAAGAG 17
||||| ||| | ||
Db 19 GCGTACCTGTAAAG 6

RESULT 11
AJ587417/c
LOCUS AJ587417 10 bp DNA linear GSS 15-JAN-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 275G07, genomic survey sequence.
ACCESSION AJ587417
VERSION AJ587417.1 GI:37937041
KEYWORDS GSS; left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G., Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE 22363535
PUBMED 12446565
REFERENCE 2 (bases 1 to 10)
AUTHORS Balzergue,S.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
FEATURES Location/Qualifiers
source 1. .10
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassillewskija"
/db_xref="taxon:3702"
/clone="275G07"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
misc_feature 1. .10
/note="T-DNA flanking sequence left border"

ORIGIN

Query Match 42.9%; Score 9; DB 9; Length 10;

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  Best Local Similarity   100.0%;  Pred. No. 8.5e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          13 AAGAGTCTG 21
               |||||||||
Db           9 AAGAGTCTG 1


RESULT 12
AJ684587
LOCUS       AJ684587                  16 bp    mRNA    linear   EST 29-JUN-2004
DEFINITION  AJ684587 CSEQRAN04 Sus scrofa cDNA clone C0001805_G15, mRNA
            sequence.
ACCESSION   AJ684587
VERSION     AJ684587.1  GI:49417177
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
  TITLE     Development of cDNA and EST resources for studying reproduction and
            embryo development in pigs and cattle
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Anderson SI
            Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
            Single pass sequencing. Bases called and trimmed with phred
            v0.020425.c. Vector identified by cross_match with the -minscore 20
            and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site1: EcoRI
            R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
            from pig uterus. Clones available from UK Centre for Functional
            Genomics in Farm Animals, Roslin Institite, Roslin, Midlothian, UK,
            EH25 9PS, www.arkgenomics.org.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /clone="C0001805_G15"
                     /tissue_type="uterus"
                     /clone_lib="CSEQRAN04"
                     /note="Vector: pBlueScriptII(KS+); Site_1: EcoRI; Site_2:
                     NotI; Single pass sequencing. Normalised library
                     constructed from pig uterus."
ORIGIN

  Query Match             42.9%;  Score 9;  DB 1;  Length 16;
  Best Local Similarity   100.0%;  Pred. No. 9e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          12 GAAGAGTCT 20
               |||||||||
Db           1 GAAGAGTCT 9


RESULT 13
AZ625776
LOCUS       AZ625776                  20 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0465C08R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0465C08 R, genomic survey sequence.
ACCESSION   AZ625776
VERSION     AZ625776.1  GI:11747966
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0465  row: C  column: 08
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0465C08"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             42.9%;  Score 9;  DB 8;  Length 20;
  Best Local Similarity   70.6%;  Pred. No. 9.3e+06;
  Matches   12;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy           4 GCGTATCTGAAGAGTCT 20
               |||  |  | ||||  |||
Db           2 GCGCACTTCAAGATTCT 18


RESULT 14
BG924548/c
LOCUS       BG924548                  21 bp    mRNA    linear   EST 06-NOV-2001
DEFINITION  HNC27-1-G10.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
            sequence.
ACCESSION   BG924548
VERSION     BG924548.1  GI:14319071
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
            Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
```

```
            Lark,M.W.
  TITLE     Identification and initial characterization of 5000 expressed
            sequenced tags (ESTs) each from adult human normal and
            osteoarthritic cartilage cDNA libraries
  JOURNAL   Osteoarthr. Cartil. 9 (7), 641-653 (2001)
  MEDLINE   21482651
   PUBMED   11597177
COMMENT     Contact: Sanjay Kumar
            UW2109
            GlaxoSmithKline
            709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
            Tel: 610-270-7245
            Fax: 610-270-5598
            Email: sanjay_kumar-1@gsk.com
            Seq primer: T7.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="cartilage"
                     /lab_host="E.coli DH10 B"
                     /clone_lib="HNC (Human Normal Cartilage)"
                     /note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
                     Directional"
ORIGIN

  Query Match             42.9%;  Score 9;  DB 4;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 9.3e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CTGGCGTAT 9
              |||||||||
Db         12 CTGGCGTAT 4


RESULT 15
AJ587168/c
LOCUS       AJ587168                 17 bp    DNA     linear   GSS 15-JAN-2004
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
            233H03, genomic survey sequence.
ACCESSION   AJ587168
VERSION     AJ587168.1  GI:37936757
KEYWORDS    GSS; left border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 17)
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="233H03"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature    1. .17
                     /note="T-DNA flanking sequence
                     left border"
ORIGIN

  Query Match             41.9%;  Score 8.8;  DB 9;  Length 17;
  Best Local Similarity   83.3%;  Pred. No. 1.1e+07;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 CGTATCTGAAGA 16
              ||||  ||||||
Db         12 CGTAGTTGAAGA 1


RESULT 16
C00979
LOCUS       C00979                   20 bp    mRNA    linear   EST 31-DEC-2002
DEFINITION  HUMGS0003365 Human adult (K.Okubo) Homo sapiens cDNA, mRNA
            sequence.
ACCESSION   C00979
VERSION     C00979.1  GI:1433209
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Okubo,K.
  TITLE     BodyMap; human gene expression database
  JOURNAL   Unpublished (1995)
COMMENT     Contact: Okubo,K.
            Institute for Molecular and Cellular Biol
            Osaka University
            1-3,Yamada-oka, Suita, Osaka Pref. 565, Japan
            Tel: 06-877-5111(ex.3315)
            Email: kousaku@imcb.osaka-u.ac.jp
            We are not submitting the same cDNA sequence redundantly to DDBJ
            since 1993. For the abundance information of clones with this
            sequence in this library and as well as in other 3'-directed
            libraries, see ' http://www.imcb.osaka- u.ac.jp/bodymap'. The
            sequences of the clones represented by this GS sequences is also
            found there.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="adult"
                     /clone_lib="Human adult (K.Okubo)"
                     /note="One or more human adult tissue"
ORIGIN

  Query Match             41.9%;  Score 8.8;  DB 6;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 1.2e+07;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 ATCTGAAGAGTC 19
              ||||  ||||||
Db          2 ATCTCTAGAGTC 13


RESULT 17
CF325351/c
LOCUS       CF325351                 20 bp    mRNA    linear   EST 18-AUG-2003
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DEFINITION  JMT1--03-A01.g1 AtJMT-overexpressing transgenic rice lambda phage
            cDNA library (JMT1) Oryza sativa (japonica cultivar-group) cDNA
            clone JMT1--03-A01, mRNA sequence.
ACCESSION   CF325351
VERSION     CF325351.1  GI:33798984
KEYWORDS    EST.
SOURCE      Oryza sativa (japonica cultivar-group)
  ORGANISM  Oryza sativa (japonica cultivar-group)
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Ehrhartoideae; Oryzeae; Oryza.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Kim,J.S., Jun,K.M., Cheong,P.J., Kim,M.J., Lee,T.H., Shin,Y.C.,
            Song,S.I., Kim,J.K., Kim,Y.-K. and Nahm,B.H.
  TITLE     Large-scale Sequencing Analysis of Rice ESTs
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Nahm B.H.
            Genomics and Genetics Institute, GreenGene Biotech Inc.; Division
            of Bioscience and Bioinformatics, MyongJi University
            Yongin, Kyeonggi, Korea
            Tel: 82 31 330 6193
            Fax: 82 31 321 6355
            Email: bhnahm@ggbio.com, bhnahm@bio.myongji.ac.kr.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Oryza sativa (japonica cultivar-group)"
                     /mol_type="mRNA"
                     /cultivar="Nackdong"
                     /db_xref="taxon:39947"
                     /clone="JMT1--03-A01"
                     /tissue_type="leaf"
                     /dev_stage="14 days after germination"
                     /lab_host="E.coli SOLR"
                     /clone_lib="AtJMT-overexpressing transgenic rice lambda
                     phage cDNA library (JMT1)"
                     /note="Vector: pBluescript SK(+); Site_1: EcoRI; Site_2:
                     XhoI; cDNA was inserted into lamda Uni-ZAP XR vector at 5'
                     end with EcoRI and 3' end with XhoI site. mRNA was
                     prepared from Arabidopsis Jasmoinate Carboxyl
                     methyltransferase overexpression line."
ORIGIN

  Query Match           41.9%;  Score 8.8;  DB 7;  Length 20;
  Best Local Similarity  83.3%;  Pred. No. 1.2e+07;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 CTGGCGTATCTG 12
              |||||| ||| |
Db         16 CTGGCGAATCAG 5


RESULT 18
D20709
LOCUS       D20709                    20 bp    mRNA    linear   EST 30-JUL-1996
DEFINITION  HUMGS01685 Human promyelocyte Homo sapiens cDNA clone pm2147 3',
            mRNA sequence.
ACCESSION   D20709
VERSION     D20709.1  GI:501805
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Okubo,K., Fukushima,A., Yoshii,J., Niiyama,T., Kojima,Y.,
            Yoshinari,H., Arimoto,J. and Matsubara,K.
  TITLE     Gene expression of human promyelocytic cell line HL60 before and
            after induction of differentiation. A new application of 3'directed
            cDNA sequencing
  JOURNAL   Unpublished (1993)
COMMENT     Contact: Okubo,K., Fukushima,A., Yoshii,J., Niiyama,T., Kojima,Y.,
            Yoshinari,H., Arimoto,J. and Matsubara,K.
            Institute for Molecular and Cellular Biology
            Osaka University
            3-1 Yamada-oka,Suita,Osaka 565,Japan.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="pm2147"
                     /clone_lib="Human promyelocyte"
                     /note="Female, adult, cell_line = HL60, cell_type =
                     promyelocyte. "
ORIGIN

  Query Match           41.9%;  Score 8.8;  DB 7;  Length 20;
  Best Local Similarity  83.3%;  Pred. No. 1.2e+07;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          8 ATCTGAAGAGTC 19
              |||| |||| ||
Db          2 ATCTCAAGACTC 13


RESULT 19
AJ671616/c
LOCUS       AJ671616                  19 bp    mRNA    linear   EST 28-JUN-2004
DEFINITION  AJ671616 KN224 Bos taurus cDNA clone KN224-006_N20, mRNA sequence.
ACCESSION   AJ671616
VERSION     AJ671616.1  GI:49356473
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
  TITLE     Development of cDNA and EST resources for studying reproduction and
            embryo development in pigs and cattle
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Anderson SI
            Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
            Single pass sequencing. Bases called and trimmed with phred
            v0.020425.c. Vector identified by cross_match with the -minscore 20
            and -minmatch 12 options. Vector: pBluescriptII(SK+) R. Site 1:
            EcoRI R. Site 2: NotI 5' Seq primer M13F Description: Normalised
            library constructed from Bovine Uterus tissue. Clones available
            from UK Centre for Functional Genomics in Farm Animals, Roslin
            Institite, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /clone="KN224-006_N20"
                     /tissue_type="uterus"
                     /clone_lib="KN224"
                     /note="Vector: pBluescriptII(SK+); Site_1: EcoRI; Site_2:
                     NotI; Single pass sequencing. Normalised library
                     constructed from Bovine Uterus tissue."
ORIGIN

  Query Match           41.0%;  Score 8.6;  DB 1;  Length 19;
  Best Local Similarity  73.3%;  Pred. No. 1.5e+07;
  Matches   11;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GGCGTATCTGAAGAG 17
              | | |||||||  ||
Db         19 GTCATATCTGAGAAG 5


RESULT 20
```

```
CO778852/c
LOCUS       CO778852                 19 bp    mRNA    linear   EST 05-AUG-2004
DEFINITION  BL004D_H08 6-Day Axolotl Tail Blastema (6DAxBL) Ambystoma mexicanum
            cDNA 5' similar to hypothetical protein, mRNA sequence.
ACCESSION   CO778852
VERSION     CO778852.1  GI:50994832
KEYWORDS    EST.
SOURCE      Ambystoma mexicanum (axolotl)
  ORGANISM  Ambystoma mexicanum
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
            Ambystoma.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Habermann,B., Bebin,A.G., Herklotz,S., Volkmer,M., Eckelt,K.,
            Pehlke,K., Epperlein,H.H., Schackert,H.K., Wiebe,G. and Tanaka,E.M.
  TITLE     An Ambystoma mexicanum EST sequencing project: Analysis of 17,352
            expressed sequence tags from embryonic and regenerating blastema
            cDNA libraries
  JOURNAL   Genome Biol. (2004) In press
COMMENT     Contact: Elly M. Tanaka
            Tanaka Lab
            Max Planck Institute of Molecular Cell Biology and Genetics,
            Dresden
            Pfotenhauerstrasse 108,01307 Dresden, Germany
            Tel: 0049 351 210 2620
            Fax: 0049 351 210 1489
            Email: tanaka@mpi-cbg.de
            Plate: BL004D  row: 08  column: H
            Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Ambystoma mexicanum"
                     /mol_type="mRNA"
                     /db_xref="taxon:8296"
                     /tissue_type="Tail Blastema"
                     /cell_type="regenerating tail blastema"
                     /clone_lib="6-Day Axolotl Tail Blastema (6DAxBL)"
                     /note="Vector: pCMVSport6; Site_1: NotI; Site_2: SalI;
                     Unnormalized cDNA plasmid library prepared by Invitrogen.
                     Size fractionated mRNA was polydT primed and cloned into
                     NotI-SalI site of pCMVSport6. Bacterial host is
                     EMDH10B-TONA. Average insert size is 1.67 kB.
                     TAG_LIB=6DAxBL"
ORIGIN
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  Query Match            41.0%;  Score 8.6;  DB 7;  Length 19;
  Best Local Similarity   73.3%;  Pred. No. 1.5e+07;
  Matches   11;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 CTGGCGTATCTGAAG 15
              | ||||||  | |||
Db         16 CAGGCGTACTTAAAG 2
```

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RESULT 21
AZ480596/c
LOCUS       AZ480596                 20 bp    DNA     linear   GSS 04-OCT-2000
DEFINITION  1M0302D18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0302D18 F, genomic survey sequence.
ACCESSION   AZ480596
VERSION     AZ480596.1  GI:10641661
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0302  row: D  column: 18
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0302D18"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN
```

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  Query Match            41.0%;  Score 8.6;  DB 8;  Length 20;
  Best Local Similarity   73.3%;  Pred. No. 1.5e+07;
  Matches   11;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 GGCGTATCTGAAGAG 17
              ||  | | |||||||
Db         18 GGAATCTATGAAGAG 4
```

```
RESULT 22
AZ658035/c
LOCUS       AZ658035                 20 bp    DNA     linear   GSS 14-DEC-2000
DEFINITION  1M0534P03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0534P03 R, genomic survey sequence.
ACCESSION   AZ658035
VERSION     AZ658035.1  GI:11795181
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
```

```
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0534  row: P  column: 03
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0534P03"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             41.0%;  Score 8.6;  DB 8;  Length 20;
  Best Local Similarity   73.3%;  Pred. No. 1.5e+07;
  Matches   11;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 TGGCGTATCTGAAGA 16
              |||| |||   ||||
Db         17 TGGCATATGGCAAGA 3


RESULT 23
AG194535/c
LOCUS       AG194535                 21 bp    DNA     linear   GSS 06-MAR-2004
DEFINITION  Pan troglodytes DNA, clone: RP43-072L24.T7, genomic survey
            sequence.
ACCESSION   AG194535
VERSION     AG194535.1  GI:45226711
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1
  AUTHORS   Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
            Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
  TITLE     BAC end sequences of Library RP-43
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 21)
  AUTHORS   Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
            Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
            Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
            52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
            (E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,
            Tel:82-42-866-7181, Fax:82-42-860-4409)
COMMENT     Clones are derived from the chimpanzee BAC library RP-43 This BAC
            end was generated during the R&D process and may have higher chance
            of clone tracking errors.
             PRIMERS
                 Sequencing: T7
             LIBRARY
                 Vector    : pBACe3.6
                 R.Site 1  : EcoRI
                 R.Site 2  : EcoRI.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
                     /clone="RP43-072L24.T7"
                     /sex="male"
                     /cell_type="lymphocytes"
                     /clone_lib="RP-43 Chimpanzee Male BAC Library"
ORIGIN

  Query Match             41.0%;  Score 8.6;  DB 9;  Length 21;
  Best Local Similarity   73.3%;  Pred. No. 1.5e+07;
  Matches   11;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          7 TATCTGAAGAGTCTG 21
              | |||| ||  ||||
Db         16 TTTCTGTAGCATCTG 2


RESULT 24
AZ623493/c
LOCUS       AZ623493                 19 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0461M13F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0461M13 F, genomic survey sequence.
ACCESSION   AZ623493
VERSION     AZ623493.1  GI:11745683
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0461  row: M  column: 13
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
```

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                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0461M13"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match            40.0%;  Score 8.4;  DB 8;  Length 19;
  Best Local Similarity  90.0%;  Pred. No. 1.8e+07;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 TATCTGAAGA 16
              || |||||||
Db         11 TAACTGAAGA 2


RESULT 25
AZ818271
LOCUS       AZ818271                 20 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0088M08F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0088M08 F, genomic survey sequence.
ACCESSION   AZ818271
VERSION     AZ818271.1  GI:12988179
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0088  row: M  column: 08
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0088M08"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match            40.0%;  Score 8.4;  DB 8;  Length 20;
  Best Local Similarity  90.0%;  Pred. No. 1.9e+07;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 ATCTGAAGAG 17
              ||||||| ||
Db          4 ATCTGAATAG 13


RESULT 26
AG199044/c
LOCUS       AG199044                 20 bp    DNA     linear   GSS 06-MAR-2004
DEFINITION  Pan troglodytes DNA, clone: RP43-080D07.TJ, genomic survey
            sequence.
ACCESSION   AG199044
VERSION     AG199044.1  GI:45231220
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1
  AUTHORS   Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
            Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
  TITLE     BAC end sequences of Library RP-43
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 20)
  AUTHORS   Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
            Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
            Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
            52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
            (E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,
            Tel:82-42-866-7181, Fax:82-42-860-4409)
COMMENT     Clones are derived from the chimpanzee BAC library RP-43 This BAC
            end was generated during the R&D process and may have higher chance
            of clone tracking errors.
             PRIMERS
                 Sequencing: TJ
             LIBRARY
                 Vector    : pBACe3.6
                 R.Site 1  : EcoRI
                 R.Site 2  : EcoRI.
FEATURES             Location/Qualifiers
     source          1. .20
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```
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
                     /clone="RP43-080D07.TJ"
                     /sex="male"
                     /cell_type="lymphocytes"
                     /clone_lib="RP-43 Chimpanzee Male BAC Library"
ORIGIN

  Query Match             40.0%;  Score 8.4;  DB 9;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+07;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          9 TCTGAAGAGT 18
              | ||||||||
Db         18 TATGAAGAGT 9


RESULT 27
AG203835
LOCUS       AG203835                 20 bp    DNA     linear   GSS 06-MAR-2004
DEFINITION  Pan troglodytes DNA, clone: RP43-088M10.TJ, genomic survey
            sequence.
ACCESSION   AG203835
VERSION     AG203835.1  GI:45236010
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1
  AUTHORS   Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
            Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
  TITLE     BAC end sequences of Library RP-43
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 20)
  AUTHORS   Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
            Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
            Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
            52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
            (E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,
            Tel:82-42-866-7181, Fax:82-42-860-4409)
COMMENT     Clones are derived from the chimpanzee BAC library RP-43 This BAC
            end was generated during the R&D process and may have higher chance
            of clone tracking errors.
             PRIMERS
                 Sequencing: TJ
             LIBRARY
                 Vector    : pBACe3.6
                 R.Site 1  : EcoRI
                 R.Site 2  : EcoRI.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
                     /clone="RP43-088M10.TJ"
                     /sex="male"
                     /cell_type="lymphocytes"
                     /clone_lib="RP-43 Chimpanzee Male BAC Library"
ORIGIN

  Query Match             40.0%;  Score 8.4;  DB 9;  Length 20;
  Best Local Similarity   90.0%;  Pred. No. 1.9e+07;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 CTGGCGTATC 10
              ||||||| ||
Db          3 CTGGCGTGTC 12
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```
RESULT 28
AZ787920/c
LOCUS       AZ787920                 21 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  2M0034M09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0034M09 R, genomic survey sequence.
ACCESSION   AZ787920
VERSION     AZ787920.1  GI:12927197
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0034  row: M  column: 09
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 21.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0034M09"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             40.0%;  Score 8.4;  DB 8;  Length 21;
  Best Local Similarity   66.7%;  Pred. No. 1.9e+07;
  Matches   12;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 TGGCGTATCTGAAGAGTC 19
              |||  |||||  |  |||
Db         18 TGGTTTATCTTCAATGTC 1
```

```
RESULT 29
CL694050
LOCUS       CL694050                  13 bp    DNA     linear   GSS 10-JUL-2004
DEFINITION  PRI0163a_H11_2 - PRI0163a.BR (13) Mixed stage fosmid library of P.
            pacificus var. California Pristionchus pacificus genomic, genomic
            survey sequence.
ACCESSION   CL694050
VERSION     CL694050.1  GI:50215958
KEYWORDS    GSS.
SOURCE      Pristionchus pacificus
  ORGANISM  Pristionchus pacificus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
            Neodiplogasteridae; Pristionchus.
REFERENCE   1  (bases 1 to 13)
  AUTHORS   Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
  TITLE     AppaDB: an AcedB database for the nematode satellite organism
            Pristionchus pacificus
  JOURNAL   Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT     Contact: Sommer RJ
            Evolutionary Biology
            Max-Planck-Institute for Developmental Biology
            Spemannstr. 37-39, Tuebingen D-72076, Germany
            Tel: 00497071601371
            Fax: 00497071601498
            Email: ralf.sommer@tuebingen.mpg.de
            This library was generated at Caltech, Pasadena, USA and end
            sequenced at Vancouver, Canada.
            Seq primer: T7
            Class: fosmid ends.
FEATURES             Location/Qualifiers
     source          1. .13
                     /organism="Pristionchus pacificus"
                     /mol_type="genomic DNA"
                     /strain="California"
                     /db_xref="taxon:54126"
                     /clone_lib="Mixed stage fosmid library of P. pacificus
                     var. California"
                     /note="Vector: pEpifos-5 Fosmid vector"
ORIGIN

  Query Match           39.0%;  Score 8.2;  DB 9;  Length 13;
  Best Local Similarity   76.9%;  Pred. No. 2.2e+07;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 CTGGCGTATCTGA 13
              |||   |||||||
Db          1 CTGCGTTATCTGA 13


RESULT 30
CL423467
LOCUS       CL423467                  17 bp    DNA     linear   GSS 16-MAR-2004
DEFINITION  01S0557-03A1-C12 UniformMu MuTAIL Library Zea mays genomic clone
            01S0557-03A1-C12, genomic survey sequence.
ACCESSION   CL423467
VERSION     CL423467.1  GI:45501511
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Latshaw,S., Tan,B-.C., Settles,A.M. and McCarty,D.R.
  TITLE     Sequence tagged transposon insertions from the UniformMu maize
            population
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Donald R. McCarty
            Plant Molecular and Cellular Biology Program
            University of Florida
            PO 110690 Gainesville, FL 32611-0690, USA
            Tel: 352-392-1928 x322
            Email: drm@ufl.edu
            Sequence Sequence flanking probable Mu insertion site in UniformMu
            line: 01S0557-03, Primer set: A
            Class: transposon insertion site.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="W22 (ACR, bz1-m9)"
                     /cultivar="UniformMu"
                     /db_xref="taxon:4577"
                     /clone="01S0557-03A1-C12"
                     /clone_lib="UniformMu MuTAIL Library"
                     /note="Vector: TOPO-PCR4; DNA flanking Mu transposon
                     insertions in Mu inactive lines were extracted from the
                     UniformMu maize population by the thermo assymmetric
                     interlaced PCR (TAIL) protocol using primers specific for
                     the Mu terminal inverted repeat and a set of 16 arbitrary
                     primers. Amplicons were size enriched using Sepharose 400
                     spin columns and cloned into the TOPO PCR4 vector."
ORIGIN

  Query Match           39.0%;  Score 8.2;  DB 9;  Length 17;
  Best Local Similarity   76.9%;  Pred. No. 2.3e+07;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          8 ATCTGAAGAGTCT 20
              ||||| | ||| |
Db          2 ATCTGGACAGTTT 14


RESULT 31
AJ662026
LOCUS       AJ662026                  18 bp    mRNA    linear   EST 28-JUN-2004
DEFINITION  AJ662026 CSEQRAN09 Sus scrofa cDNA clone C0000023_O15, mRNA
            sequence.
ACCESSION   AJ662026
VERSION     AJ662026.1  GI:49346149
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
  TITLE     Development of cDNA and EST resources for studying reproduction and
            embryo development in pigs and cattle
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Anderson SI
            Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
            Single pass sequencing. Bases called and trimmed with phred
            v0.020425.c. Vector identified by cross_match with the -minscore 20
            and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site 1:
            EcoRI R. Site 2: NotI Description: Normalised library constructed
            from pooled tissue from day 30 placentas. Clones available from UK
            Centre for Functional Genomics in Farm Animals, Roslin Institite,
            Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /clone="C0000023_O15"
                     /tissue_type="placenta"
                     /clone_lib="CSEQRAN09"
                     /note="Vector: pBlueScriptII(KS+); Site_1: EcoRI; Site_2:
                     NotI; Single pass sequencing. Normalised library
                     constructed from pooled tissue from day 30 placentas."
ORIGIN

  Query Match           39.0%;  Score 8.2;  DB 1;  Length 18;
  Best Local Similarity   76.9%;  Pred. No. 2.3e+07;
```

```
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 GGCGTATCTGAAG 15
              ||||| | || ||
Db          2 GGCGTCTTTGGAG 14


RESULT 32
AJ588865
LOCUS       AJ588865                 18 bp    DNA     linear   GSS 15-JAN-2004
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, right border, clone
            539G02, genomic survey sequence.
ACCESSION   AJ588865
VERSION     AJ588865.1  GI:37938489
KEYWORDS    GSS; right border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 18)
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="539G02"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature    1. .18
                     /note="T-DNA flanking sequence
                     right border"
ORIGIN

  Query Match           39.0%;  Score 8.2;  DB 9;  Length 18;
  Best Local Similarity   76.9%;  Pred. No. 2.3e+07;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          8 ATCTGAAGAGTCT 20
              |||||| | | ||
Db          4 ATCTGATGGGCCT 16


RESULT 33
AZ358656/c
LOCUS       AZ358656                 19 bp    DNA     linear   GSS 02-OCT-2000
DEFINITION  1M0101K12F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0101K12 F, genomic survey sequence.
ACCESSION   AZ358656
VERSION     AZ358656.1  GI:10472356
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0101  row: K  column: 12
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0101K12"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match           39.0%;  Score 8.2;  DB 8;  Length 19;
  Best Local Similarity   76.9%;  Pred. No. 2.3e+07;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          9 TCTGAAGAGTCTG 21
              | ||| |||| ||
Db         19 TGTGAGGAGTGTG 7


RESULT 34
BQ595520
LOCUS       BQ595520                 20 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012693-024-022-L12-SP6 MPIZ-ADIS-024-developing root Beta vulgaris
            cDNA clone 024-022-L12 5-PRIME, mRNA sequence.
ACCESSION   BQ595520
```

```
VERSION     BQ595520.1  GI:26125103
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 20   Std Error: 0.00
            Plate: 22  row: L  column: 12
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:191330"
                     /db_xref="taxon:161934"
                     /clone="024-022-L12"
                     /tissue_type="developing root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-developing root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN

  Query Match            39.0%;  Score 8.2;  DB 5;  Length 20;
  Best Local Similarity  76.9%;  Pred. No. 2.3e+07;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          8 ATCTGAAGAGTCT 20
              |||| || | |||
Db          5 ATCTCAATATTCT 17


RESULT 35
AZ320114
LOCUS       AZ320114                 20 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0040D05F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0040D05 F, genomic survey sequence.
ACCESSION   AZ320114
VERSION     AZ320114.1  GI:10371567
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0040  row: D  column: 05
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0040D05"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match            39.0%;  Score 8.2;  DB 8;  Length 20;
  Best Local Similarity  76.9%;  Pred. No. 2.3e+07;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          6 GTATCTGAAGAGT 18
              ||| || || |||
Db          2 GTACCTAAACAGT 14


RESULT 36
AZ436082
LOCUS       AZ436082                 20 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0233A10R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0233A10 R, genomic survey sequence.
ACCESSION   AZ436082
VERSION     AZ436082.1  GI:10560095
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
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          Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
          Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE   Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
  JOURNAL Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
          University of Utah Genome Center
          University of Utah
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: ddunn@genetics.utah.edu
          Insert Length: 10000   Std Error: 0.00
          Plate: 0233  row: A  column: 10
          Seq primer: CACACAGGAAACAGCTATGACC
          Class: plasmid ends
          High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0233A10"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             39.0%;  Score 8.2;  DB 8;  Length 20;
  Best Local Similarity   76.9%;  Pred. No. 2.3e+07;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 TGGCGTATCTGAA 14
              |||  || |||||
Db          5 TGGGATAGCTGAA 17


RESULT 37
AZ772787/c
LOCUS       AZ772787                 20 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  1M0583M24R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0583M24 R, genomic survey sequence.
ACCESSION   AZ772787
VERSION     AZ772787.1  GI:12896465
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
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          Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
          Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE   Mouse whole genome scaffolding with paired end reads from 10kb
          plasmid inserts
  JOURNAL Unpublished (2000)
COMMENT   Contact: Robert B. Weiss
          University of Utah Genome Center
          University of Utah
          Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
          84112, USA
          Tel: 801 585 5606
          Fax: 801 585 7177
          Email: ddunn@genetics.utah.edu
          Insert Length: 10000   Std Error: 0.00
          Plate: 0583  row: M  column: 24
          Seq primer: CACACAGGAAACAGCTATGACC
          Class: plasmid ends
          High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0583M24"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             39.0%;  Score 8.2;  DB 8;  Length 20;
  Best Local Similarity   76.9%;  Pred. No. 2.3e+07;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          9 TCTGAAGAGTCTG 21
              ||| |||||  ||
Db         13 TCTTAAGAGAGTG 1


RESULT 38
AZ807038
LOCUS       AZ807038                 20 bp    DNA     linear   GSS 20-FEB-2001
DEFINITION  2M0069C06R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC2M0069C06 R, genomic survey sequence.
ACCESSION   AZ807038
VERSION     AZ807038.1  GI:12970987
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
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            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0069  row: C  column: 06
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0069C06"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             39.0%;  Score 8.2;  DB 8;  Length 20;
  Best Local Similarity   76.9%;  Pred. No. 2.3e+07;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 GGCGTATCTGAAG 15
              |||  | ||||||
Db          8 GGCTGACCTGAAG 20


RESULT 39
CL436802
LOCUS       CL436802                 21 bp    DNA     linear   GSS 18-MAR-2004
DEFINITION  PST3869-NR.Seq MICB1 Mus musculus genomic clone PST3869-NR.Seq
            similar to 6820402O20Rik, genomic survey sequence.
ACCESSION   CL436802
VERSION     CL436802.1  GI:45571964
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 21)
  AUTHORS   Hicks,G.G.
  TITLE     www.EScells.ca
  JOURNAL   Unpublished (2002)
COMMENT     Contact: Hicks GG
            Mammalian Functional Genomics Centre
            Manitoba Institute of Cell Biology, Universitry of Manitoba
            ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
            Tel: 204 787 2133
            Fax: 204 787 2190
            Email: hicksgg@cc.umanitoba.ca
            U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional
            sequence information and target gene cloning can be generated. ES
            cell line harboring insertion mutation of target gene is available.
            Sequence analysis available from
            http://140.193.242.7/esdb/public_search_frame.php?PST=PST3869-NR.Se
            q
            Class: Gene Trap.
FEATURES             Location/Qualifiers
     source          1. .21
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="129 sv"
                     /db_xref="taxon:10090"
                     /clone="PST3869-NR.Seq"
                     /sex="Male"
                     /cell_type="Embryonic stem cell"
                     /cell_line="D3H (J1 subclone)"
                     /clone_lib="MICB1"
                     /note="Vector: U3NeoSV1"
ORIGIN

  Query Match             39.0%;  Score 8.2;  DB 9;  Length 21;
  Best Local Similarity   61.9%;  Pred. No. 2.3e+07;
  Matches   13;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 CTGGCGTATCTGAAGAGTCTG 21
              |||||    || ||| |  ||
Db          1 CTGGCTGCCCTTAAGGGCATG 21


RESULT 40
BG927412/c
LOCUS       BG927412                 11 bp    mRNA    linear   EST 06-NOV-2001
DEFINITION  HNC1-1-G11.R HNC (Human Normal Cartilage) Homo sapiens cDNA, mRNA
            sequence.
ACCESSION   BG927412
VERSION     BG927412.1  GI:14321935
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 11)
  AUTHORS   Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J.,
            Sathe,G., Mui,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and
            Lark,M.W.
  TITLE     Identification and initial characterization of 5000 expressed
            sequenced tags (ESTs) each from adult human normal and
            osteoarthritic cartilage cDNA libraries
  JOURNAL   Osteoarthr. Cartil. 9 (7), 641-653 (2001)
  MEDLINE   21482651
   PUBMED   11597177
COMMENT     Contact: Sanjay Kumar
            UW2109
            GlaxoSmithKline
            709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
            Tel: 610-270-7245
            Fax: 610-270-5598
            Email: sanjay_kumar-1@gsk.com
            Seq primer: T7.
FEATURES             Location/Qualifiers
     source          1. .11
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
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/tissue_type="cartilage"
/lab_host="E.coli DH10 B"
/clone_lib="HNC (Human Normal Cartilage)"
/note="Vector: pSPORT I; Site_1: SalI; Site_2: NotI;
Directional"

ORIGIN

Query Match 38.1%; Score 8; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.7e+07;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 CTGGCGTA 8
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Db          9 CTGGCGTA 2
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Search completed: August 12, 2005, 11:03:27
Job time : 1812 secs

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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 12, 2005, 10:33:19 ; Search time 1581 Seconds
(without alignments)
612.969 Million cell updates/sec

Title: US-09-743-825-10
Perfect score: 20
Sequence: 1 gaccgcatagacttctcaga 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 790860

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :
GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	13.8	69.0	20	6	AR312275	AR312275 Sequence
c	2	12.2	61.0	18	6	AR096404	AR096404 Sequence
c	3	12.2	61.0	18	6	BD217452	BD217452 Antisense
	4	12	60.0	20	6	AR031072	AR031072 Sequence
	5	12	60.0	20	6	AR152833	AR152833 Sequence
	6	12	60.0	20	6	BD134289	BD134289 Detection
c	7	11.8	59.0	17	6	AX735344	AX735344 Sequence
	8	11.8	59.0	17	6	AX759065	AX759065 Sequence
	9	11.8	59.0	18	6	A65727	A65727 Sequence 8
c	10	11.8	59.0	18	6	AR048183	AR048183 Sequence
c	11	11.8	59.0	18	6	E10136	E10136 PCR primer
	12	11.8	59.0	20	6	AR023697	AR023697 Sequence
c	13	11.6	58.0	19	6	AX207008	AX207008 Sequence
	14	11.6	58.0	20	6	AX353519	AX353519 Sequence
	15	11.4	57.0	15	6	I61735	I61735 Sequence 28
	16	11.4	57.0	15	6	AX636229	AX636229 Sequence
c	17	11.4	57.0	17	6	AR111392	AR111392 Sequence
c	18	11.4	57.0	17	6	AR364674	AR364674 Sequence
c	19	11.4	57.0	17	6	AX734698	AX734698 Sequence
c	20	11.4	57.0	19	6	AX130020	AX130020 Sequence
c	21	11.4	57.0	19	6	AX130021	AX130021 Sequence
	22	11.4	57.0	20	6	AX269412	AX269412 Sequence
	23	11.4	57.0	20	6	AX270943	AX270943 Sequence
	24	11.2	56.0	18	6	AR292962	AR292962 Sequence
c	25	11.2	56.0	19	6	AX378663	AX378663 Sequence
	26	11.2	56.0	20	6	AR072310	AR072310 Sequence
c	27	11.2	56.0	20	6	AR123092	AR123092 Sequence
	28	11.2	56.0	20	6	CQ770343	CQ770343 Sequence
	29	11.2	56.0	20	6	I26421	I26421 Sequence 11
c	30	11.2	56.0	20	6	AR313207	AR313207 Sequence
c	31	11.2	56.0	20	6	AR359611	AR359611 Sequence
c	32	11.2	56.0	20	6	AR559459	AR559459 Sequence
c	33	11.2	56.0	20	6	AX259854	AX259854 Sequence
c	34	11.2	56.0	20	6	AX259855	AX259855 Sequence
	35	11	55.0	17	6	BD254799	BD254799 Regulatio
	36	11	55.0	17	6	BD254800	BD254800 Regulatio
	37	11	55.0	17	6	BD254801	BD254801 Regulatio
	38	11	55.0	17	6	AX110604	AX110604 Sequence
c	39	11	55.0	18	6	AR567503	AR567503 Sequence
c	40	11	55.0	18	6	AX277553	AX277553 Sequence
c	41	11	55.0	18	6	AX418117	AX418117 Sequence
	42	11	55.0	19	6	AX816790	AX816790 Sequence
	43	11	55.0	20	6	E30865	E30865 Oligonucleo
	44	11	55.0	20	6	E37662	E37662 Method for
	45	11	55.0	20	6	I58336	I58336 Sequence 4
	46	10.8	54.0	15	6	AR180134	AR180134 Sequence
	47	10.8	54.0	15	6	AR180675	AR180675 Sequence
c	48	10.8	54.0	17	6	AX693268	AX693268 Sequence
c	49	10.8	54.0	17	6	AX693269	AX693269 Sequence
c	50	10.8	54.0	17	6	AX693270	AX693270 Sequence
c	51	10.8	54.0	17	6	AX693271	AX693271 Sequence
c	52	10.8	54.0	17	6	AX736308	AX736308 Sequence
c	53	10.8	54.0	17	6	AX758685	AX758685 Sequence
c	54	10.8	54.0	17	6	AX759814	AX759814 Sequence
c	55	10.8	54.0	17	10	MMTC1X5AC	Z49012 M.musculus
	56	10.8	54.0	18	6	BD223754	BD223754 Endogenou
	57	10.8	54.0	20	6	BD176767	BD176767 Method of
c	58	10.8	54.0	20	6	AR208738	AR208738 Sequence
c	59	10.6	53.0	17	6	A92171	A92171 Sequence 5
c	60	10.6	53.0	17	6	AR189852	AR189852 Sequence
c	61	10.6	53.0	17	6	AR324840	AR324840 Sequence
	62	10.6	53.0	17	6	AR402059	AR402059 Sequence
c	63	10.6	53.0	17	6	AX226904	AX226904 Sequence
	64	10.6	53.0	17	6	AX761103	AX761103 Sequence
c	65	10.6	53.0	17	6	BD009147	BD009147 Herbicide
	66	10.6	53.0	17	6	BD067559	BD067559 Enzymatic
	67	10.6	53.0	18	6	CQ786884	CQ786884 Sequence
	68	10.6	53.0	18	6	CQ786886	CQ786886 Sequence
	69	10.6	53.0	18	6	AR392133	AR392133 Sequence
	70	10.6	53.0	19	6	AR108171	AR108171 Sequence
	71	10.6	53.0	19	6	AR148621	AR148621 Sequence
c	72	10.6	53.0	19	6	AR156552	AR156552 Sequence
	73	10.6	53.0	19	6	E26923	E26923 Vascular en
	74	10.6	53.0	19	6	AR206672	AR206672 Sequence
c	75	10.6	53.0	20	6	AR097061	AR097061 Sequence
	76	10.6	53.0	20	6	AR165231	AR165231 Sequence
c	77	10.6	53.0	20	6	BD205208	BD205208 Method of
	78	10.6	53.0	20	6	BD231398	BD231398 Isolated
	79	10.6	53.0	20	6	E36220	E36220 Japanese ci
	80	10.6	53.0	20	6	E47018	E47018 Simulataneo
	81	10.6	53.0	20	6	AR201402	AR201402 Sequence
	82	10.6	53.0	20	6	AR225050	AR225050 Sequence
c	83	10.6	53.0	20	6	AR252980	AR252980 Sequence
	84	10.6	53.0	20	6	AR264191	AR264191 Sequence
c	85	10.6	53.0	20	6	AR297463	AR297463 Sequence
c	86	10.6	53.0	20	6	AR336993	AR336993 Sequence
c	87	10.6	53.0	20	6	AX118550	AX118550 Sequence
	88	10.6	53.0	20	6	AX459958	AX459958 Sequence
c	89	10.6	53.0	20	6	AX777573	AX777573 Sequence
	90	10.4	52.0	15	6	I61736	I61736 Sequence 29
	91	10.4	52.0	15	6	AX636230	AX636230 Sequence
c	92	10.4	52.0	17	6	AX673751	AX673751 Sequence

c 93	10.4	52.0	17	6	AX693266	AX693266	Sequence
c 94	10.4	52.0	17	6	AX693267	AX693267	Sequence
c 95	10.4	52.0	17	6	AX725386	AX725386	Sequence
c 96	10.4	52.0	17	6	AX733563	AX733563	Sequence
97	10.4	52.0	17	6	AX745403	AX745403	Sequence
98	10.4	52.0	17	6	AX745404	AX745404	Sequence
99	10.4	52.0	17	6	AX745405	AX745405	Sequence
100	10.4	52.0	17	6	AX745406	AX745406	Sequence

ALIGNMENTS

RESULT 1
AR312275
LOCUS AR312275 20 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 2812 from patent US 6559294.
ACCESSION AR312275
VERSION AR312275.1 GI:31705701
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A., Sankaran,B. and Fletcher,L.D.
TITLE Chlamydia pneumoniae polynucleotides and uses thereof
JOURNAL Patent: US 6559294-A 2812 06-MAY-2003;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN

Query Match 69.0%; Score 13.8; DB 6; Length 20;
Best Local Similarity 88.2%; Pred. No. 7.3e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GACCGCATAGACTTCTC 17
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Db 3 GACCGCATAAACTTATC 19

RESULT 2
AR096404/c
LOCUS AR096404 18 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 75 from patent US 6007995.
ACCESSION AR096404
VERSION AR096404.1 GI:10025180
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Baker,B.F. and Cowsert,L.M.
TITLE Antisense inhibition of TNFR1 expression
JOURNAL Patent: US 6007995-A 75 28-DEC-1999;
FEATURES Location/Qualifiers
source 1. .18
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Query Match 61.0%; Score 12.2; DB 6; Length 18;
Best Local Similarity 82.4%; Pred. No. 6.4e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CGCATAGACTTCTCAGA 20
||| || |||||||||
Db 18 CGCCCAGTCTTCTCAGA 2

RESULT 3
BD217452/c
LOCUS BD217452 18 bp DNA linear PAT 17-JUL-2003
DEFINITION Antisense modulation of TNFR1 expression.
ACCESSION BD217452
VERSION BD217452.1 GI:33027222
KEYWORDS JP 2002519015-A/75.
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 18)
AUTHORS Baker,B.F. and Cowsert,L.M.
TITLE Antisense modulation of TNFR1 expression
JOURNAL Patent: JP 2002519015-A 75 02-JUL-2002;
ISIS PHARMACEUTICALS INC
COMMENT OS Unidentified
PN JP 2002519015-A/75
PD 02-JUL-2002
PF 17-JUN-1999 JP 2000557265
PR 26-JUN-1998 US 09/106038
PI BRENDA F BAKER,LEX M COWSERT
PC
C12N15/09,A61K31/7105,A61K31/711,A61K48/00,A61P29/00,A61P43/00, PC C12Q1/68,
PC C12N15/00
CC Strandedness: Single;
CC Topology: Linear;
CC Antisense modulation of TNFR1 expression
FH Key Location/Qualifiers
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FT /organism='Unidentified'.
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
ORIGIN

Query Match 61.0%; Score 12.2; DB 6; Length 18;
Best Local Similarity 82.4%; Pred. No. 6.4e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CGCATAGACTTCTCAGA 20
||| || |||||||||
Db 18 CGCCCAGTCTTCTCAGA 2

RESULT 4
AR031072
LOCUS AR031072 20 bp DNA linear PAT 29-SEP-1999
DEFINITION Sequence 60 from patent US 5861504.
ACCESSION AR031072
VERSION AR031072.1 GI:5944286
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 20)
AUTHORS Polymeropoulos,M.H. and Merril,C.R.
TITLE Eleven highly informative microsatelite repeat polymorphic DNA markers
JOURNAL Patent: US 5861504-A 60 19-JAN-1999;
FEATURES Location/Qualifiers
source 1. .20
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN

Query Match 60.0%; Score 12; DB 6; Length 20;
Best Local Similarity 75.0%; Pred. No. 8.5e+04;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GACCGCATAGACTTCTCAGA 20
|||| || || || |||||

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Db          1 GACCCCACAGCCTATTCAGA 20


RESULT 5
AR152833
LOCUS       AR152833                  20 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 113 from patent US 6235470.
ACCESSION   AR152833
VERSION     AR152833.1  GI:15120365
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Sidransky,D.
  TITLE     Detection of neoplasia by analysis of saliva
  JOURNAL   Patent: US 6235470-A 113 22-MAY-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match          60.0%;  Score 12;  DB 6;  Length 20;
  Best Local Similarity   75.0%;  Pred. No. 8.5e+04;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GACCGCATAGACTTCTCAGA 20
              |||| || || ||  |||||
Db          1 GACCCCACAGCCTATTCAGA 20


RESULT 6
BD134289
LOCUS       BD134289                  20 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  Detection of neoplasia by analysis of saliva.
ACCESSION   BD134289
VERSION     BD134289.1  GI:23229234
KEYWORDS    JP 2002505888-A/113.
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Sidlanski,D.
  TITLE     Detection of neoplasia by analysis of saliva
  JOURNAL   Patent: JP 2002505888-A 113 26-FEB-2002;
            THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE
COMMENT     OS   Artificial Sequence
            PN   JP 2002505888-A/113
            PD   26-FEB-2002
            PF   10-MAR-1999 JP 2000535774
            PR   10-MAR-1998 US    09/038637
            PI   DAVID SIDLANSKI
            PC   C12N15/09,C12Q1/68,C12N15/00
            CC   nucleotide
            FH   Key             Location/Qualifiers
            FT   source          1. .20
            FT                   /organism='Artificial Sequence'.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32630"
ORIGIN

  Query Match          60.0%;  Score 12;  DB 6;  Length 20;
  Best Local Similarity   75.0%;  Pred. No. 8.5e+04;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GACCGCATAGACTTCTCAGA 20
              |||| || || ||  |||||
Db          1 GACCCCACAGCCTATTCAGA 20


RESULT 7
AX735344/c
LOCUS       AX735344                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 934 from Patent WO03025177.
ACCESSION   AX735344
VERSION     AX735344.1  GI:30514621
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 934 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match          59.0%;  Score 11.8;  DB 6;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 1.1e+05;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 CATAGACTTCTCAGA 20
              |||| ||||||| ||
Db         17 CATAAACTTCTCTGA 3


RESULT 8
AX759065
LOCUS       AX759065                  17 bp    DNA     linear   PAT 25-JUN-2003
DEFINITION  Sequence 2386 from Patent WO03040369.
ACCESSION   AX759065
VERSION     AX759065.1  GI:32253681
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in tumoral suppression, tumoral reversion,
            apoptosis and/or viral resistance phenomena and their use as
            medicines
  JOURNAL   Patent: WO 03040369-A 2386 15-MAY-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match          59.0%;  Score 11.8;  DB 6;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 1.1e+05;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GACCGCATAGACTTC 15
              || | ||||||||||
Db          1 GATCACATAGACTTC 15


RESULT 9
A65727
LOCUS       A65727                    18 bp    DNA     linear   PAT 29-MAR-1999
DEFINITION  Sequence 8 from Patent WO9735973.
```

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ACCESSION   A65727
VERSION     A65727.1  GI:4531346
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Lenzen,G., Pietri-Rouxel,F., Drumare, Marie-Francoise and
            Strosberg,A.D.
  TITLE     CANINE beta 2- AND beta 3-ADRENERGIC RECEPTORS AND USE THEREOF
  JOURNAL   Patent: WO 9735973-A 8 02-OCT-1997;
            VETIGEN (FR)
COMMENT     Other publication FR 2746813 19971003.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             59.0%;  Score 11.8;  DB 6;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 1.1e+05;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 CCGCATAGACTTCTC 17
              ||||| |||| ||||
Db          3 CCGCAGAGACGTCTC 17


RESULT 10
AR048183/c
LOCUS       AR048183                  18 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1 from patent US 5821062.
ACCESSION   AR048183
VERSION     AR048183.1  GI:5970526
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Komai,K., Kaneko,H. and Nakatsuka,I.
  TITLE     Oligonucleotide for use in checking presence or absence of mutation
            in human-derived cytochrome P450IIC18 gene
  JOURNAL   Patent: US 5821062-A 1 13-OCT-1998;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             59.0%;  Score 11.8;  DB 6;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 1.1e+05;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 CATAGACTTCTCAGA 20
              ||||||||| | |||
Db         16 CATAGACTTTTGAGA 2


RESULT 11
E10136/c
LOCUS       E10136                    18 bp    DNA     linear   PAT 29-SEP-1997
DEFINITION  PCR primer to amplify mutated genes encoding human cytochrome
            P450IIC18.
ACCESSION   E10136
VERSION     E10136.1  GI:22026764
KEYWORDS    JP 1995285987-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Komai,K., Kaneko,H. and Nakatsuka,I.
  TITLE     OLIGONUCLEOTIDE FOR AMPLIFYING MUTATION TYPE GENE OF HUMAN DERIVED
            CYTOCHROME P450IIC18
  JOURNAL   Patent: JP 1995285987-A 1 31-OCT-1995;
            SUMITOMO CHEM CO LTD
COMMENT     OS   None
            OC   Artificial sequences.
            PN   JP 1995285987-A/1
            PD   31-OCT-1995
            PF   29-MAR-1994 JP 1994059386
            PI   KOMAI KOICHIRO, KANEKO HIDEO, NAKATSUKA IWAO
            PC   C07H21/04,C12Q1/68//C12N15/09;
            CC   strandedness: Single;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
            FH
            FT   source          1. .18
            FT                   /organism='Artificial sequences'.
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             59.0%;  Score 11.8;  DB 6;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 1.1e+05;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 CATAGACTTCTCAGA 20
              ||||||||| | |||
Db         16 CATAGACTTTTGAGA 2


RESULT 12
AR023697
LOCUS       AR023697                  20 bp    DNA     linear   PAT 05-DEC-1998
DEFINITION  Sequence 8 from patent US 5795722.
ACCESSION   AR023697
VERSION     AR023697.1  GI:3976991
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Lacroix,J.-M. and Dunn,J.M.
  TITLE     Method and kit for quantitation and nucleic acid sequencing of
            nucleic acid analytes in a sample
  JOURNAL   Patent: US 5795722-A 8 18-AUG-1998;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             59.0%;  Score 11.8;  DB 6;  Length 20;
  Best Local Similarity   86.7%;  Pred. No. 1.1e+05;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 GCATAGACTTCTCAG 19
              ||||| |||||| ||
Db          3 GCATAAACTTCTGAG 17


RESULT 13
AX207008/c
LOCUS       AX207008                  19 bp    DNA     linear   PAT 30-AUG-2001
DEFINITION  Sequence 31 from Patent WO0155214.
ACCESSION   AX207008
VERSION     AX207008.1  GI:15394779
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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REFERENCE   1
  AUTHORS   Whittaker,P.A., Jones,S.J. and Hanley,M.T.
  TITLE     Disease-associated gene
  JOURNAL   Patent: WO 0155214-A 31 02-AUG-2001;
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match           58.0%;  Score 11.6;  DB 6;  Length 19;
  Best Local Similarity   77.8%;  Pred. No. 1.5e+05;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GACCGCATAGACTTCTCA 18
              ||| |||  ||| |||||
Db         18 GACGGCAGCGACATCTCA 1


RESULT 14
AX353519
LOCUS       AX353519                  20 bp    DNA     linear   PAT 06-FEB-2002
DEFINITION  Sequence 51 from Patent WO0204636.
ACCESSION   AX353519
VERSION     AX353519.1  GI:18618594
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   van Roy,F., Goossens,S., Janssens,B. and Vanpoucke,G.
  TITLE     Novel _g(a) expressed in heart and testis
  JOURNAL   Patent: WO 0204636-A 51 17-JAN-2002;
            Vlaams Interuniversitair Instituut voor Biotechnologie vzw. (BE)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="upper primer FVR2521"
ORIGIN

  Query Match           58.0%;  Score 11.6;  DB 6;  Length 20;
  Best Local Similarity   77.8%;  Pred. No. 1.5e+05;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GACCGCATAGACTTCTCA 18
              ||| | | || |||||||
Db          2 GACTGAACAGGCTTCTCA 19


RESULT 15
I61735
LOCUS       I61735                    15 bp    DNA     linear   PAT 07-OCT-1997
DEFINITION  Sequence 289 from patent US 5658780.
ACCESSION   I61735
VERSION     I61735.1  GI:2479683
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 15)
  AUTHORS   Stinchcomb,D.T., Draper,K.G. and McSwiggen,J.
  TITLE     Rel a targeted ribozymes
  JOURNAL   Patent: US 5658780-A 289 19-AUG-1997;
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           57.0%;  Score 11.4;  DB 6;  Length 15;
  Best Local Similarity   92.3%;  Pred. No. 1.9e+05;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 ATAGACTTCTCAG 19
              || ||||||||||
Db          1 ATGGACTTCTCAG 13


RESULT 16
AX636229
LOCUS       AX636229                  15 bp    RNA     linear   PAT 21-FEB-2003
DEFINITION  Sequence 3368 from Patent EP1260586.
ACCESSION   AX636229
VERSION     AX636229.1  GI:28471843
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1
  AUTHORS   Stinchcomb,D.T., Dudycz,L.W., Chowrira,B., Grimm,S., Direnzo,A.,
            Karpeisky,A., Draper,K.G., Kisich,K., Matulic-Adamic,J.,
            Mcswiggen,J.A., Modak,A., Pavco,P., Beigelman,L., Sullivan,S.M.,
            Sweedler,D., Thompson,J.D., Tracz,D., Usman,N., Wincott,F.E. and
            Woolf,T.
  TITLE     Method and reagent for inhibiting the expression of disease related
            genes
  JOURNAL   Patent: EP 1260586-A 3368 27-NOV-2002;
            RIBOZYME PHARMACEUTICALS, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .15
                     /organism="unidentified"
                     /mol_type="unassigned RNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match           57.0%;  Score 11.4;  DB 6;  Length 15;
  Best Local Similarity   92.3%;  Pred. No. 1.9e+05;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 ATAGACTTCTCAG 19
              || ||||||||||
Db          1 ATGGACTTCTCAG 13


RESULT 17
AR111392/c
LOCUS       AR111392                  17 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 4 from patent US 6127133.
ACCESSION   AR111392
VERSION     AR111392.1  GI:12828240
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Akong,M.Anthony., Harpold,M.Miller., Velicelebi,G. and Brust,P.
  TITLE     Automated analysis equipment and assay method for detecting cell
            surface protein function using same
  JOURNAL   Patent: US 6127133-A 4 03-OCT-2000;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match           57.0%;  Score 11.4;  DB 6;  Length 17;
  Best Local Similarity   92.3%;  Pred. No. 1.9e+05;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 ATAGACTTCTCAG 19
              ||||| |||||||
Db         13 ATAGAATTCTCAG 1
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RESULT 18
AR364674/c
LOCUS       AR364674                  17 bp    DNA     linear   PAT 03-SEP-2003
DEFINITION  Sequence 5 from patent US 5401629.
ACCESSION   AR364674
VERSION     AR364674.1  GI:34427598
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Harpold,M.M. and Brust,P.
  TITLE     Assay methods and compositions useful for measuring the
            transduction of an intracellular signal
  JOURNAL   Patent: US 5401629-A 5 28-MAR-1995;
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             57.0%;  Score 11.4;  DB 6;  Length 17;
  Best Local Similarity   92.3%;  Pred. No. 1.9e+05;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 ATAGACTTCTCAG 19
              ||||| |||||||
Db         13 ATAGAATTCTCAG 1


RESULT 19
AX734698/c
LOCUS       AX734698                  17 bp    DNA     linear   PAT 08-MAY-2003
DEFINITION  Sequence 288 from Patent WO03025177.
ACCESSION   AX734698
VERSION     AX734698.1  GI:30513975
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Telerman,A., Amson,R. and Tuijnder,M.
  TITLE     Sequences involved in phenomena of tumour suppression, tumour
            reversion, apoptosis and/or resistance to viruses and the use
            thereof as medicaments
  JOURNAL   Patent: WO 03025177-A 288 27-MAR-2003;
            Molecular Engines Laboratories (FR)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             57.0%;  Score 11.4;  DB 6;  Length 17;
  Best Local Similarity   92.3%;  Pred. No. 1.9e+05;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 TAGACTTCTCAGA 20
              |||| ||||||||
Db         15 TAGAGTTCTCAGA 3


RESULT 20
AX130020/c
LOCUS       AX130020                  19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 1238 from Patent WO0130362.
ACCESSION   AX130020
VERSION     AX130020.1  GI:14136325
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 1238 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Cdk-we-hu ribozyme binding site"
ORIGIN

  Query Match             57.0%;  Score 11.4;  DB 6;  Length 19;
  Best Local Similarity   92.3%;  Pred. No. 1.9e+05;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GCATAGACTTCTC 17
              ||||| |||||||
Db         15 GCATATACTTCTC 3


RESULT 21
AX130021/c
LOCUS       AX130021                  19 bp    DNA     linear   PAT 15-MAY-2001
DEFINITION  Sequence 1239 from Patent WO0130362.
ACCESSION   AX130021
VERSION     AX130021.1  GI:14136326
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Robbins,J.M. and Tritz,R.
  TITLE     Ribozyme therapy for the treatment of proliferative skin and eye
            diseases
  JOURNAL   Patent: WO 0130362-A 1239 03-MAY-2001;
            IMMUSOL, INC. (US)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
                     /note="Cdk-we-hu ribozyme binding site"
ORIGIN

  Query Match             57.0%;  Score 11.4;  DB 6;  Length 19;
  Best Local Similarity   92.3%;  Pred. No. 1.9e+05;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GCATAGACTTCTC 17
              ||||| |||||||
Db         13 GCATATACTTCTC 1


RESULT 22
AX269412
LOCUS       AX269412                  20 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 43 from Patent WO0164876.
ACCESSION   AX269412
VERSION     AX269412.1  GI:16542188
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Stefansson,H., Steinthorsdottir,V. and Gulcher,J.R.
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```
  TITLE     Human schizophrenia gene
  JOURNAL   Patent: WO 0164876-A 43 07-SEP-2001;
            Decode Genetics EHF. (IS)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             57.0%;  Score 11.4;  DB 6;  Length 20;
  Best Local Similarity   92.3%;  Pred. No. 1.9e+05;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GCATAGACTTCTC 17
              ||||||| |||||
Db          6 GCATAGAATTCTC 18


RESULT 23
AX270943
LOCUS       AX270943                  20 bp    DNA     linear   PAT 30-NOV-2001
DEFINITION  Sequence 43 from Patent WO0164877.
ACCESSION   AX270943
VERSION     AX270943.1  GI:16543680
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Stefansson,H., Steinthorsdottir,V. and Gulcher,J.R.
  TITLE     Human schizophrenia gene
  JOURNAL   Patent: WO 0164877-A 43 07-SEP-2001;
            Decode Genetics EHF. (IS)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             57.0%;  Score 11.4;  DB 6;  Length 20;
  Best Local Similarity   92.3%;  Pred. No. 1.9e+05;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GCATAGACTTCTC 17
              ||||||| |||||
Db          6 GCATAGAATTCTC 18


RESULT 24
AR292962
LOCUS       AR292962                  18 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 4697 from patent US 6537751.
ACCESSION   AR292962
VERSION     AR292962.1  GI:31680246
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Cohen,D., Chumakov,I. and Blumenfeld,M.
  TITLE     Biallelic markers for use in constructing a high density
            disequilibrium map of the human genome
  JOURNAL   Patent: US 6537751-A 4697 25-MAR-2003;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             56.0%;  Score 11.2;  DB 6;  Length 18;
  Best Local Similarity   81.2%;  Pred. No. 2.5e+05;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 GCATAGACTTCTCAGA 20
              ||| |||||||  |||
Db          1 GCACAGACTTCAAAGA 16


RESULT 25
AX378663/c
LOCUS       AX378663                  19 bp    DNA     linear   PAT 18-MAR-2002
DEFINITION  Sequence 452 from Patent WO0206525.
ACCESSION   AX378663
VERSION     AX378663.1  GI:19574516
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Cohen,D., Blumenfeld,M., Chumakov,I., Abderrahim,H. and Bihain,B.
  TITLE     Obesity associated biallelic marker maps
  JOURNAL   Patent: WO 0206525-A 452 24-JAN-2002;
            GENSET (FR)
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     primer_bind     1. .19
                     /note="downstream amplification primer 99-48212 for SEQ
                     110, in complement"
ORIGIN

  Query Match             56.0%;  Score 11.2;  DB 6;  Length 19;
  Best Local Similarity   81.2%;  Pred. No. 2.5e+05;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 GCATAGACTTCTCAGA 20
              ||||| | ||||| ||
Db         17 GCATAAAGTTCTCTGA 2


RESULT 26
AR072310
LOCUS       AR072310                  20 bp    DNA     linear   PAT 28-AUG-2000
DEFINITION  Sequence 113 from patent US 5948611.
ACCESSION   AR072310
VERSION     AR072310.1  GI:9999074
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Prockop,D.J., Ala-Kokko,L., Williams,C.J., Ritvaniemi,P.,
            Baldwin,C., Hopkinson,I. and Ahmad,N.Nina.
  TITLE     Primers and methods for detecting mutations in the procollagen II
            gene (COL2A1) that indicate a genetic predisposition for a
            COL2A1-associated disease
  JOURNAL   Patent: US 5948611-A 113 07-SEP-1999;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             56.0%;  Score 11.2;  DB 6;  Length 20;
  Best Local Similarity   81.2%;  Pred. No. 2.5e+05;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 ACCGCATAGACTTCTC 17
              || |||  ||||||||
Db          4 ACTGCAGGGACTTCTC 19
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RESULT 27
AR123092/c
LOCUS       AR123092                  20 bp    DNA     linear   PAT 16-MAY-2001
DEFINITION  Sequence 36 from patent US 6168950.
ACCESSION   AR123092
VERSION     AR123092.1  GI:14108058
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Monia,B.P., Gaarde,W., Ward,D.T. and Cowsert,L.M.
  TITLE     Antisense modulation of MEKK1 expression
  JOURNAL   Patent: US 6168950-A 36 02-JAN-2001;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            56.0%;  Score 11.2;  DB 6;  Length 20;
  Best Local Similarity  81.2%;  Pred. No. 2.5e+05;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 GCATAGACTTCTCAGA 20
              ||||||||||   ||
Db         19 GCATAGACTTCAGGGA 4


RESULT 28
CQ770343
LOCUS       CQ770343                  20 bp    DNA     linear   PAT 04-MAR-2004
DEFINITION  Sequence 14 from Patent WO2004009842.
ACCESSION   CQ770343
VERSION     CQ770343.1  GI:45125013
KEYWORDS    .
SOURCE      Rattus sp.
  ORGANISM  Rattus sp.
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1
  AUTHORS   Larsen,L.K., Vrang,N. and Larsen,P.J.
  TITLE     Methods for identifying genes related to malfunctions of the
            central nervous system
  JOURNAL   Patent: WO 2004009842-A 14 29-JAN-2004;
            Rheoscience A/S (DK)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Rattus sp."
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:10118"
ORIGIN

  Query Match            56.0%;  Score 11.2;  DB 6;  Length 20;
  Best Local Similarity  81.2%;  Pred. No. 2.5e+05;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 ACCGCATAGACTTCTC 17
              ||||||  || ||| ||
Db          5 ACCGCACAGCCTTGTC 20


RESULT 29
I26421
LOCUS       I26421                    20 bp    DNA     linear   PAT 07-OCT-1996
DEFINITION  Sequence 113 from patent US 5558988.
ACCESSION   I26421
VERSION     I26421.1  GI:1606291
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Prockop,D.J., Ala-Kokko,L. and Ritvaniemi,P.
  TITLE     Primers and methods for detecting mutations in the procollagen II
            gene that indicate a genetic predisposition for osteoarthritis
  JOURNAL   Patent: US 5558988-A 113 24-SEP-1996;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match            56.0%;  Score 11.2;  DB 6;  Length 20;
  Best Local Similarity  81.2%;  Pred. No. 2.5e+05;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 ACCGCATAGACTTCTC 17
              || |||  ||||||||
Db          4 ACTGCAGGGACTTCTC 19


RESULT 30
AR313207/c
LOCUS       AR313207                  20 bp    DNA     linear   PAT 12-JUN-2003
DEFINITION  Sequence 3744 from patent US 6559294.
ACCESSION   AR313207
VERSION     AR313207.1  GI:31706633
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Griffais,R., Hoiseth,S.K., Zagursky,R.J., Metcalf,B.J., Peek,J.A.,
            Sankaran,B. and Fletcher,L.D.
  TITLE     Chlamydia pneumoniae polynucleotides and uses thereof
  JOURNAL   Patent: US 6559294-A 3744 06-MAY-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match            56.0%;  Score 11.2;  DB 6;  Length 20;
  Best Local Similarity  81.2%;  Pred. No. 2.5e+05;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 ACCGCATAGACTTCTC 17
              | | ||  |||||||||
Db         20 ATCTCAGAGACTTCTC 5


RESULT 31
AR359611/c
LOCUS       AR359611                  20 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 204 from patent US 6593305.
ACCESSION   AR359611
VERSION     AR359611.1  GI:33766334
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Wright,J.A.
  TITLE     Antitumor antisense sequences directed against R1 and R2 components
            of ribonucleotide reductase
  JOURNAL   Patent: US 6593305-A 204 15-JUL-2003;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN
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  Query Match             56.0%;  Score 11.2;  DB 6;  Length 20;
  Best Local Similarity   81.2%;  Pred. No. 2.5e+05;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 CGCATAGACTTCTCAG 19
              |||| || ||| ||||
Db         20 CGCAGAGTCTTGTCAG 5


RESULT 32
AR559459/c
LOCUS       AR559459                  20 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 28 from patent US 6750019.
ACCESSION   AR559459
VERSION     AR559459.1  GI:53968875
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Freier,S.M.
  TITLE     Antisense modulation of insulin-like growth factor binding protein
            5 expression
  JOURNAL   Patent: US 6750019-A 28 15-JUN-2004;
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             56.0%;  Score 11.2;  DB 6;  Length 20;
  Best Local Similarity   81.2%;  Pred. No. 2.5e+05;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GACCGCATAGACTTCT 16
              ||||||| ||  ||||
Db         17 GACCGCAAAGGATTCT 2


RESULT 33
AX259854/c
LOCUS       AX259854                  20 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 81 from Patent WO0172822.
ACCESSION   AX259854
VERSION     AX259854.1  GI:16508928
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hugot,J.P., Thomas,G., Zouali,M., Lesage,S. and Chamaillard,M.
  TITLE     Genes involved in intestinal inflammatory diseases and use thereof
  JOURNAL   Patent: WO 0172822-A 81 04-OCT-2001;
            Fondation Jean Dausset-Ceph (FR)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             56.0%;  Score 11.2;  DB 6;  Length 20;
  Best Local Similarity   81.2%;  Pred. No. 2.5e+05;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 GCATAGACTTCTCAGA 20
              |||  | |||||||||
Db         17 GCAGGGCCTTCTCAGA 2


RESULT 34
AX259855/c
LOCUS       AX259855                  20 bp    DNA     linear   PAT 26-OCT-2001
DEFINITION  Sequence 82 from Patent WO0172822.
ACCESSION   AX259855
VERSION     AX259855.1  GI:16508929
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hugot,J.P., Thomas,G., Zouali,M., Lesage,S. and Chamaillard,M.
  TITLE     Genes involved in intestinal inflammatory diseases and use thereof
  JOURNAL   Patent: WO 0172822-A 82 04-OCT-2001;
            Fondation Jean Dausset-Ceph (FR)
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             56.0%;  Score 11.2;  DB 6;  Length 20;
  Best Local Similarity   81.2%;  Pred. No. 2.5e+05;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 GCATAGACTTCTCAGA 20
              |||  | |||||||||
Db         17 GCAGGGCCTTCTCAGA 2


RESULT 35
BD254799
LOCUS       BD254799                  17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD254799
VERSION     BD254799.1  GI:33064569
KEYWORDS    JP 2002541795-A/2592.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 2592 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/2592
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
            C12P21/02,C12P21/02//A61K31/711,(C12N5/10,C12R1:91),(C12P21/02, PC
             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             55.0%;  Score 11;  DB 6;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+05;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          10 GACTTCTCAGA 20
               ||||||||||
Db           5 GACTTCTCAGA 15


RESULT 36
BD254800
LOCUS       BD254800                 17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD254800
VERSION     BD254800.1  GI:33064570
KEYWORDS    JP 2002541795-A/2593.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 2593 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/2593
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
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             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             55.0%;  Score 11;  DB 6;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+05;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          10 GACTTCTCAGA 20
               ||||||||||
Db           4 GACTTCTCAGA 14


RESULT 37
BD254801
LOCUS       BD254801                 17 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Regulation of repressor genes using nucleic acid molecules.
ACCESSION   BD254801
VERSION     BD254801.1  GI:33064571
KEYWORDS    JP 2002541795-A/2594.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Blatt,L., Zwick,M., Pavco,P. and Mcswiggen,J.
  TITLE     Regulation of repressor genes using nucleic acid molecules
  JOURNAL   Patent: JP 2002541795-A 2594 10-DEC-2002;
            RIBOZYME PHARMACEUTICALS INC
COMMENT     OS   Eukaryote
            PN   JP 2002541795-A/2594
            PD   10-DEC-2002
            PF   11-APR-2000 JP 2000611654
            PR   12-APR-1999 US    60/129390
            PI   LAWRENCE BLATT,MICHAEL ZWICK,PAMELA PAVCO,JAMES MCSWIGGEN PC
            C12N15/09,A61K38/00,A61K48/00,A61P43/00,A61P43/00,C12N5/10, PC
            C12P21/02,
            PC
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             C12R1:91),
            PC   (C12P21/02,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,C12N5/00,
            PC   A61K37/02,
            PC   (C12N5/00,C12R1:91)
            CC   Regulation of repressor genes using nucleic acid molecules FH
             Key             Location/Qualifiers
            FT   source          1. .17
            FT                   /organism='Eukaryote'.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="unidentified"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:32644"
ORIGIN

  Query Match             55.0%;  Score 11;  DB 6;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+05;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          10 GACTTCTCAGA 20
               ||||||||||
Db           2 GACTTCTCAGA 12


RESULT 38
AX110604
LOCUS       AX110604                 17 bp    DNA     linear   PAT 29-MAY-2002
DEFINITION  Sequence 1337 from Patent WO0123604.
ACCESSION   AX110604
VERSION     AX110604.1  GI:13926896
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C., Ouellette,M.,
            Picard,F.J. and Roy,P.H.
  TITLE     Highly conserved genes and their use to generate probes and primers
            for detection of microorganisms
  JOURNAL   Patent: WO 0123604-A 1337 05-APR-2001;
            Infectio Diagnostic (I.D.I.) INC. (CA)
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Oligonucleotide"
ORIGIN

  Query Match             55.0%;  Score 11;  DB 6;  Length 17;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+05;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy           9 AGACTTCTCAG 19
               ||||||||||
Db           4 AGACTTCTCAG 14


RESULT 39
AR567503/c
LOCUS       AR567503                 18 bp    DNA     linear   PAT 08-OCT-2004
DEFINITION  Sequence 32 from patent US 6780609.
ACCESSION   AR567503
VERSION     AR567503.1  GI:53985285
KEYWORDS    .
SOURCE      Unknown.
```

```
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Carulli,J.P., Little,R.D., Recker,R.R. and Johnson,M.L.
  TITLE     High bone mass gene of 1.1q13.3
  JOURNAL   Patent: US 6780609-A 32 24-AUG-2004;
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             55.0%;  Score 11;  DB 6;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+05;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GACTTCTCAGA 20
              ||||||||||
Db         17 GACTTCTCAGA 7


RESULT 40
AX277553/c
LOCUS       AX277553                  18 bp    DNA     linear   PAT 01-NOV-2001
DEFINITION  Sequence 32 from Patent WO0177327.
ACCESSION   AX277553
VERSION     AX277553.1  GI:16604752
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            other sequences; artificial sequences.
REFERENCE   1
  AUTHORS   Carulli,J.P., Little,R.D., Recker,R.R. and Johnson,M.L.
  TITLE     The high bone mass gene of 11q13.3
  JOURNAL   Patent: WO 0177327-A 32 18-OCT-2001;
            Genome Therapeutics Corporation (US)
FEATURES             Location/Qualifiers
     source          1. .18
                     /organism="synthetic construct"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
                     /note="Artificial sequence is a primer."
ORIGIN

  Query Match             55.0%;  Score 11;  DB 6;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 3.3e+05;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GACTTCTCAGA 20
              ||||||||||
Db         17 GACTTCTCAGA 7


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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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Title: US-09-743-825-10
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Searched: 4390206 seqs, 2959870667 residues

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6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	20	100.0	20	3	AAZ50446	Aaz50446 Human PB3
	2	13.8	69.0	20	2	AAX93486	Aax93486 PCR prime
c	3	13.2	66.0	20	10	AAD62200	Aad62200 Human hae
	4	12.6	63.0	20	13	ADT00440	Adt00440 Novel mut
	5	12.4	62.0	17	8	ACA08287	Aca08287 Necrosis
	6	12.4	62.0	17	8	ACA06680	Aca06680 NFKB sub-
c	7	12.2	61.0	18	3	AAZ48549	Aaz48549 Human TNF
c	8	12.2	61.0	18	6	ABT05045	Abt05045 TNFR1 exp
c	9	12.2	61.0	18	13	ADR06077	Adr06077 Human TNF
	10	12.2	61.0	19	10	ADG73193	Adg73193 Pseudomon
	11	12.2	61.0	19	10	ADL12249	Adl12249 Pseudomon
	12	12.2	61.0	20	12	ADI79866	Adi79866 Mouse HMG
c	13	12.2	61.0	20	12	ADI79673	Adi79673 Mouse HMG
	14	12	60.0	20	2	AAQ32840	Aaq32840 Microsate
	15	12	60.0	20	2	AAQ57863	Aaq57863 Primer pa
	16	12	60.0	20	2	AAZ21763	Aaz21763 Exemplary
	17	12	60.0	20	3	AAC60963	Aac60963 TATA box-
	18	11.8	59.0	17	10	ADB42063	Adb42063 Tumour su
c	19	11.8	59.0	17	10	ADI48431	Adi48431 Human tum
c	20	11.8	59.0	18	2	AAQ94315	Aaq94315 Human cyt
	21	11.8	59.0	18	2	AAV30475	Aav30475 Canine be
	22	11.8	59.0	20	2	AAV33985	Aav33985 Primer CT
	23	11.8	59.0	20	3	AAZ24116	Aaz24116 Primer CT
c	24	11.8	59.0	20	10	ABZ91284	Abz91284 Human oli
c	25	11.8	59.0	20	11	ABD27514	Abd27514 AA486238-
c	26	11.6	58.0	19	4	AAD11750	Aad11750 Human AAG
	27	11.6	58.0	20	6	ABK41518	Abk41518 Human CTN
	28	11.6	58.0	20	6	ABS59713	Abs59713 Human dam
c	29	11.6	58.0	20	12	ADK78853	Adk78853 Chimeric
c	30	11.6	58.0	20	12	ADK78455	Adk78455 Chimeric
c	31	11.6	58.0	20	12	ADK78852	Adk78852 Chimeric
	32	11.4	57.0	15	2	AAT55168	Aat55168 Human rel
	33	11.4	57.0	17	8	ACA09062	Aca09062 NFKB sub-
c	34	11.4	57.0	17	10	ADI47785	Adi47785 Human tum
c	35	11.4	57.0	19	3	AAA83653	Aaa83653 cdk-we-hu
c	36	11.4	57.0	19	3	AAA83652	Aaa83652 cdk-we-hu
c	37	11.4	57.0	19	5	AAH58814	Aah58814 Cdk-we-hu
c	38	11.4	57.0	19	5	AAH58815	Aah58815 Cdk-we-hu
c	39	11.4	57.0	19	12	ADQ61886	Adq61886 Anti-KCNH
c	40	11.4	57.0	20	2	AAX77133	Aax77133 PCR prime
	41	11.4	57.0	20	4	AAK95244	Aak95244 Neureguli
c	42	11.4	57.0	20	4	AAD08232	Aad08232 Human DNA
	43	11.4	57.0	20	4	AAD08233	Aad08233 Human DNA
	44	11.4	57.0	20	4	AAK96737	Aak96737 Neureguli
	45	11.4	57.0	20	6	ABT00014	Abt00014 Human neu
	46	11.4	57.0	20	6	ABT01507	Abt01507 Human neu
	47	11.4	57.0	20	12	ADI29181	Adi29181 Human MAR
c	48	11.4	57.0	20	12	ADI29115	Adi29115 Antisense
	49	11.4	57.0	20	12	ADH77528	Adh77528 Human neu
c	50	11.4	57.0	20	12	ADK95401	Adk95401 Primer of
	51	11.4	57.0	20	12	ADP43749	Adp43749 Human fib
	52	11.2	56.0	17	8	ACC74121	Acc74121 Human CYP
c	53	11.2	56.0	17	8	ACC74122	Acc74122 Human CYP
c	54	11.2	56.0	17	10	ADB89105	Adb89105 Human tum
c	55	11.2	56.0	17	10	ADC24452	Adc24452 Human tum
c	56	11.2	56.0	17	10	ADD67722	Add67722 Human TNF
c	57	11.2	56.0	17	10	ADE10435	Ade10435 Minicell
c	58	11.2	56.0	17	10	ADE11357	Ade11357 Human TNF
c	59	11.2	56.0	17	10	ADE12535	Ade12535 Human TNF
c	60	11.2	56.0	17	10	ADE12298	Ade12298 Human TNF
c	61	11.2	56.0	17	10	ADG25432	Adg25432 Tumour ne
c	62	11.2	56.0	17	10	ADJ47831	Adj47831 Human TNF
c	63	11.2	56.0	17	10	ADJ61852	Adj61852 Novel min
c	64	11.2	56.0	17	11	ADP70598	Adp70598 Minicell
c	65	11.2	56.0	17	12	ADF56265	Adf56265 Human TNF
c	66	11.2	56.0	17	12	ADG43293	Adg43293 Human TNF
c	67	11.2	56.0	17	12	ADG43550	Adg43550 Human TNF
c	68	11.2	56.0	17	12	ADG68614	Adg68614 Human TNF
c	69	11.2	56.0	17	12	ADH56754	Adh56754 PCR prime
c	70	11.2	56.0	17	12	ADI12846	Adi12846 PCR prime
c	71	11.2	56.0	17	12	ADI27748	Adi27748 PCR prime
c	72	11.2	56.0	17	12	ADI33817	Adi33817 Human TNF
c	73	11.2	56.0	17	12	ADK51551	Adk51551 PCR prime
c	74	11.2	56.0	17	12	ADM18033	Adm18033 Human TNF
c	75	11.2	56.0	17	12	ADL82631	Adl82631 PCR prime
c	76	11.2	56.0	17	12	ADM46269	Adm46269 PCR prime
	77	11.2	56.0	18	3	AAZ70341	Aaz70341 Human bia
c	78	11.2	56.0	19	6	ABK41204	Abk41204 Human obe
	79	11.2	56.0	20	2	AAQ65840	Aaq65840 Type II p
c	80	11.2	56.0	20	2	AAZ02195	Aaz02195 PCR prime
c	81	11.2	56.0	20	2	AAX94418	Aax94418 PCR prime
c	82	11.2	56.0	20	3	AAA90858	Aaa90858 Ribonucle
c	83	11.2	56.0	20	4	AAF27114	Aaf27114 Human MEK
c	84	11.2	56.0	20	4	AAI65670	Aai65670 Primer fo
c	85	11.2	56.0	20	4	AAI65669	Aai65669 Primer fo
c	86	11.2	56.0	20	8	AAD48077	Aad48077 PCR prime
c	87	11.2	56.0	20	10	ACF58321	Acf58321 Mouse IL-
c	88	11.2	56.0	20	10	ABZ86038	Abz86038 Human oli
c	89	11.2	56.0	20	10	ABZ82699	Abz82699 Human HSL
c	90	11.2	56.0	20	10	ACC47652	Acc47652 Human IGF
c	91	11.2	56.0	20	11	ABD22268	Abd22268 Human sta
	92	11.2	56.0	20	12	ADI56702	Adi56702 Rat hypot
c	93	11.2	56.0	20	12	ADL88532	Adl88532 Probe 32

94	11.2	56.0	20	12	ADL27440	Adl27440 PCR prime
95	11	55.0	17	3	AAF02601	Aaf02601 Hammerhea
96	11	55.0	17	3	AAF02603	Aaf02603 Hammerhea
97	11	55.0	17	3	AAF02602	Aaf02602 Hammerhea
98	11	55.0	17	4	AAH01346	Aah01346 parC resi
c 99	11	55.0	18	5	ABA82646	Aba82646 Human Zma
c 100	11	55.0	18	5	ABA82604	Aba82604 HBM1 poly

ALIGNMENTS

RESULT 1
AAZ50446
ID AAZ50446 standard; DNA; 20 BP.
XX
AC AAZ50446;
XX
DT 18-MAY-2000 (first entry)
XX
DE Human PB39 specific 3' RACE primer.
XX
KW PB39; human; prostate cancer; PC; chromosome 11p11.1-11.2; cancer;
KW prostate epithelium; splicing mechanism; early diagnosis; progression;
KW precancerous cell; metastatic potential; non-neoplastic prostate disease;
KW expressed sequence tag; EST; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200005376-A1.
XX
PD 03-FEB-2000.
XX
PF 23-JUL-1999; 99WO-US016831.
XX
PR 24-JUL-1998; 98US-0094137P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Chuaqui RF, Cole KA, Liotta LA;
XX
DR WPI; 2000-182700/16.
XX
PT Novel gene which is dysregulated in prostate cancer useful for diagnosing
PT cancer.
XX
PS Claim 5; Page 18; 51pp; English.
XX
CC The present sequence is the human PB39 3' specific RACE primer, from EST
CC clone AAR00504. It is used to determine the complete nucleotide sequence
CC of PB39 cDNA, isolated from human pancreas cDNA library using RACE. The
CC PB39 gene that is dysregulated in prostate cancer has homology to the EST
CC AAR00504. PB39 gene is located on chromosome 11p11.1-11.2. Abnormally
CC high concentrations of PB39 are found in prostate tissue derived from
CC prostate cancer (PC) epithelium. PB39 sequence is useful for detection of
CC precancerous or cancer cells in the prostate. PB39 is useful for early
CC diagnosis of the progression of prostate cancer, especially in aggressive
CC prostate carcinoma. It can also distinguish PC from other non-neoplastic
CC prostate disease. The diagnostic method is selective and specific for
CC various types of PC and also facilitates identifying prostate cancer of
CC differing aggressiveness and metastatic potential
XX
SQ Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GACCGCATAGACTTCTCAGA 20
              ||||||||||||||||||||
Db          1 GACCGCATAGACTTCTCAGA 20
```

RESULT 2
AAX93486
ID AAX93486 standard; DNA; 20 BP.
XX
AC AAX93486;
XX
DT 13-SEP-1999 (first entry)
XX
DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
XX
KW Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;
KW sinusitis; purulent otitis media; erythema nodosum; pharyngitis; vaccine;
KW neutralising epitope; PCR primer; ss.
XX
OS Synthetic.
OS Chlamydophila pneumoniae.
XX
PN WO9927105-A2.
XX
PD 03-JUN-1999.
XX
PF 20-NOV-1998; 98WO-IB001890.
XX
PR 21-NOV-1997; 97FR-00014673.
PR 04-NOV-1998; 98US-0107078P.
XX
PA (GEST) GENSET.
XX
PI Griffais R;
XX
DR WPI; 1999-357842/30.
XX
PT Genome sequence of Chlamydia pneumoniae.
XX
PS Page 1595; Disclosure; 1912pp; English.
XX
CC AAX91991-X97517 represent PCR primers used to amplify open reading frames
CC and other nucleic acid sequences from the genome of Chlamydia pneumoniae
CC (see AAX91990). C. pneumoniae causes respiratory disease such as
CC pneumonia and bronchitis and is thought to be a contributing factor in
CC heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema
CC nodosum or pharyngitis. The polypeptides encoded by the open reading
CC frames of the C. pneumoniae genome (see AAY34584- AAY35879) can be used
CC in immunogenic compositions as vaccines. Vectors containing C. pneumoniae
CC nucleotides sequences can also be used as immunogenic compositions,
CC especially where the vector directs the expression of a neutralising
CC epitope of C. pneumoniae
XX
SQ Sequence 20 BP; 7 A; 6 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 69.0%; Score 13.8; DB 2; Length 20;
Best Local Similarity 88.2%; Pred. No. 2.3e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 GACCGCATAGACTTCTC 17
              ||||||||| |||| ||
Db          3 GACCGCATAAACTTATC 19
```

RESULT 3
AAD62200/c
ID AAD62200 standard; DNA; 20 BP.
XX
AC AAD62200;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human haematopoietic cell tyrosine kinase antisense oligo ISIS #150755.
XX
KW Haematopoietic cell; tyrosine kinase; hyperproliferative disorder;
KW cancer; therapy; inflammation; diabetes; viral infection; inflammation;
KW tumour; cytostatic; virucide; antisense therapy; antisense; human;
KW phosphorothioate backbone; ss.

```
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag= a
FT                   /mod_base= OTHER
FT                   /note= "Phosphorothioate backbone; All cytidines are 5-
FT                   methyl cytidines"
FT   modified_base   1. .5
FT                   /*tag= b
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) nucleotides"
FT   modified_base   16. .20
FT                   /*tag= c
FT                   /mod_base= OTHER
FT                   /note= "2'-O-methoxyethyl (2'-MOE) nucleotides"
XX
PN   US2003125275-A1.
XX
PD   03-JUL-2003.
XX
PF   04-DEC-2001; 2001US-00007010.
XX
PR   04-DEC-2001; 2001US-00007010.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Borchers AH,  Dobie KW;
XX
DR   WPI; 2003-811000/76.
XX
PT   New antisense oligonucleotides targeted to nucleic acids encoding
PT   hematopoietic cell protein tyrosine kinase, useful for diagnosing or
PT   treating cancer (e.g. leukemia), inflammation, diabetes or viral
PT   infections.
XX
PS   Example 15; Page 26; 59pp; English.
XX
CC   The invention relates to a compound targetted to a nucleic acid molecule
CC   encoding haematopoietic cell protein tyrosine kinase. The compound
CC   inhibits the expression of haematopoietic cell protein tyrosine kinase
CC   and it specifically hybridises with the nucleic acid molecule encoding
CC   the tyrosine kinase or with at least an 8-nucleobase portion of an active
CC   site on the nucleic acid molecule encoding the tyrosine kinase. The
CC   antisense compounds are useful for modulating the expression of
CC   haematopoietic cell protein tyrosine kinase and treating diseases or
CC   conditions associated with the expression of the tyrosine kinase, such as
CC   hyperproliferative disorders (e.g. cancer), inflammation, diabetes or a
CC   viral infection. The antisense compounds are also useful for diagnostics,
CC   therapeutics, prophylaxis, e.g. to prevent or delay infection,
CC   inflammation or tumour formation, as research reagents and kits and in
CC   distinguishing between functions of various members of a biological
CC   pathway. The present sequence is human haematopoietic cell tyrosine
CC   kinase antisense oligonucleotide
XX
SQ   Sequence 20 BP; 6 A; 2 C; 7 G; 5 T; 0 U; 0 Other;

  Query Match             66.0%;  Score 13.2;  DB 10;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 4.8e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 ACCGCATAGACTTCTCAG 19
              | | ||| ||||||||||
Db         20 AACTCATTGACTTCTCAG 3


RESULT 4
ADT00440
ID   ADT00440 standard; DNA; 20 BP.
XX
AC   ADT00440;
XX
DT   16-DEC-2004  (first entry)
XX
DE   Novel mutant protein tyrosine kinase-related oligonucleotide SeqID428.
XX
KW   tyrosine kinase; cancer; anti-cancer agent; signalling molecule;
KW   tumourigenesis; somatic alteration; colorectal cancer; NTRK3; FES;
KW   GUCY2F; MCCK; MLK4; kinase domain; cytostatic; tyrosine kinase inhibitor;
KW   guanylate cyclase stimulator; ss.
XX
OS   Homo sapiens.
XX
PN   WO2004082458-A2.
XX
PD   30-SEP-2004.
XX
PF   18-FEB-2004; 2004WO-US004452.
XX
PR   21-FEB-2003; 2003US-0448537P.
PR   29-MAY-2003; 2003US-0473895P.
XX
PA   (UYJO ) UNIV JOHNS HOPKINS.
XX
PI   Bardelli A,  Parsons W,  Velculescu V,  Kinzler KW,  Vogelstein B;
XX
DR   WPI; 2004-718702/70.
XX
PT   Activated mutant protein tyrosine kinases (e.g. NTRK3, FES and MCCK) and
PT   associated methods for diagnosing cancer and screening for anti-cancer
PT   agents.
XX
PS   Disclosure; SEQ ID NO 428; 363pp; English.
XX
CC   This invention relates to a novel activated mutant protein tyrosine
CC   kinases and associated methods for diagnosing cancer and screening for
CC   anti-cancer agents. Protein kinases are signalling molecules involved in
CC   tumourigenesis. Mutational analysis of the human tyrosine kinase gene
CC   family identified somatic alteration sin 1 in 5 colorectal cancers, with
CC   the majority of mutations occurring in the NTRK3, FES, GUCY2F and
CC   MCCK/MLK4 genes. Most were identified in the kinase domain. The invention
CC   may be useful for the production of compounds with a cytostatic activity
CC   acting as protein tyrosine kinase inhibitors or guanylate cyclase
CC   stimulators. The invention may be useful for developing methods for
CC   detecting mutations involved in cancer or screening for anti-cancer
CC   agents. The present sequence is that of a human-derived oligonucleotide
CC   which is related to the invention.
XX
SQ   Sequence 20 BP; 4 A; 7 C; 5 G; 4 T; 0 U; 0 Other;

  Query Match             63.0%;  Score 12.6;  DB 13;  Length 20;
  Best Local Similarity   78.9%;  Pred. No. 1e+04;
  Matches   15;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GACCGCATAGACTTCTCAG 19
              |||| | ||| | ||||||
Db          2 GACCCCGTAGTCATCTCAG 20


RESULT 5
ACA08287
ID   ACA08287 standard; DNA; 17 BP.
XX
AC   ACA08287;
XX
DT   03-JUN-2003  (first entry)
XX
DE   Necrosis factor kappa B (NFKB) sub-unit modulating DNAzyme #56.
XX
KW   Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;
KW   G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; lung cancer;
KW   prostate cancer; colorectal cancer; brain cancer; oesophageal cancer;
KW   stomach cancer; bladder cancer; pancreatic cancer; cervical cancer;
KW   head and neck cancer; ovarian cancer; melanoma; lymphoma; glioma;
```

KW multidrug resistant cancer; REL-A-specific inhibitor; chemotherapy;
KW paclitaxel; docetaxel; cisplatin; methotrexate; cyclophosphamide;
KW doxorubin; fluorouracil carboplatin; edatrexate; gemcitabine;
KW radiation therapy; inflammatory disease; asthma; diabetes;
KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
KW transplant/graft rejection; reperfusion injury; glomerulonephritis;
KW allergic airway inflammation; inflammatory bowel disease; infection; ss.
XX
OS Synthetic.
XX
PN US2002177568-A1.
XX
PD 28-NOV-2002.
XX
PF 23-MAY-2001; 2001US-00864785.
XX
PR 07-DEC-1992; 92US-00987132.
PR 18-MAY-1994; 94US-00245466.
PR 15-AUG-1994; 94US-00291932.
PR 23-DEC-1996; 96US-00777916.
XX
PA (STIN/) STINCHCOMB D T.
PA (MCSW/) MCSWIGGEN J.
PA (DRAP/) DRAPER K G.
XX
PI Stinchcomb DT, Mcswiggen J, Draper KG;
XX
DR WPI; 2003-340953/32.
XX
PT Novel enzymatic nucleic acid molecules which down regulates expression of
PT a sequence encoding a subunit of nuclear factor kappa B useful for
PT treating cancer, inflammatory disorders and autoimmune diseases.
XX
PS Claim 3; Page 46; 72pp; English.
XX
CC The invention describes an enzymatic nucleic acid molecule (I) which down
CC regulates expression of a sequence encoding a subunit of nuclear factor
CC kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
CC configuration. The enzymatic nucleic acid molecule is adapted to treat
CC cancer and is useful for down-regulating REL-A activity in a cell, for
CC treating a patient having a condition associated with the level of REL-A.
CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
CC the presence of a divalent cation, especially Mg^2^+. The enzymatic and
CC antisense nucleic acid molecules are useful for treating breast, lung,
CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
CC multidrug resistant cancer. The method involves use of other drug
CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or
CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,
CC cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,
CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic
CC acid molecules are also useful for treating inflammatory disease such as
CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
CC rejection, gene therapy applications, ischaemia/reperfusion injury
CC (central nervous system (CNS) and myocardial), glomerulonephritis,
CC sepsis, allergic airway inflammation, inflammatory bowel disease or
CC infection. This sequence represents an enzymatic nucleic acid used to
CC modulate the function of a necrosis factor kappa B sub-unit
XX
SQ Sequence 17 BP; 4 A; 4 C; 5 G; 0 T; 4 U; 0 Other;

Query Match 62.0%; Score 12.4; DB 8; Length 17;
Best Local Similarity 64.3%; Pred. No. 1.3e+04;
Matches 9; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CATAGACTTCTCAG 19
||: |||::|:|||
Db 4 CAUGGACUUCUCAG 17

RESULT 6

ACA06680
ID ACA06680 standard; RNA; 17 BP.
XX
AC ACA06680;
XX
DT 03-JUN-2003 (first entry)
XX
DE NFKB sub-unit modulating inozyme substrate #499.
XX
KW Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;
KW G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;
KW lung cancer; prostate cancer; colorectal cancer; brain cancer;
KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;
KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
KW cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;
KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
KW transplant/graft rejection; reperfusion injury; glomerulonephritis;
KW allergic airway inflammation; inflammatory bowel disease; infection; ss.
XX
OS Homo sapiens.
XX
PN US2002177568-A1.
XX
PD 28-NOV-2002.
XX
PF 23-MAY-2001; 2001US-00864785.
XX
PR 07-DEC-1992; 92US-00987132.
PR 18-MAY-1994; 94US-00245466.
PR 15-AUG-1994; 94US-00291932.
PR 23-DEC-1996; 96US-00777916.
XX
PA (STIN/) STINCHCOMB D T.
PA (MCSW/) MCSWIGGEN J.
PA (DRAP/) DRAPER K G.
XX
PI Stinchcomb DT, Mcswiggen J, Draper KG;
XX
DR WPI; 2003-340953/32.
XX
PT Novel enzymatic nucleic acid molecules which down regulates expression of
PT a sequence encoding a subunit of nuclear factor kappa B useful for
PT treating cancer, inflammatory disorders and autoimmune diseases.
XX
PS Claim 3; Page 34; 72pp; English.
XX
CC The invention describes an enzymatic nucleic acid molecule (I) which down
CC regulates expression of a sequence encoding a subunit of nuclear factor
CC kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
CC configuration. The enzymatic nucleic acid molecule is adapted to treat
CC cancer and is useful for down-regulating REL-A activity in a cell, for
CC treating a patient having a condition associated with the level of REL-A.
CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
CC the presence of a divalent cation, especially Mg^2^+. The enzymatic and
CC antisense nucleic acid molecules are useful for treating breast, lung,
CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
CC multidrug resistant cancer. The method involves use of other drug
CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or
CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,
CC cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,
CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic
CC acid molecules are also useful for treating inflammatory disease such as
CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
CC rejection, gene therapy applications, ischaemia/reperfusion injury
CC (central nervous system (CNS) and myocardial), glomerulonephritis,
CC sepsis, allergic airway inflammation, inflammatory bowel disease or
CC infection. This sequence represents the substrate of a novel enzymatic

```
CC   nucleic acid molecule
XX
SQ   Sequence 17 BP; 4 A; 6 C; 3 G; 0 T; 4 U; 0 Other;

  Query Match             62.0%;  Score 12.4;  DB 8;  Length 17;
  Best Local Similarity   64.3%;  Pred. No. 1.3e+04;
  Matches    9;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CATAGACTTCTCAG 19
              ||: |||::|:|||
Db          2 CAUGGACUUCUCAG 15


RESULT 7
AAZ48549/c
ID   AAZ48549 standard; DNA; 18 BP.
XX
AC   AAZ48549;
XX
DT   31-MAR-2000  (first entry)
XX
DE   Human TNFR1 mRNA inhibiting antisense oligo ISIS# 18942.
XX
KW   Tumour necrosis factor receptor type 1; TNFR1; antisense; infection;
KW   inflammation; tumour formation; TNFR1; anticancer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   US6007995-A.
XX
PD   28-DEC-1999.
XX
PF   26-JUN-1998;   98US-00106038.
XX
PR   26-JUN-1998;   98US-00106038.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Baker BF,  Cowsert LM;
XX
DR   WPI; 2000-105333/09.
XX
PT   Antisense inhibition of tumor necrosis factor type 1 expression for
PT   diagnosis, treatment and prevention of disease, particularly tumors.
XX
PS   Example 10; Col 25; 34pp; English.
XX
CC   The invention provides antisense compounds targeted to human tumour
CC   necrosis factor receptor type 1 (TNFR1) RNA. These antisense compounds
CC   can be used in a method of inhibiting the expression of TNFR1 human cells
CC   or tissues. The antisense compounds specifically hybridize with one or
CC   more nucleic acids encoding TNFR1 modulating the function of nucleic acid
CC   molecules encoding TNFR1, ultimately modulating the amount of TNFR1
CC   produced. The antisense compounds and method are useful as research
CC   reagents and diagnostics, and in the treatment and prophylaxis of
CC   infection, inflammation or tumour formation. Sequences AAZ48482-565
CC   represent antisense oligos used for inhibition of the human TNFR1 mRNA
XX
SQ   Sequence 18 BP; 5 A; 3 C; 7 G; 3 T; 0 U; 0 Other;

  Query Match             61.0%;  Score 12.2;  DB 3;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 1.6e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 CGCATAGACTTCTCAGA 20
              |||  || |||||||||
Db         18 CGCCCAGTCTTCTCAGA 2


RESULT 8
ABT05045/c
ID   ABT05045 standard; DNA; 18 BP.
XX
AC   ABT05045;
XX
DT   11-OCT-2002  (first entry)
XX
DE   TNFR1 expression modulation related antisense oligo SEQ ID No 75.
XX
KW   Antisense compound; tumour necrosis factor receptor 1; liver disease;
KW   TNFR1; hepatitis; liver injury; hyperproliferative disorder; cancer;
KW   human; ds.
XX
OS   Homo sapiens.
XX
PN   WO200248168-A1.
XX
PD   20-JUN-2002.
XX
PF   22-OCT-2001; 2001WO-US051224.
XX
PR   24-OCT-2000; 2000US-00695451.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Baker BF,  Cowsert LM,  Zhang H,  Dean NM;
XX
DR   WPI; 2002-583481/62.
XX
PT   Novel antisense compound targeted to nucleic acid molecule encoding tumor
PT   necrosis factor receptor 1 (TNFR1), useful for treating humans having
PT   disease associated with TNFR1 e.g. hepatitis, liver injury, liver cancer.
XX
PS   Example 10; Page 45; 121pp; English.
XX
CC   The invention relates to an antisense compound 8 to 30 nucleotides in
CC   length targeted to nucleic acid molecule encoding tumour necrosis factor
CC   receptor 1 (TNFR1), where the antisense compound inhibits expression of
CC   TNFR1. The antisense compound is useful for inhibiting the expression of
CC   TNFR1 in cells or tissues. The antisense compound is also useful for
CC   treating an animal (preferably human) having a disease or condition
CC   associated with TNFR1, e.g. a liver disease (such as hepatitis, or liver
CC   injury) or a hyperproliferative disorder such as cancer, by inhibiting
CC   the expression of TNFR1. The antisense compound is useful for
CC   diagnostics, therapeutics, prophylaxis and as research reagents and kits.
CC   This polynucleotide sequence represents a human oligonucleotide relating
CC   to the TNFR1 of the invention
XX
SQ   Sequence 18 BP; 5 A; 3 C; 7 G; 3 T; 0 U; 0 Other;

  Query Match             61.0%;  Score 12.2;  DB 6;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 1.6e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 CGCATAGACTTCTCAGA 20
              |||  || |||||||||
Db         18 CGCCCAGTCTTCTCAGA 2


RESULT 9
ADR06077/c
ID   ADR06077 standard; DNA; 18 BP.
XX
AC   ADR06077;
XX
DT   21-OCT-2004  (first entry)
XX
DE   Human TNFR1 antisense oligonucleotide seqid 75.
XX
KW   cytostatic; gene therapy; apoptosis inhibitor;
KW   radiation-induced apoptosis; tumour necrosis factor receptor 1; TNFR1;
KW   human; antisense oligonucleotide; antisense technology; ss.
XX
OS   Homo sapiens.
XX
```

```
FH   Key             Location/Qualifiers
FT   modified_base   1. .18
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "OTHER= Phosphorothioate backbone"
FT   modified_base   1. .4
FT                   /*tag=  a
FT                   /mod_base= OTHER
FT                   /note= "OTHER= Optionally 2'-O-Methoxyethyl (2'-MOE)
FT                   nucleotides"
FT   modified_base   15. .18
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "OTHER= Optionally 2'-O-Methoxyethyl (2'-MOE)
FT                   nucleotides"
XX
PN   US2004147471-A1.
XX
PD   29-JUL-2004.
XX
PF   06-NOV-2003; 2003US-00702817.
XX
PR   26-JUN-1998;   98US-00106038.
PR   17-JUN-1999;   99WO-US013763.
PR   24-OCT-2000; 2000US-00695451.
XX
PA   (ZHAN/) ZHANG H.
XX
PI   Zhang H;
XX
DR   WPI; 2004-561407/54.
XX
PT   Inhibiting radiation-induced apoptosis in a cell or tissue comprises
PT   administering to the cell or tissue an antisense oligonucleotide targeted
PT   to a nucleic acid molecule encoding tumor necrosis factor receptor 1.
XX
PS   Example 10; SEQ ID NO 75; 24pp; English.
XX
CC   The invention describes a method of inhibiting radiation-induced
CC   apoptosis in a cell or tissue comprising administering to the cell or
CC   tissue an antisense oligonucleotide of 8-30 nucleotides in length
CC   targeted to a nucleic acid molecule encoding tumour necrosis factor
CC   receptor 1 (TNFR1). The method and antisense oligonucleotides are useful
CC   for inhibiting radiation-induced apoptosis in a cell or tissue, and for
CC   treating diseases associated with the expression of TNFR1. This sequence
CC   represents a human tumour necrosis factor receptor 1 (TNFR1) antisense
CC   oligonucleotide.
XX
SQ   Sequence 18 BP; 5 A; 3 C; 7 G; 3 T; 0 U; 0 Other;

  Query Match             61.0%;  Score 12.2;  DB 13;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 1.6e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 CGCATAGACTTCTCAGA 20
              |||  || |||||||||
Db         18 CGCCCAGTCTTCTCAGA 2


RESULT 10
ADG73193
ID   ADG73193 standard; DNA; 19 BP.
XX
AC   ADG73193;
XX
DT   11-MAR-2004  (first entry)
XX
DE   Pseudomonas syringae pv. tomato DC3000 Hop gene PCR primer #40.
XX
KW   Avr; Hop; transgenic plant; disease resistance; cancer; bacteria;
KW   metabolic pathway; eukaryotic cell death; programmed cell death;
KW   cytostatic; PCR; primer; ss.
XX
OS   Pseudomonas syringae; pv. tomato str. DC3000.
XX
PN   US2003204868-A1.
XX
PD   30-OCT-2003.
XX
PF   12-FEB-2003; 2003US-00365742.
XX
PR   12-FEB-2002; 2002US-0356408P.
PR   10-MAY-2002; 2002US-0380185P.
XX
PA   (COLL/) COLLMER A.
PA   (ALFA/) ALFANO J R.
PA   (CART/) CARTINHOUR S W.
PA   (SCHN/) SCHNEIDER D J.
PA   (TANG/) TANG X.
XX
PI   Collmer A,  Alfano JR,  Cartinhour SW,  Schneider DJ,  Tang X;
XX
DR   WPI; 2003-875735/81.
XX
PT   New nucleic acid, useful in imparting disease resistance to a plant or in
PT   preparing a composition for treating cancer.
XX
PS   Example; SEQ ID NO 187; 209pp; English.
XX
CC   The present invention relates to the isolation of Pseudomonas syringae
CC   pv. tomato DC3000 Avr/Hop proteins, and the polynucleotide sequences
CC   encoding them. Also disclosed are expression vectors, host cells, and
CC   transgenic plants comprising polynucleotide sequences of the invention.
CC   The polynucleotide and polypeptide sequences are useful in imparting
CC   disease resistance to a plant or in preparing a composition for treating
CC   cancer. The sequences may also be used to make a plant hypersusceptible
CC   to colonisation by nonpathogenic bacteria, modify a metabolic pathway in
CC   a cell, cause eukaryotic cell death, and inhibit programmed cell death.
CC   The present sequence represents a PCR primer used in the examples of the
CC   present invention.
XX
SQ   Sequence 19 BP; 4 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

  Query Match             61.0%;  Score 12.2;  DB 10;  Length 19;
  Best Local Similarity   82.4%;  Pred. No. 1.6e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 CCGCATAGACTTCTCAG 19
              |||||||||| | || |
Db          3 CCGCATAGACCTGTCTG 19


RESULT 11
ADL12249
ID   ADL12249 standard; DNA; 19 BP.
XX
AC   ADL12249;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Pseudomonas syringae anti-cancer gene primer #60.
XX
KW   cytostatic; gene therapy; Avr; Hop; cancer; primer; ss.
XX
OS   Pseudomonas syringae; pv tomato DC3000.
XX
PN   WO2003068930-A2.
XX
PD   21-AUG-2003.
XX
PF   12-FEB-2003; 2003WO-US004450.
XX
PR   12-FEB-2002; 2002US-0356408P.
PR   10-MAY-2002; 2002US-0380185P.
XX
PA   (CORR ) CORNELL RES FOUND INC.
```

PA (USDA) US SEC OF AGRIC.
PA (UYNE-) UNIV NEBRASKA.
PA (UNIV) UNIV KANSAS STATE RES FOUND.
XX
PI Collmer A, Alfano JR, Cartinhour SW, Schneider DJ, Tang X;
XX
DR WPI; 2003-679632/64.
XX
PT New nucleic acid molecule, useful for preparing a composition for
PT treating cancer.
XX
PS Disclosure; SEQ ID NO 187; 284pp; English.
XX
CC The invention relates to novel Pseudomonas Avr and Hop genes, a sequence
CC that hybridizes with these sequences under stringency conditions
CC comprising a hybridization medium that includes 0.9 x saline sodium
CC citrate (SSC) buffer at a temperature of 42 deg C. The nucleic acid
CC molecule is useful for preparing a composition for treating cancer. This
CC sequence corresponds to a PCR to isolate and amplify one of the genes of
CC the invention.
XX
SQ Sequence 19 BP; 4 A; 7 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 61.0%; Score 12.2; DB 10; Length 19;
Best Local Similarity 82.4%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 CCGCATAGACTTCTCAG 19
||||||||||.|.||.|
Db 3 CCGCATAGACCTGTCTG 19

RESULT 12
ADI79866
ID ADI79866 standard; DNA; 20 BP.
XX
AC ADI79866;
XX
DT 22-APR-2004 (first entry)
XX
DE Mouse HMG-CoA reductase antisense oligonucleotide, SEQ ID No 389.
XX
KW HMG-CoA reductase; 3-hydroxy-3-methylglutaryl-Coenzyme A;
KW HMG-CoA reductase; cardiant; antiarteriosclerotic; antilipaemic;
KW antisense gene therapy; cardiovascular disorder; cholesterol metabolism;
KW mouse; murine; ss.
XX
OS Mus musculus.
XX
PN US2004006031-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00190366.
XX
PR 02-JUL-2002; 2002US-00190366.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Dean NM, Freier SM, Dobie KW;
XX
DR WPI; 2004-081743/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding HMG-CoA reductase, useful for treating
PT atherosclerosis, or a disease involving cholesterol metabolism or
PT angiogenesis.
XX
PS Example 16; SEQ ID NO 389; 110pp; English.
XX
CC The invention relates to novel compounds of 8-80 nucleobases in length
CC targeted to, and which specifically hybridises with, a nucleic acid
CC molecule encoding 3-hydroxy-3-methylglutaryl-Coenzyme A (HMG-CoA)
CC reductase, and inhibits the expression of HMG-CoA reductase. The novel
CC compounds have cardiant, antiarteriosclerotic, and antilipaemic
CC activities. The compound can be used to treat disorders by antisense gene
CC therapy. The compounds, compositions and methods are useful for treating
CC a disease or condition associated with HMG-CoA reductase, such as a
CC cardiovascular disorder e.g. atherosclerosis, or a disease or condition
CC involving cholesterol metabolism. They are also useful in research and
CC diagnostics for modulating the expression of HMG-CoA reductase. This
CC polynucleotide sequence represents an antisense oligonucleotide of the
CC invention.
XX
SQ Sequence 20 BP; 6 A; 6 C; 4 G; 4 T; 0 U; 0 Other;

Query Match 61.0%; Score 12.2; DB 12; Length 20;
Best Local Similarity 82.4%; Pred. No. 1.6e+04;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CGCATAGACTTCTCAGA 20
| || ||||| ||||||
Db 3 CACAGAGACTCCTCAGA 19

RESULT 13
ADI79673/c
ID ADI79673 standard; DNA; 20 BP.
XX
AC ADI79673;
XX
DT 22-APR-2004 (first entry)
XX
DE Mouse HMG-CoA reductase antisense oligonucleotide, SEQ ID No 196.
XX
KW HMG-CoA reductase; 3-hydroxy-3-methylglutaryl-Coenzyme A;
KW HMG-CoA reductase; cardiant; antiarteriosclerotic; antilipaemic;
KW antisense gene therapy; cardiovascular disorder; cholesterol metabolism;
KW mouse; murine; ss.
XX
OS Mus musculus.
XX
PN US2004006031-A1.
XX
PD 08-JAN-2004.
XX
PF 02-JUL-2002; 2002US-00190366.
XX
PR 02-JUL-2002; 2002US-00190366.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Dean NM, Freier SM, Dobie KW;
XX
DR WPI; 2004-081743/08.
XX
PT New compounds, particularly antisense oligonucleotides targeted to a
PT nucleic acid encoding HMG-CoA reductase, useful for treating
PT atherosclerosis, or a disease involving cholesterol metabolism or
PT angiogenesis.
XX
PS Example 16; SEQ ID NO 196; 110pp; English.
XX
CC The invention relates to novel compounds of 8-80 nucleobases in length
CC targeted to, and which specifically hybridises with, a nucleic acid
CC molecule encoding 3-hydroxy-3-methylglutaryl-Coenzyme A (HMG-CoA)
CC reductase, and inhibits the expression of HMG-CoA reductase. The novel
CC compounds have cardiant, antiarteriosclerotic, and antilipaemic
CC activities. The compound can be used to treat disorders by antisense gene
CC therapy. The compounds, compositions and methods are useful for treating
CC a disease or condition associated with HMG-CoA reductase, such as a
CC cardiovascular disorder e.g. atherosclerosis, or a disease or condition
CC involving cholesterol metabolism. They are also useful in research and
CC diagnostics for modulating the expression of HMG-CoA reductase. This
CC polynucleotide sequence represents an antisense oligonucleotide of the
CC invention.

```
XX
SQ   Sequence 20 BP; 4 A; 4 C; 6 G; 6 T; 0 U; 0 Other;

  Query Match             61.0%;  Score 12.2;  DB 12;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 1.6e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 CGCATAGACTTCTCAGA 20
              | || ||||| ||||||
Db         18 CACAGAGACTCCTCAGA 2


RESULT 14
AAQ32840
ID   AAQ32840 standard; DNA; 20 BP.
XX
AC   AAQ32840;
XX
DT   25-MAR-2003  (revised)
DT   05-MAY-1993  (first entry)
XX
DE   Microsatellite repeat polymorphic DNA marker PCR primer.
XX
KW   PIC; high polymorphism information content; forensic; screening;
KW   polymerase chain reaction; genetic mapping; paternity; prenatal.
XX
OS   Synthetic.
XX
PN   WO9221693-A1.
XX
PD   10-DEC-1992.
XX
PF   27-MAY-1992;   92WO-US004195.
XX
PR   29-MAY-1991;   91US-00707501.
PR   27-NOV-1991;   91US-00799828.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICE.
XX
PI   Polymeropoulos MH,  Merrill CR;
XX
DR   WPI; 1992-433606/52.
XX
PT   Oligo-nucleotide primers for polymerase chain reaction amplification -
PT   which detect DNA polymorphisms and are useful for prenatal and paternity
PT   screening, and genetic mapping.
XX
PS   Disclosure; Fig 60; 44pp; English.
XX
CC   This is a PCR primer which is used (with AAQ32841) to characterise a
CC   unique microsatellite repeat polymorphic DNA marker which has a high
CC   polymorphism information content. The marker is useful for human
CC   individualisation, in forensic screening, in paternity and prenatal
CC   screening as well as in genetic mapping. (Updated on 25-MAR-2003 to
CC   correct PN field.)
XX
SQ   Sequence 20 BP; 6 A; 8 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             60.0%;  Score 12;  DB 2;  Length 20;
  Best Local Similarity   75.0%;  Pred. No. 2.1e+04;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GACCGCATAGACTTCTCAGA 20
              |||| || || ||  |||||
Db          1 GACCCCACAGCCTATTCAGA 20


RESULT 15
AAQ57863
ID   AAQ57863 standard; DNA; 20 BP.
XX
AC   AAQ57863;
XX
DT   25-MAR-2003  (revised)
DT   21-AUG-1994  (first entry)
XX
DE   Primer pair 26A II-D detection primer #1.
XX
KW   Primer; assay; subtle difference; dinucleotide; tetranucleotide; repeat;
KW   polymorphism; PCR; polymerase chain reaction; amplify; PAGE;
KW   autoradiography; migration pattern; length variation; genetic mapping;
KW   forensic screening; paternity; prenatal; screening; microsatellite;
KW   human; ss.
XX
OS   Synthetic.
XX
PN   WO9403640-A1.
XX
PD   17-FEB-1994.
XX
PF   30-JUL-1993;   93WO-US007183.
XX
PR   31-JUL-1992;   92US-00922723.
PR   28-SEP-1992;   92US-00952277.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Polymeropolous MH,  Merril CR;
XX
DR   WPI; 1994-065727/08.
XX
PT   New polynucleotide sequences - derived from polymorphic micro:satellite
PT   repeats, used for characterising human individuals for forensic,
PT   paternity and prenatal screening and genetic mapping.
XX
PS   Disclosure; Page 47; 72pp; English.
XX
CC   The sequences given in AAQ57782-866 are primers which were used in an
CC   assay for measuring the subtle differences in genetic material regarding
CC   an added or omitted set of dinucleotide or tetranucleotide repeat
CC   polymorphisms. The method comprises obtaining polynucleotide segments
CC   comprising the repeat polymorphisms in an amount effective for testing
CC   and amplifying the segments by a PCR procedure using a pair of
CC   oligonucleotide primers capable of amplifying the polymorphism containing
CC   sequence. The amplified sequences are resolved using PAGE and the
CC   resolved sequences are compared by autoradiography to observe the
CC   differences in migration pattern due to length variation. The
CC   polynucleotides provide a fast and accurate test for measuring the subtle
CC   differences in individuals in eg. forensic screening, paternity and
CC   prenatal screening and genetic mapping. The polynucleotides are specific
CC   for polymorphic microsatellite repeats based on previously sequenced
CC   human genes. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 20 BP; 6 A; 8 C; 3 G; 3 T; 0 U; 0 Other;

  Query Match             60.0%;  Score 12;  DB 2;  Length 20;
  Best Local Similarity   75.0%;  Pred. No. 2.1e+04;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GACCGCATAGACTTCTCAGA 20
              |||| || || ||  |||||
Db          1 GACCCCACAGCCTATTCAGA 20


RESULT 16
AAZ21763
ID   AAZ21763 standard; DNA; 20 BP.
XX
AC   AAZ21763;
XX
DT   01-DEC-1999  (first entry)
XX
DE   Exemplary oligonucleotide primer TBP (For).
XX
KW   neoplasia; mutant; target nucleotide; hybridization; lung cancer; ss;
KW   neck cancer; head cancer; saliva test; chemotherapy; early detection;
```

KW primer; PCR; amplification.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9946408-A1.
XX
PD 16-SEP-1999.
XX
PF 10-MAR-1999; 99WO-US005220.
XX
PR 10-MAR-1998; 98US-00038637.
XX
PA (UYJO) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
XX
PI Sidransky D;
XX
DR WPI; 1999-551428/46.
XX
PT Detection of cancers comprises assaying for a genetic mutation associated
PT with cancer.
XX
PS Disclosure; Page 27; 99pp; English.
XX
CC This is an exemplary oligonucleotide primer, for use in the detection of
CC neoplasmic related gene mutations. There are over 40 known proto-
CC oncogenes and suppressor genes to date, which control growth,
CC development, and cell differentiation. Regulation of these genes can,
CC under certain circumstances, be altered and normal cells can assume
CC neoplastic growth characteristics. The invention provides a method for
CC detecting a neoplastic disorder of the head and neck or lung in a
CC subject. The detection of a target mutant nucleotide sequence in the
CC saliva is indicative of a neoplastic disorder of the head, neck or lung.
CC This allows early detection and therefore treatment of the preneoplasia
CC or cancer, and can also be used to monitor high risk patients undergoing
CC chemoprevention or chemotherapy
XX
SQ Sequence 20 BP; 6 A; 8 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 60.0%; Score 12; DB 2; Length 20;
Best Local Similarity 75.0%; Pred. No. 2.1e+04;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GACCGCATAGACTTCTCAGA 20
|||| || || || |||||
Db 1 GACCCCACAGCCTATTCAGA 20

RESULT 17
AAC60963
ID AAC60963 standard; DNA; 20 BP.
XX
AC AAC60963;
XX
DT 13-FEB-2001 (first entry)
XX
DE TATA box-binding protein short tandem repeat primer SEQ ID NO:23.
XX
KW Short tandem repeat; primer; STR; susceptibility; HIV; infection; AIDS;
KW detection; polymorphism; interleukin 10 promoter; IL-10;
KW chromosome position 6q27; TATA box-binding protein; ss.
XX
OS Homo sapiens.
XX
PN WO200061811-A2.
XX
PD 19-OCT-2000.
XX
PF 06-APR-2000; 2000WO-US009355.
XX
PR 09-APR-1999; 99US-0128521P.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Smith MW, Shin HD, O'brien SJ;
XX
DR WPI; 2000-687051/67.
XX
PT Predicting susceptibility to HIV infection or progression useful for
PT selection of therapeutic treatment for persons infected with HIV virus,
PT comprises detecting polymorphism in human interleukin-10 promoter.
XX
PS Example 1; Page 12; 40pp; English.
XX
CC The present invention describes a method for predicting susceptibility to
CC HIV infection or HIV progression in a subject. The method involves
CC detecting a polymorphism in a human interleukin-10 (IL-10) promoter,
CC where the presence of the polymorphism indicates susceptibility to HIV
CC infection or HIV progression. The method provides prognostic information
CC to persons infected with HIV virus and is useful to help select
CC treatments (such as administration of IL-10 or gene therapy with IL-10).
CC The presence of polymorphism is useful as predictor that very aggressive
CC treatment could substantially eradicate the virus from the infected
CC person. The method is useful for the generation of normograms or other
CC predictive algorithms that can be used, in association with allele
CC status, to prognose probable survival or years to development of AIDS
CC following HIV seroconversion. It indicates that increased expression of
CC the IL-10 gene helps to reduce HIV-1 infection and pathogenic progression
CC and enables a variety of new therapeutic interventions in the treatment
CC of HIV disease. The present sequence represents a short tandem repeat
CC (STR) primer which is used in an example from the present invention
XX
SQ Sequence 20 BP; 6 A; 8 C; 3 G; 3 T; 0 U; 0 Other;

Query Match 60.0%; Score 12; DB 3; Length 20;
Best Local Similarity 75.0%; Pred. No. 2.1e+04;
Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 GACCGCATAGACTTCTCAGA 20
|||| || || || |||||
Db 1 GACCCCACAGCCTATTCAGA 20

RESULT 18
ADB42063
ID ADB42063 standard; DNA; 17 BP.
XX
AC ADB42063;
XX
DT 18-DEC-2003 (revised)
DT 04-DEC-2003 (first entry)
XX
DE Tumour suppression/reversion associated nucleotide #2386.
XX
KW cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
KW primer; probe; tumour suppression; tumour reversion; apoptosis;
KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
KW diagnosis.
XX
OS Homo sapiens.
XX
PN WO2003040369-A2.
XX
PD 15-MAY-2003.
XX
PF 17-SEP-2002; 2002WO-IB004219.
XX
PR 17-SEP-2001; 2001FR-00011981.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-441574/41.
XX
PT New nucleic acid encoding human prostate membrane-specific antigen,

```
PT   useful e.g. for treatment of tumors and viral infection, also related
PT   polypeptide and antibodies.
XX
PS   Disclosure; Page 311; 771pp; French.
XX
CC   The invention relates to the isolation of 6327 nucleotide sequences,
CC   fragments of at least 15 consecutive nucleotides of these nucleotides, a
CC   sequence having at least 80% identity, after optimal alignment, with the
CC   nucleotides, a sequence that hybridizes under stringent conditions with
CC   the nucleotides, or the complement, or corresponding RNA, of the
CC   nucleotides. The nucleotides are used as probes or primers for detecting,
CC   identifying, quantifying and/or amplifying nucleic acids, as in vitro
CC   sense and antisense sequences, of nucleotides involved in tumour
CC   suppression or reversion, apoptosis and or viral resistance, to produce
CC   recombinant polypeptides, and to prepare transgenic animals, as
CC   experimental models. The nucleotides (also vectors containing them and
CC   cells containing the vectors), the encoded polypeptides and antibodies
CC   (Ab) against the polypeptide are useful for prevention and/or treatment
CC   of viral infections or diseases characterized by development of tumours
CC   or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
CC   Analysis of the expression of the nucleotides can be used for diagnosis
CC   and/or prognosis of these diseases. The nucleotides and polypeptides can
CC   also be used to screen for their specific interactive molecules,
CC   potentially useful for treating diseases associated with abnormal
CC   expression of the nucleotides.
XX
SQ   Sequence 17 BP; 6 A; 5 C; 2 G; 4 T; 0 U; 0 Other;

  Query Match             59.0%;  Score 11.8;  DB 10;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 2.6e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GACCGCATAGACTTC 15
              || | ||||||||||
Db          1 GATCACATAGACTTC 15


RESULT 19
ADI48431/c
ID   ADI48431 standard; DNA; 17 BP.
XX
AC   ADI48431;
XX
DT   15-APR-2004  (first entry)
XX
DE   Human tumour suppression/reversion-related DNA sequence SeqID934.
XX
KW   tumour suppression; tumour reversion; apoptosis; virus resistance;
KW   cytostatic; virucide; neuroprotective; nootropic; neuroleptic; probe;
KW   primer; PCR; gene chip; antisense; viral disease; tumour;
KW   cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX
OS   Homo sapiens.
XX
PN   WO2003025177-A2.
XX
PD   27-MAR-2003.
XX
PF   17-SEP-2002; 2002WO-IB004523.
XX
PR   17-SEP-2001; 2001FR-00011980.
XX
PA   (MOLE-) MOLECULAR ENGINES LAB.
XX
PI   Telerman A,  Amson R,  Tuijnder M;
XX
DR   WPI; 2003-313354/30.
XX
PT   New isolated nucleic acid, useful for treating viral diseases associated
PT   with tumors and cell degeneration, also related polypeptides, antibodies
PT   and transfected cells.
XX
PS   Disclosure; SEQ ID NO 934; 30pp; French.
XX
CC   This invention relates to novel isolated nucleic acid sequences involved
CC   in the phenomena of tumour suppression, tumour reversion, apoptosis
CC   and/or resistance to viruses. The invention may be useful for the
CC   development of compounds with a cytostatic, virucide, neuroprotective,
CC   nootropic or neuroleptic activity. The DNA sequences may be useful as
CC   probes and primers for detecting, indentifying, quantifying and/or
CC   amplifying nucleic acid, for example as one component of a gene chip, in
CC   vitro as antisense reagents and for production of recombinant
CC   polypeptides. The invention may therefore be useful for preparation of
CC   pharmaceuticals for prevention and/or treatment of viral diseases that
CC   are characterised by development of tumours or cell degeneration,
CC   specifically cancer but also Alzheimer's disease and schizophrenia. The
CC   present sequence is that of a nucleic acid sequence of the invention.
CC   Note: The sequence data for this patent did not form part of the printed
CC   specification, but was obtained in electronic format directly from WIPO
CC   at ftp.wipo.int/pub/publishedpct_sequences
XX
SQ   Sequence 17 BP; 6 A; 1 C; 5 G; 5 T; 0 U; 0 Other;

  Query Match             59.0%;  Score 11.8;  DB 10;  Length 17;
  Best Local Similarity   86.7%;  Pred. No. 2.6e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 CATAGACTTCTCAGA 20
              |||| ||||||| ||
Db         17 CATAAACTTCTCTGA 3


RESULT 20
AAQ94315/c
ID   AAQ94315 standard; DNA; 18 BP.
XX
AC   AAQ94315;
XX
DT   09-MAY-1996  (first entry)
XX
DE   Human cytochrome P450IIC18 exon 2 point mutant 204 PCR primer.
XX
KW   Human-derived; cytochrome P450IIC18 gene; point mutant; exon 2;
KW   position 204; PCR primer; polymorphism; medicine metabolism; tricyclics;
KW   benzodiazepines; beta blockers; barbiturates; ss.
XX
OS   Synthetic.
XX
PN   WO9526415-A1.
XX
PD   05-OCT-1995.
XX
PF   28-MAR-1995;   95WO-JP000570.
XX
PR   29-MAR-1994;   94JP-00059385.
PR   29-MAR-1994;   94JP-00059386.
XX
PA   (SUMO ) SUMITOMO CHEM CO LTD.
XX
PI   Komai K,  Kaneko H,  Nakatsuka I;
XX
DR   WPI; 1995-351329/45.
XX
PT   Oligo:nucleotide which hybridises to human cytochrome P450IIC18 gene -
PT   for detection of mutation(s) in the gene when establishing safe
PT   medication dosage in individual patients.
XX
PS   Claim 4; Page 20; 34pp; Japanese.
XX
CC   The oligos AAQ94315-27 which hybridise to the human-derived cytochrome
CC   P450IIC18 gene, esp. to the gene having a point mutation at position 204
CC   in exon 2, can be used as PCR amplification primers which discriminate
CC   between the normal and mutated gene, allowing the degree of genetic
CC   polymorphism in a patient to be determined. As the gene prod.
CC   participates in the metabolism of medicines (e.g. tricyclics,
CC   benzodiazepines, beta blockers and barbiturates), patients with mutant
```

```
CC   genes differ in their drug metabolising ability and therefore knowledge
CC   of this allows the safe dosage of medicine to be more accurately assessed
XX
SQ   Sequence 18 BP; 5 A; 4 C; 3 G; 6 T; 0 U; 0 Other;

  Query Match             59.0%;  Score 11.8;  DB 2;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 2.6e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 CATAGACTTCTCAGA 20
              ||||||||| | |||
Db         16 CATAGACTTTTGAGA 2


RESULT 21
AAV30475
ID   AAV30475 standard; DNA; 18 BP.
XX
AC   AAV30475;
XX
DT   14-OCT-1998  (first entry)
XX
DE   Canine beta-3 adrenergic receptor antisense primer TR21.
XX
KW   Canine; beta-adrenergic receptor; brown adipose tissue; probe; human;
KW   hybridisation; ligand; primer; ss.
XX
OS   Synthetic.
OS   Canis familiaris.
XX
PN   WO9735973-A2.
XX
PD   02-OCT-1997.
XX
PF   26-MAR-1997;   97WO-FR000537.
XX
PR   26-MAR-1996;   96FR-00003730.
XX
PA   (VETI-) VETIGEN.
XX
PI   Lenzen G,  Pietri-Rouxel F,  Drumare M,  Strosberg AD;
XX
DR   WPI; 1998-032136/03.
XX
PT   Canine beta 2 and beta 3 adrenergic receptors and coding sequences -
PT   useful for identifying specific ligands and (ant)agonists to develop
PT   specific treatments for obesity in dogs.
XX
PS   Claim 17; Page 49; 79pp; French.
XX
CC   Primers AAV30470-V30490 were used for sequencing the coding region of the
CC   canine beta 3-adrenergic receptor (RA-Ca-b3) gene (AAV30469). RA-Ca-b3
CC   has been implicated in obesity and obesity-related metabolic disorders
CC   e.g. diabetes. The canine version of RA-Ca-b3 can be used to develop
CC   treatments specific for dogs. The sequence can also be used in
CC   differential screening for ligands for RA-Ca-b3 as compared to the beta-2
CC   adrenergic receptor (AAW44932)
XX
SQ   Sequence 18 BP; 3 A; 8 C; 5 G; 2 T; 0 U; 0 Other;

  Query Match             59.0%;  Score 11.8;  DB 2;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 2.6e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 CCGCATAGACTTCTC 17
              ||||| |||| ||||
Db          3 CCGCAGAGACGTCTC 17


RESULT 22
AAV33985
ID   AAV33985 standard; DNA; 20 BP.
XX
AC   AAV33985;
XX
DT   25-JAN-1999  (first entry)
XX
DE   Primer CT1431F for C. trachomatis cryptic plasmid sequence.
XX
KW   Primer; PCR; amplification; gag; qualitative; quantitative; analysis;
KW   infection; diagnosis; detection; serotype; ss.
XX
OS   Synthetic.
OS   Chlamydia trachomatis.
XX
PN   US5795722-A.
XX
PD   18-AUG-1998.
XX
PF   18-MAR-1997;   97US-00819912.
XX
PR   18-MAR-1997;   97US-00819912.
XX
PA   (VISI-) VISIBLE GENETICS INC.
XX
PI   Dunn JM,  Lacroix J;
XX
DR   WPI; 1998-466660/40.
XX
PT   Simultaneous qualitative and quantitative analysis of target nucleic acid
PT   - by simultaneous amplification of analyte and control with one primer
PT   pair and of sequencing fragment with second primer pair that includes
PT   label for immobilisation, especially for HIV-1 detection.
XX
PS   Disclosure; Col 8; 18pp; English.
XX
CC   Primers AAV33985-V33986 are used to amplify a fragment of the Chlamydia
CC   trachomatis cryptic plasmid sequence. The primers are used in a method
CC   for the qualitative and quantitative analysis of a nucleic acid analyte
CC   in a sample. The method comprises adding a control nucleic acid to the
CC   sample and two primer pairs, one pair which can amplify a conserved
CC   region of the sample nucleic acid and a region of the control nucleic
CC   acid to produce fragments (F1, F2) of differing lengths, while the other
CC   pair amplifies a second region of the sample nucleic acid to form a
CC   sequencing fragment (F3). The method generates a mixture of all 3
CC   fragments if the sample nucleic acid is present but only F2 if it is
CC   absent. The resultant mixture is analysed for relative amounts of F1 and
CC   F2, to quantify the level of sample nucleic acid; and fragment F3 is
CC   sequenced to determine the nature of sample nucleic acid. The method can
CC   be used for any infectious organism, e.g. human papilloma virus or
CC   Chlamydia trachomatis. By using primers specific for the disease to be
CC   tested e.g. HIV-1, the disease can be detected and by the amount of
CC   amplification product formed, the viral load i.e. the extent of the
CC   disease can be assessed. Then by using in the same assay a pair of
CC   sequencing primers, the serotype of the disease organism can be
CC   determined, leading to a more exact treatment
XX
SQ   Sequence 20 BP; 6 A; 3 C; 5 G; 6 T; 0 U; 0 Other;

  Query Match             59.0%;  Score 11.8;  DB 2;  Length 20;
  Best Local Similarity   86.7%;  Pred. No. 2.7e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 GCATAGACTTCTCAG 19
              ||||| |||||| ||
Db          3 GCATAAACTTCTGAG 17


RESULT 23
AAZ24116
ID   AAZ24116 standard; DNA; 20 BP.
XX
AC   AAZ24116;
XX
DT   03-FEB-2000  (first entry)
XX
```

DE Primer CT1431F-Cy5.5.
XX
KW Detection; target; diagnosis; mutant; human leucocyte antigen typing;
KW transplantation; pathogen; amplification; primer; ss.
XX
OS Synthetic.
XX
PN DE19917871-A1.
XX
PD 11-NOV-1999.
XX
PF 20-APR-1999; 99DE-01017871.
XX
PR 24-APR-1998; 98US-00065748.
XX
PA (VISI-) VISIBLE GENETICS INC.
XX
PI Leushner J, Lacroix J, Hui M, Dunn J, Larson MT;
XX
DR WPI; 2000-040351/04.
XX
PT Nucleic acid sequencing involving chain extension reaction in presence of
PT chain terminator e.g. for detecting mutations.
XX
PS Example 1; Page 9; 18pp; German.
XX
CC This invention describes a novel method for determining the position of
CC at least one nucleotide (A) within a segment of a target nucleic acid
CC (present in a sample). The method comprises (i) combining the sample with
CC a reaction mixture to synthesize, from the sample, chain-extension
CC products which display the presence of (A) and (ii) evaluating the
CC products. The method is used for diagnosis, e.g. (I) detecting mutations,
CC in human, animal, plant or microbial sequences, particularly medically
CC significant mutations, (II) for human leucocyte antigen typing (in
CC transplantation), (III) detecting or identifying microbes, particularly
CC pathogens; or in situ sequencing in histological samples, especially
CC archival samples for retrospective analysis. The method makes it possible
CC to sequence segments of a target nucleic acid, even when this is present
CC in its natural concentration in a highly complex sample. It is suitable
CC for automation; the system represents a way of mimimizing errors caused
CC by contaminants or carried-over nucleic acid; only minimal sample
CC pretreatment is involved and only a single batch of reagent, and single
CC vessel, are required. AAZ24114-Z24122 represent primers used in the
CC method of the invention
XX
SQ Sequence 20 BP; 6 A; 3 C; 5 G; 6 T; 0 U; 0 Other;

Query Match 59.0%; Score 11.8; DB 3; Length 20;
Best Local Similarity 86.7%; Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GCATAGACTTCTCAG 19
||||| |||||| ||
Db 3 GCATAAACTTCTGAG 17

RESULT 24
ABZ91284/c
ID ABZ91284 standard; DNA; 20 BP.
XX
AC ABZ91284;
XX
DT 17-OCT-2003 (first entry)
XX
DE Human oligonucleotide sequence.
XX
KW Human; antisense; lung dysfunction; nasal airway dysfunction;
KW antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic;
KW antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy;
KW antisense gene therapy; respiratory; lung; adenosine sensitivity;
KW adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
KW lung inflammation; respiratory disease; ds.
XX
OS Homo sapiens.
XX
PN WO200285308-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013135.
XX
PR 24-APR-2001; 2001US-0286137P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-229219/22.
XX
PT Pharmaceutical composition for treating ailments associated with impaired
PT respiration, has oligo(s) antisense to specific gene(s) or its
PT corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
PT ubiquinone.
XX
PS Disclosure; SEQ ID NO 6526; 872pp; English.
XX
CC The invention relates to a novel pharmaceutical composition, which has a
CC first active agent comprising an oligonucleotide antisense to the
CC initiation codon, coding region, 5' or 3' end genomic flanking regions,
CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of
CC junctions of genes encoding a polypeptide associated with lung and/or
CC nasal airway dysfunction and a second active agent comprising an
CC antiinflammatory steroid and ubiquinone. A composition of the invention
CC has antiinflammatory, antiallergic, antiasthmatic, hypotensive,
CC immunosuppressive, and cytostatic activity. The composition may have a
CC use in antisense gene therapy. The composition is useful for treating or
CC preventing a respiratory, lung or malignant disease or condition, also
CC for enhancing the prophylactic or therapeutic respiratory effect of an
CC antiinflammatory steroid in a subject, for reducing or depleting levels
CC of, or reducing sensitivity to adenosine, reducing levels of adenosine
CC receptor, producing bronchodilation, increasing levels of ubiquinone or
CC lung surfactant in a subject's tissue, or treating bronchoconstriction,
CC lung inflammation, lung allergies, or a respiratory disease or condition.
CC Note: The sequence data for this patent is not represented in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 59.0%; Score 11.8; DB 10; Length 20;
Best Local Similarity 86.7%; Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CATAGACTTCTCAGA 20
| || ||||||||||
Db 19 CTTACACTTCTCAGA 5

RESULT 25
ABD27514/c
ID ABD27514 standard; DNA; 20 BP.
XX
AC ABD27514;
XX
DT 29-JUL-2004 (first entry)
XX
DE AA486238-derived oligonucleotide SEQ ID 6526.
XX
KW Human; antisense; bronchoconstriction; allergy; hyposecretion; pain;
KW respiratory tract inflammation; adenosine sensitivity; lung; cancer;
KW surfactant depletion; antiallergic; antiinflammatory; antiasthmatic;
KW analgesic; hypotensive; immunosuppressive; cytostatic; cystic fibrosis;
KW beta-adrenergic agonist; respiratory disease; pulmonary vasoconstriction;
KW respiratory distress syndrome; allergic rhinitis; pulmonary hypertension;
KW emphysema; chronic obstructive pulmonary disease; cancer; bronchitis;

KW pulmonary transplantation rejection; ss; primer.
XX
OS Homo sapiens.
XX
PN WO200285309-A2.
XX
PD 31-OCT-2002.
XX
PF 23-APR-2002; 2002WO-US013143.
XX
PR 24-APR-2001; 2001US-0286036P.
XX
PA (EPIG-) EPIGENESIS PHARM INC.
XX
PI Nyce JW, Li Y, Sandrasagra A, Katz E, Pabalan J, Aguilar D;
PI Miller S, Tang L, Shahabuddin S;
XX
DR WPI; 2003-093058/08.
XX
PT Pharmaceutical composition for treating asthma, has antisense
PT oligonucleotide containing less percentage of adenosine, targeted to
PT nucleic acids associated with lung airway or lung dysfunction, and
PT bronchodilating agent.
XX
PS Claim 15; SEQ ID NO 6526; 763pp; English.
XX
CC This invention describes a novel composition (a) a first active agent,
CC comprising oligonucleotides, effective for alleviating
CC bronchoconstriction, respiratory tract inflammation, allergies and
CC reducing adenosine sensitivity, levels of adenosine (A) or (A) receptors,
CC surfactant depletion or hyposecretion, when administered to a mammal. The
CC oligonucleotides are derived from a gene encoding or regulating
CC expression of a target polypeptide associated with lung airway or lung
CC dysfunction or cancer and can be anti-sense to the corresponding mRNA.
CC The invention also describes a kit, that comprises: (a) a delivery
CC device, in separate containers, (b) the oligonucleotides, (c)
CC instructions for adding a carrier and for use of the kit. The composition
CC of the invention has antiallergic, antiinflammatory, antiasthmatic,
CC analgesic, hypotensive, immunosuppressive and cytostatic activity, is a
CC beta-adrenergic agonist. The composition is useful for preventing or
CC treating a respiratory, lung or malignant disease. The administered
CC composition comprises oligo and is administered to reduce the production
CC or availability, or to increase the degradation of the target mRNA or to
CC reduce the amount of target polypeptide present in the lungs. The
CC pulmonary obstruction, and/or bronchoconstriction and/or lung
CC inflammation, allergies and/or surfactant hypoproduction are associated
CC with a disease or condition such as pulmonary vasoconstriction,
CC inflammation, allergies, asthma, impeded respiration, respiratory
CC distress syndrome, pain, cystic fibrosis, allergic rhinitis, pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease, pulmonary
CC transplantation rejection, pulmonary infections, bronchitis or cancer.
CC The reduced adenosine content of the anti-sense oligos corresponding to
CC thymidines present in the target RNA serves to prevent the breakdown of
CC the oligonucleotides into products that free adenosine into the system
CC e.g., lung, brain, heart, kidney, etc, tissue environment and thereby, to
CC prevent any unwanted effects due to it
XX
SQ Sequence 20 BP; 6 A; 4 C; 6 G; 4 T; 0 U; 0 Other;

Query Match 59.0%; Score 11.8; DB 11; Length 20;
Best Local Similarity 86.7%; Pred. No. 2.7e+04;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 CATAGACTTCTCAGA 20
|| |||||||||||
Db 19 CTTACACTTCTCAGA 5

RESULT 26
AAD11750/c
ID AAD11750 standard; DNA; 19 BP.
XX
AC AAD11750;
XX
DT 24-SEP-2001 (first entry)
XX
DE Human AAG6 DNA exon 1.13 amplifying reverse PCR primer #13.
XX
KW Human; asthma-associated gene; AAG6; antiinflammatory; gene therapy;
KW obstructive airway disease; asthma; chronic bronchitis; eosinophila;
KW adult respiratory distress syndrome; ARDS; dyspnoea; emphysema; COPD;
KW COAD; chronic obstructive or pulmonary disease; pneumoconiosis;
KW eosinophil related disorder; bronchopulmonary aspergillosis;
KW Loffler's syndrome; polyarteritis nodosa; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200155214-A2.
XX
PD 02-AUG-2001.
XX
PF 23-JAN-2001; 2001WO-EP000719.
XX
PR 25-JAN-2000; 2000US-00490616.
XX
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX
PI Whittaker PA, Jones SJ, Hanley MT;
XX
DR WPI; 2001-457719/49.
XX
PT Novel polypeptide AAG6 useful for treating an inflammatory or obstructive
PT airways disease, e.g., asthma.
XX
PS Example 2; Page 26; 62pp; English.
XX
CC The invention relates to human asthma-associated gene designated as AAG6.
CC AAG6 is used in the diagnosis, prognosis and treatment of inflammatory or
CC obstructive airway diseases such as asthma, adult respiratory distress
CC syndrome (ARDS), chronic obstructive or pulmonary disease (COPD or COAD),
CC chronic bronchitis, dyspnoea, emphysema and pneumoconiosis. AAG6 is also
CC used in the treatment of eosinophil related disorders such as
CC eosinophila, eosinophilic pneumonia, Loffler's syndrome, bronchopulmonary
CC aspergillosis, polyarteritis nodosa and eosinophilic granuloma. AAG6 DNA
CC is useful in gene therapy. The present sequence is a PCR primer used for
CC amplifying human AAG6 DNA
XX
SQ Sequence 19 BP; 2 A; 5 C; 6 G; 6 T; 0 U; 0 Other;

Query Match 58.0%; Score 11.6; DB 4; Length 19;
Best Local Similarity 77.8%; Pred. No. 3.4e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GACCGCATAGACTTCTCA 18
||| ||| ||| |||||
Db 18 GACGGCAGCGACATCTCA 1

RESULT 27
ABK41518
ID ABK41518 standard; DNA; 20 BP.
XX
AC ABK41518;
XX
DT 21-MAY-2002 (first entry)
XX
DE Human CTNNA3 exon-specific upper PCR primer #5.
XX
KW Human; mouse; alpha-catenin; primer; ss; cytostatic; antiinfertility;
KW cadherin-catenin related pathway; heart testis; cancer; gene therapy;
KW cadherin-catenin related disease; specifically dilated cardiomyopathy;
KW cardiomyopathy; male infertility; CTNNA3; PCR; alpha T-catenin.
XX
OS Homo sapiens.
XX

```
PN   WO200204636-A1.
XX
PD   17-JAN-2002.
XX
PF   28-JUN-2001; 2001WO-EP007392.
XX
PR   12-JUL-2000; 2000EP-00202472.
PR   14-JUL-2000; 2000US-0218309P.
XX
PA   (VLAA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
XX
PI   Van Roy F,  Goossens S,  Janssens B,  Vanpoucke G;
XX
DR   WPI; 2002-171717/22.
XX
PT   New alpha catenin polypeptides and polynucleotides encoding them, useful
PT   for predicting, diagnosing or treating cadherin-catenin related diseases,
PT   particularly cardiomyopathies, cancer and male infertility.
XX
PS   Example; Page 35; 132pp; English.
XX
CC   The invention relates to human and mouse alpha-catenin polypeptides and
CC   their associated polynucleotides. The polypeptides and related antibodies
CC   are useful for modulating the cadherin-catenin related pathway in
CC   selected organs, such as the heart and testis. The nucleic acids and the
CC   antibodies are useful in the diagnosis and/or prediction of the
CC   likelihood of developing cadherin-catenin related diseases. The nucleic
CC   acids may also be used to predict the likelihood of developing cancer or
CC   in diagnosing cancer, and in gene therapy. The polypeptide, the nucleic
CC   acid or the antibody is useful in manufacturing a medicament for treating
CC   cadherin-catenin related diseases, such as cancer, cardiomyopathy,
CC   specifically dilated cardiomyopathy, and male infertility. Sequences
CC   ABK41510-ABK41599 represent PCR primers used to amplify DNA encoding
CC   human and mouse alpha-catenin polypeptides, including the CTNNA3 gene
CC   which encodes human alpha T-catenin
XX
SQ   Sequence 20 BP; 5 A; 5 C; 5 G; 5 T; 0 U; 0 Other;

  Query Match             58.0%;  Score 11.6;  DB 6;  Length 20;
  Best Local Similarity   77.8%;  Pred. No. 3.4e+04;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GACCGCATAGACTTCTCA 18
              ||| | | || |||||||
Db          2 GACTGAACAGGCTTCTCA 19


RESULT 28
ABS59713
ID   ABS59713 standard; DNA; 20 BP.
XX
AC   ABS59713;
XX
DT   05-NOV-2002  (first entry)
XX
DE   Human damage specific DNA binding protein 1 antisense oligonucleotide #5.
XX
KW   Antisense; cytostatic; hepatotrophic; antiinflammatory; virucide;
KW   Damage-specific DNA-binding protein 1; p127; cancer; human; ss;
KW   hyperproliferative disorder; haematopoietic cancer; hepatitis.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   modified_base   1. .20
FT                   /*tag=  a
FT                   /mod_base= m5c
FT                   /note= "All cytosines are 5-methyl cytosine"
FT   modified_base   1. .20
FT                   /*tag=  c
FT                   /mod_base= OTHER
FT                   /note= "OTHER= phosphorothioate backbone"
FT   modified_base   1. .5
FT                   /*tag=  b
FT                   /mod_base= OTHER
FT                   /note= "OTHER= 2'-O-methoxyethyl nucleotide"
FT   modified_base   16. .20
FT                   /*tag=  d
FT                   /mod_base= OTHER
FT                   /note= "OTHER= 2'-O-methoxyethyl nucleotide"
XX
PN   WO200246206-A1.
XX
PD   13-JUN-2002.
XX
PF   04-DEC-2001; 2001WO-US046485.
XX
PR   06-DEC-2000; 2000US-00731457.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Popoff I,  Wyatt JR;
XX
DR   WPI; 2002-599454/64.
XX
PT   Novel antisense compound targeted to nucleic acid molecule encoding
PT   Damage-specific DNA-binding protein 1, p127, useful for treating animal
PT   having disease associated with the protein such as liver cancer, or
PT   hepatitis.
XX
PS   Page 89; Claim 3; 121pp; English.
XX
CC   This invention relates to a novel antisense compound 8 to 50 nucleobases
CC   in length targeted to nucleic acid molecule encoding Damage-specific DNA-
CC   binding protein 1, p127 where the antisense compound specifically
CC   hybridises with and inhibits expression of the damage specific DNA
CC   binding protein-1 gene. The compounds of the invention may be used in
CC   antisense therapy as an inhibitor of expression of Damage-specific DNA-
CC   binding protein 1, p127. The antisense compounds of the invention are
CC   useful for inhibiting the expression of damage specific DNA binding
CC   protein 1, p127 in cells or tissues and are also useful for treating an
CC   animal having a disease or condition associated with expression of p127,
CC   such as a hyperproliferative disorder (e.g., cancer such as breast, skin,
CC   liver, or haematopoietic cancer), or hepatitis, by inhibiting the
CC   expression of p127. All antisense oligonucleotides of the invention are
CC   chimeric oligonucleotides (gapmers) 20 nucleotides in length, composed of
CC   a central gap region consisting of ten 2'-deoxynucleotides, which are
CC   flanked on both sides (5' and 3' directions) by five- nucleotide wings.
CC   The wings are composed of 2'-methoxyethyl (2'-MOE) nucleotides. The
CC   internucleoside (backbone) linkages are phosphorothioate (P=S) throughout
CC   the oligonucleotide and all cytidine residues are 5-methylcytidines. The
CC   present sequence represents a damage-specific DNA binding protein 1, p127
CC   antisense oligonucleotide of the invention
XX
SQ   Sequence 20 BP; 7 A; 5 C; 2 G; 6 T; 0 U; 0 Other;

  Query Match             58.0%;  Score 11.6;  DB 6;  Length 20;
  Best Local Similarity   77.8%;  Pred. No. 3.4e+04;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GACCGCATAGACTTCTCA 18
              |||| ||||||  ||| |
Db          2 GACCACATAGATCTCTAA 19


RESULT 29
ADK78853/c
ID   ADK78853 standard; DNA; 20 BP.
XX
AC   ADK78853;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Chimeric phosphorothioate oligonucleotide to target Nav1.3 #6187.
XX
```

KW Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
KW diabetic neuropathy; arthritic pain; migraine headache;
KW infantile epilepsy; ataxia; ss.
XX
OS Synthetic.
XX
PN WO2004016754-A2.
XX
PD 26-FEB-2004.
XX
PF 14-AUG-2003; 2003WO-US025465.
XX
PR 14-AUG-2002; 2002US-0403416P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Roberds SL;
XX
DR WPI; 2004-203785/19.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT Nav1.3, useful for useful for treating a disease or condition associated
PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
PT disorder, or ataxia.
XX
PS Claim 4; SEQ ID NO 6187; 417pp; English.
XX
CC The present invention relates to an antisense compound targeted to a
CC nucleic acid molecule encoding Nav1.3, where the antisense compound
CC specifically hybridizes with and inhibits the expression of Nav1.3. The
CC compound and composition are useful for treating a disease or condition
CC associated with Nav1.3, e.g. pain including but not limited to
CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
CC pain from burns, migraine headache, cluster headache, mild-to-moderate
CC headache; seizure disorder such as childhood seizure disorder, including
CC but not limited to neonatal or infantile epilepsy; or ataxia. The present
CC sequence represents a chimeric phosphorothioate oligonucleotide with
CC 2'MOE wings and a deoxy gap. Used during the antisense inhibition of
CC human Nav1.3 expression, the oligonucleotides are designed to target
CC different regions of the human Nav1.3 RNA.
XX
SQ Sequence 20 BP; 7 A; 5 C; 3 G; 5 T; 0 U; 0 Other;

Query Match 58.0%; Score 11.6; DB 12; Length 20;
Best Local Similarity 77.8%; Pred. No. 3.4e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GACCGCATAGACTTCTCA 18
||| || |||| || |||
Db 20 GACTGCTTAGAGTTTTCA 3

RESULT 30
ADK78455/c
ID ADK78455 standard; DNA; 20 BP.
XX
AC ADK78455;
XX
DT 20-MAY-2004 (first entry)
XX
DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #5789.
XX
KW Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
KW diabetic neuropathy; arthritic pain; migraine headache;
KW infantile epilepsy; ataxia; ss.
XX
OS Synthetic.
XX
PN WO2004016754-A2.
XX
PD 26-FEB-2004.
XX
PF 14-AUG-2003; 2003WO-US025465.
XX
PR 14-AUG-2002; 2002US-0403416P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Roberds SL;
XX
DR WPI; 2004-203785/19.
XX
PT New antisense compound targeted to a nucleic acid molecule encoding
PT Nav1.3, useful for useful for treating a disease or condition associated
PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
PT disorder, or ataxia.
XX
PS Claim 4; SEQ ID NO 5789; 417pp; English.
XX
CC The present invention relates to an antisense compound targeted to a
CC nucleic acid molecule encoding Nav1.3, where the antisense compound
CC specifically hybridizes with and inhibits the expression of Nav1.3. The
CC compound and composition are useful for treating a disease or condition
CC associated with Nav1.3, e.g. pain including but not limited to
CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
CC pain from burns, migraine headache, cluster headache, mild-to-moderate
CC headache; seizure disorder such as childhood seizure disorder, including
CC but not limited to neonatal or infantile epilepsy; or ataxia. The present
CC sequence represents a chimeric phosphorothioate oligonucleotide with
CC 2'MOE wings and a deoxy gap. Used during the antisense inhibition of
CC human Nav1.3 expression, the oligonucleotides are designed to target
CC different regions of the human Nav1.3 RNA.
XX
SQ Sequence 20 BP; 7 A; 4 C; 3 G; 6 T; 0 U; 0 Other;

Query Match 58.0%; Score 11.6; DB 12; Length 20;
Best Local Similarity 77.8%; Pred. No. 3.4e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GACCGCATAGACTTCTCA 18
||| || |||| || |||
Db 19 GACTGCTTAGAGTTTTCA 2

RESULT 31
ADK78852/c
ID ADK78852 standard; DNA; 20 BP.
XX
AC ADK78852;
XX
DT 20-MAY-2004 (first entry)
XX
DE Chimeric phosphorothioate oligonucleotide to target Nav1.3 #6186.
XX
KW Nav1.3; Analgesic; Nootropic; Neuroprotective; post-herpetic neuralgia;
KW diabetic neuropathy; arthritic pain; migraine headache;
KW infantile epilepsy; ataxia; ss.
XX
OS Synthetic.
XX
PN WO2004016754-A2.
XX
PD 26-FEB-2004.
XX
PF 14-AUG-2003; 2003WO-US025465.
XX
PR 14-AUG-2002; 2002US-0403416P.
XX
PA (PHAA) PHARMACIA CORP.
XX
PI Roberds SL;
XX
DR WPI; 2004-203785/19.
XX

PT New antisense compound targeted to a nucleic acid molecule encoding
PT Nav1.3, useful for useful for treating a disease or condition associated
PT with Nav1.3, e.g. pain, seizure disorder such as childhood seizure
PT disorder, or ataxia.
XX
PS Claim 4; SEQ ID NO 6186; 417pp; English.
XX
CC The present invention relates to an antisense compound targeted to a
CC nucleic acid molecule encoding Nav1.3, where the antisense compound
CC specifically hybridizes with and inhibits the expression of Nav1.3. The
CC compound and composition are useful for treating a disease or condition
CC associated with Nav1.3, e.g. pain including but not limited to
CC neuropathic pain, post-herpetic neuralgia, chronic pain, lower back pain,
CC diabetic neuropathy, trigeminal neuropathy, arthritic pain, acute pain,
CC pain from burns, migraine headache, cluster headache, mild-to-moderate
CC headache; seizure disorder such as childhood seizure disorder, including
CC but not limited to neonatal or infantile epilepsy; or ataxia. The present
CC sequence represents a chimeric phosphorothioate oligonucleotide with
CC 2'MOE wings and a deoxy gap. Used during the antisense inhibition of
CC human Nav1.3 expression, the oligonucleotides are designed to target
CC different regions of the human Nav1.3 RNA.
XX
SQ Sequence 20 BP; 7 A; 4 C; 4 G; 5 T; 0 U; 0 Other;

Query Match 58.0%; Score 11.6; DB 12; Length 20;
Best Local Similarity 77.8%; Pred. No. 3.4e+04;
Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 GACCGCATAGACTTCTCA 18
||| || |||| || |||
Db 18 GACTGCTTAGAGTTTTCA 1

RESULT 32
AAT55168
ID AAT55168 standard; RNA; 15 BP.
XX
AC AAT55168;
XX
DT 25-MAR-2003 (revised)
DT 22-APR-1997 (first entry)
XX
DE Human relA hammerhead ribozyme target sequence (nt. position 1704).
XX
KW Enzymatic nucleic acid; ribozyme; trans cleavage; inhibition;
KW gene expression; downregulation; interleukin-5; IL-5; ICAM-1;
KW intercellular adhesion molecule; rel A; tumour necrosis factor;
KW TNF-alpha; respiratory syncytial virus; RSV; bcr-abl; oncogene;
KW translocation; chronic myelogenous leukaemia; CML; cancer;
KW Philadelphia chromosome; inflammation; autoimmune disease;
KW atherosclerosis; myocardial infarction; stroke; restenosis;
KW transplant rejection; rheumatoid arthritis; psoriasis;
KW myocardial ischaemia; Kawasaki disease; septic shock; HIV;
KW human immunodeficiency virus; acquired immune deficiency syndrome; AIDS;
KW ss.
XX
OS Homo sapiens.
XX
PN WO9523225-A2.
XX
PD 31-AUG-1995.
XX
PF 23-FEB-1995; 95WO-IB000156.
XX
PR 23-FEB-1994; 94US-00201109.
PR 29-MAR-1994; 94US-00218934.
PR 04-APR-1994; 94US-00222795.
PR 07-APR-1994; 94US-00224483.
PR 15-APR-1994; 94US-00227958.
PR 15-APR-1994; 94US-00228041.
PR 18-MAY-1994; 94US-00245736.
PR 06-JUL-1994; 94US-00271280.
PR 15-AUG-1994; 94US-00291932.
PR 16-AUG-1994; 94US-00291433.
PR 17-AUG-1994; 94US-00292620.
PR 19-AUG-1994; 94US-00293520.
PR 02-SEP-1994; 94US-00300000.
PR 08-SEP-1994; 94US-00303039.
PR 23-SEP-1994; 94US-00311486.
PR 23-SEP-1994; 94US-00311749.
PR 28-SEP-1994; 94US-00314397.
PR 03-OCT-1994; 94US-00316771.
PR 07-OCT-1994; 94US-00319492.
PR 11-OCT-1994; 94US-00321993.
PR 04-NOV-1994; 94US-00334847.
PR 10-NOV-1994; 94US-00337608.
PR 28-NOV-1994; 94US-00345516.
PR 16-DEC-1994; 94US-00357577.
PR 23-DEC-1994; 94US-00363233.
PR 30-JAN-1995; 95US-00380734.
XX
PA (RIBO-) RIBOZYME PHARM INC.
XX
PI Stinchcomb DT, Chowrira B, Direnzo A, Draper KG, Dudycz LW;
PI Grimm S, Karpeisky A, Kisich K, Matulic-Adamic J, Mcswiggen JA;
PI Modak A, Pavco P, Beigleman L, Sullivan SM, Sweedler D, Thompson JD;
PI Tracz D, Usman N, Wincott FE, Woolf T;
XX
DR WPI; 1995-351090/45.
XX
PT Ribozymes having modified bases and methods for producing them - for use
PT in inhibiting disease related genes.
XX
PS Claim 2; Page 229; 407pp; English.
XX
CC The present sequence represents a preferred target sequence for an
CC enzymatic nucleic acid (i.e. a ribozyme) which cleaves relA mRNA at the
CC nucleotide base position indicated in the DE line. The relA gene product
CC is a subunit of the transcriptional regulator NF-kappaB and is implicated
CC specifically in the induction of inflammatory responses. Regions of the
CC mRNA that do not form secondary folding structures and that contain
CC potential hammerhead and hairpin ribozyme cleavage sites were identified
CC by computer analysis. Ribozymes directed against these mRNA sequences
CC were designed and synthesised with modifications that improve their
CC nuclease resistance. The ribozymes are designed to cleave the target
CC sequences and thereby inhibit relA expression, making them potentially
CC useful for treating rheumatoid arthritis, restenosis and asthma as well
CC as for increasing tolerance to transplanted tissues. The potential
CC immunosuppressive properties of a ribozyme that cleaves relA mRNA means
CC that uses are limited to local delivery, acute indications or ex vivo
CC treatment. (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 15 BP; 3 A; 5 C; 3 G; 0 T; 4 U; 0 Other;

Query Match 57.0%; Score 11.4; DB 2; Length 15;
Best Local Similarity 61.5%; Pred. No. 4.2e+04;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ATAGACTTCTCAG 19
|: |||::|:|||
Db 1 AUGGACUUCUCAG 13

RESULT 33
ACA09062
ID ACA09062 standard; RNA; 17 BP.
XX
AC ACA09062;
XX
DT 03-JUN-2003 (first entry)
XX
DE NFKB sub-unit modulating amberzyme substrate #225.
XX
KW Enzymatic nucleic acid; nuclear factor kappa B; NFKB; inozyme; zinzyme;
KW G-cleaver; amberzyme; cancer; REL-A activity; breast cancer; human;
KW lung cancer; prostate cancer; colorectal cancer; brain cancer;

KW oesophageal cancer; stomach cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; head and neck cancer; ovarian cancer; melanoma;
KW lymphoma; glioma; multidrug resistant cancer; REL-A-specific inhibitor;
KW chemotherapy; paclitaxel; docetaxel; cisplatin; methotrexate;
KW cyclophosphamide; doxorubin; fluorouracil carboplatin; edatrexate;
KW gemcitabine; radiation therapy; inflammatory disease; asthma; diabetes;
KW rheumatoid arthritis; restenosis; Crohn's disease; obesity; ischaemia;
KW gene therapy; autoimmune disease; lupus; multiple sclerosis; sepsis;
KW transplant/graft rejection; reperfusion injury; glomerulonephritis;
KW allergic airway inflammation; inflammatory bowel disease; infection; ss.
XX
OS Homo sapiens.
XX
PN US2002177568-A1.
XX
PD 28-NOV-2002.
XX
PF 23-MAY-2001; 2001US-00864785.
XX
PR 07-DEC-1992; 92US-00987132.
PR 18-MAY-1994; 94US-00245466.
PR 15-AUG-1994; 94US-00291932.
PR 23-DEC-1996; 96US-00777916.
XX
PA (STIN/) STINCHCOMB D T.
PA (MCSW/) MCSWIGGEN J.
PA (DRAP/) DRAPER K G.
XX
PI Stinchcomb DT, Mcswiggen J, Draper KG;
XX
DR WPI; 2003-340953/32.
XX
PT Novel enzymatic nucleic acid molecules which down regulates expression of
PT a sequence encoding a subunit of nuclear factor kappa B useful for
PT treating cancer, inflammatory disorders and autoimmune diseases.
XX
PS Claim 3; Page 55; 72pp; English.
XX
CC The invention describes an enzymatic nucleic acid molecule (I) which down
CC regulates expression of a sequence encoding a subunit of nuclear factor
CC kappa B (NFKB), where (I) is an inozyme, zinzyme, G-cleaver or amberzyme
CC configuration. The enzymatic nucleic acid molecule is adapted to treat
CC cancer and is useful for down-regulating REL-A activity in a cell, for
CC treating a patient having a condition associated with the level of REL-A.
CC (I) is useful for cleaving RNA comprising a sequence of REL-A gene, in
CC the presence of a divalent cation, especially Mg^2^+. The enzymatic and
CC antisense nucleic acid molecules are useful for treating breast, lung,
CC prostate, colorectal, brain, oesophageal, stomach, bladder, pancreatic,
CC cervical, head and neck, ovarian cancer, melanoma, lymphoma, glioma or
CC multidrug resistant cancer. The method involves use of other drug
CC therapies such as monoclonal antibodies, REL-A-specific inhibitors or
CC chemotherapy including paclitaxel, docetaxel, cisplatin, methotrexate,
CC cyclophosphamide, doxorubin, fluorouracil carboplatin, edatrexate,
CC gemcitabine or radiation therapy. The enzymatic and antisense nucleic
CC acid molecules are also useful for treating inflammatory disease such as
CC rheumatoid arthritis, restenosis, asthma, Crohn's disease, diabetes,
CC obesity, autoimmune disease, lupus, multiple sclerosis, transplant/graft
CC rejection, gene therapy applications, ischaemia/reperfusion injury
CC (central nervous system (CNS) and myocardial), glomerulonephritis,
CC sepsis, allergic airway inflammation, inflammatory bowel disease or
CC infection. This sequence represents the substrate of a novel enzymatic
CC nucleic acid molecule
XX
SQ Sequence 17 BP; 4 A; 5 C; 4 G; 0 T; 4 U; 0 Other;

Query Match 57.0%; Score 11.4; DB 8; Length 17;
Best Local Similarity 61.5%; Pred. No. 4.3e+04;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 6 CATAGACTTCTCA 18
||: |||::|:||
Db 5 CAUGGACUUCUCA 17

RESULT 34
ADI47785/c
ID ADI47785 standard; DNA; 17 BP.
XX
AC ADI47785;
XX
DT 15-APR-2004 (first entry)
XX
DE Human tumour suppression/reversion-related DNA sequence SeqID288.
XX
KW tumour suppression; tumour reversion; apoptosis; virus resistance;
KW cytostatic; virucide; neuroprotective; nootropic; neuroleptic; probe;
KW primer; PCR; gene chip; antisense; viral disease; tumour;
KW cell degeneration; cancer; Alzheimer's disease; schizophrenia; ds; human.
XX
OS Homo sapiens.
XX
PN WO2003025177-A2.
XX
PD 27-MAR-2003.
XX
PF 17-SEP-2002; 2002WO-IB004523.
XX
PR 17-SEP-2001; 2001FR-00011980.
XX
PA (MOLE-) MOLECULAR ENGINES LAB.
XX
PI Telerman A, Amson R, Tuijnder M;
XX
DR WPI; 2003-313354/30.
XX
PT New isolated nucleic acid, useful for treating viral diseases associated
PT with tumors and cell degeneration, also related polypeptides, antibodies
PT and transfected cells.
XX
PS Disclosure; SEQ ID NO 288; 30pp; French.
XX
CC This invention relates to novel isolated nucleic acid sequences involved
CC in the phenomena of tumour suppression, tumour reversion, apoptosis
CC and/or resistance to viruses. The invention may be useful for the
CC development of compounds with a cytostatic, virucide, neuroprotective,
CC nootropic or neuroleptic activity. The DNA sequences may be useful as
CC probes and primers for detecting, indentifying, quantifying and/or
CC amplifying nucleic acid, for example as one component of a gene chip, in
CC vitro as antisense reagents and for production of recombinant
CC polypeptides. The invention may therefore be useful for preparation of
CC pharmaceuticals for prevention and/or treatment of viral diseases that
CC are characterised by development of tumours or cell degeneration,
CC specifically cancer but also Alzheimer's disease and schizophrenia. The
CC present sequence is that of a nucleic acid sequence of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/publishedpct_sequences
XX
SQ Sequence 17 BP; 6 A; 4 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 57.0%; Score 11.4; DB 10; Length 17;
Best Local Similarity 92.3%; Pred. No. 4.3e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 TAGACTTCTCAGA 20
|||| ||||||||
Db 15 TAGAGTTCTCAGA 3

RESULT 35
AAA83653/c
ID AAA83653 standard; DNA; 19 BP.
XX
AC AAA83653;
XX
DT 04-DEC-2000 (first entry)

XX
DE cdk-we-hu ribozyme binding site #128.
XX
KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX
OS Mammalia.
XX
PN WO200032765-A2.
XX
PD 08-JUN-2000.
XX
PF 06-DEC-1999; 99WO-US028772.
XX
PR 04-DEC-1998; 98US-0110954P.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX
DR WPI; 2000-412314/35.
XX
PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1.
XX
PS Disclosure; Page 65; 109pp; English.
XX
CC The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX
SQ Sequence 19 BP; 6 A; 3 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 57.0%; Score 11.4; DB 3; Length 19;
Best Local Similarity 92.3%; Pred. No. 4.3e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCATAGACTTCTC 17
||||| |||||||
Db 13 GCATATACTTCTC 1

RESULT 36
AAA83652/c
ID AAA83652 standard; DNA; 19 BP.
XX
AC AAA83652;
XX
DT 04-DEC-2000 (first entry)
XX
DE cdk-we-hu ribozyme binding site #127.
XX
KW Ribozyme; hairpin; hammerhead; gene therapy; vasotropic; restenosis; ss.
XX
OS Mammalia.
XX
PN WO200032765-A2.
XX
PD 08-JUN-2000.
XX
PF 06-DEC-1999; 99WO-US028772.
XX
PR 04-DEC-1998; 98US-0110954P.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Tritz R, Welch PJ, Barber JR, Robbins JM;
XX
DR WPI; 2000-412314/35.
XX
PT New hairpin and hammerhead ribozyme for inhibiting restenosis, cleaves
PT RNA encoding a cyclin or cell-cycle dependent kinase other than CDK1,
PT PCNA and Cyclin B1.
XX
PS Disclosure; Page 65; 109pp; English.
XX
CC The present invention relates to a hairpin or hammerhead ribozyme,
CC designed to cleave RNA encoding a cyclin or cell-cycle dependent kinase
CC other than cell-cycle dependent kinases CDK1, PCNA and Cyclin B1.
CC Representative examples of ribozyme recognition sites are given in
CC AAA82415 to AAA86787. The ribozyme of the invention is useful for
CC inhibiting restenosis by introduction of the ribozyme into cells. The
CC ribozyme is resistant to endonuclease activity and hence is efficient in
CC restenosis treatment
XX
SQ Sequence 19 BP; 7 A; 2 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 57.0%; Score 11.4; DB 3; Length 19;
Best Local Similarity 92.3%; Pred. No. 4.3e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCATAGACTTCTC 17
||||| |||||||
Db 15 GCATATACTTCTC 3

RESULT 37
AAH58814/c
ID AAH58814 standard; DNA; 19 BP.
XX
AC AAH58814;
XX
DT 10-SEP-2001 (first entry)
XX
DE Cdk-we-hu ribozyme binding site SEQ ID NO:1238.
XX
KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW recognition site; target; ribozyme binding site; eye disease; vulnerary;
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW sickle cell retinopathy; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200130362-A2.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-US029500.
XX
PR 26-OCT-1999; 99US-0161532P.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Robbins JM, Tritz R;
XX
DR WPI; 2001-300427/31.
XX
PT Treating proliferative skin or eye diseases and scarring, using ribozymes
PT that cleave RNA encoding cytokines involved in inflammation, matrix
PT metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
PS Example 1; Page 162; 408pp; English.
XX
CC The present invention describes a method for treating a proliferative

CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC ophthalmological, vulnerary, keratolytic and virucide activities, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative skin
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 19 BP; 7 A; 2 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 57.0%; Score 11.4; DB 5; Length 19;
Best Local Similarity 92.3%; Pred. No. 4.3e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCATAGACTTCTC 17
||||| |||||||
Db 15 GCATATACTTCTC 3

RESULT 38
AAH58815/c
ID AAH58815 standard; DNA; 19 BP.
XX
AC AAH58815;
XX
DT 10-SEP-2001 (first entry)
XX
DE Cdk-we-hu ribozyme binding site SEQ ID NO:1239.
XX
KW Human; ribozyme therapy; hairpin ribozyme; hammerhead ribozyme;
KW recognition site; target; ribozyme binding site; eye disease; vulnerary;
KW proliferative disease; skin disease; psoriasis; diabetic retinopathy;
KW cytokine; inflammation; cell-cycle dependent kinase; cyclin; MMP;
KW matrix metalloproteinase; growth factor; reductase; scarring; cytostatic;
KW antipsoriatic; dermatological; antiseborrheic; antidiabetic; virucide;
KW antisickling; ophthalmological; keratolytic; gene therapy; viral wart;
KW atopic dermatitis; actinic keratosis; squamous cell carcinoma;
KW basal cell carcinoma; seborrheic wart; vitreoretinopathy; scar;
KW sickle cell retinopathy; ss.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200130362-A2.
XX
PD 03-MAY-2001.
XX
PF 26-OCT-2000; 2000WO-US029500.
XX
PR 26-OCT-1999; 99US-0161532P.
XX
PA (IMMU-) IMMUSOL INC.
XX
PI Robbins JM, Tritz R;
XX
DR WPI; 2001-300427/31.
XX
PT Treating proliferative skin or eye diseases and scarring, using ribozymes
PT that cleave RNA encoding cytokines involved in inflammation, matrix
PT metalloproteinases, growth factors and cell-cycle dependent kinases.
XX
PS Example 1; Page 162; 408pp; English.
XX
CC The present invention describes a method for treating a proliferative
CC skin or eye disease and scarring. The method involves administering a
CC ribozyme (I) which cleaves RNA encoding a cytokine involved in
CC inflammation, matrix metalloproteinase (MMP), cyclin, cell-cycle
CC dependent kinase, growth factor or a reductase, or administering a
CC nucleic acid molecule (II) comprising a promoter operably linked to a
CC nucleic acid segment encoding (I). (I) can have antipsoriatic,
CC dermatological, cytostatic, antiseborrheic, antidiabetic, antisickling,
CC ophthalmological, vulnerary, keratolytic and virucide activities, and
CC cleaves RNA encoding cytokine involved in inflammation. (I) can be used
CC in gene therapy. (I) and (II) are useful for treating proliferative skin
CC diseases such as psoriasis, atopic dermatitis, actinic keratosis,
CC squamous or basal cell carcinoma and viral or seborrheic wart. They can
CC also be used for treating proliferative eye diseases such as diabetic
CC retinopathy, vitreoretinopathy, sickle cell retinopathy, retinopathy of
CC prematurity and retinal detachment, and for treating and preventing
CC scarring such as keloid, adhesion and hypertrophic or hypertrophic burn
CC scar. AAH57577 to AAH62099 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 19 BP; 6 A; 3 C; 5 G; 5 T; 0 U; 0 Other;

Query Match 57.0%; Score 11.4; DB 5; Length 19;
Best Local Similarity 92.3%; Pred. No. 4.3e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCATAGACTTCTC 17
||||| |||||||
Db 13 GCATATACTTCTC 1

RESULT 39
ADQ61886/c
ID ADQ61886 standard; RNA; 19 BP.
XX
AC ADQ61886;
XX
DT 09-SEP-2004 (first entry)
XX
DE Anti-KCNH1 siRNA SEQ ID NO:1588.
XX
KW ss; siRNA; gene silencing; Bcl-2; optimised; short interfering RNA;
KW RNA interference.
XX
OS Synthetic.
XX
PN WO2004045543-A2.
XX
PD 03-JUN-2004.
XX
PF 14-NOV-2003; 2003WO-US036787.
XX
PR 14-NOV-2002; 2002US-0426137P.
PR 10-SEP-2003; 2003US-0502050P.
XX
PA (DHAR-) DHARMACON INC.
XX
PI Anastasia K, Angela R, Devin L, William M, Stephen S;
XX
DR WPI; 2004-420527/39.
XX
PT Selecting siRNA by selecting an siRNA molecule of 19-25 nucleoside bases
PT by selecting a target gene and measuring the functionality of the
PT nucleotide sequences that are complementary to a stretch of nucleotides
PT of the target sequence.
XX
PS Example 12; SEQ ID NO 1588; 199pp; English.
XX
CC The invention relates to a novel method for selecting siRNA (short
CC interfering RNA) comprising selecting an siRNA molecule of 19-25
CC nucleoside bases by selecting a target gene and measuring the
CC functionality of sequences of 19-25 nucleotides in length that are

CC substantially complementary to a stretch of nucleotides of the target
CC sequence, where the functionality is dependent upon non-target specific
CC criteria. Also claimed are methods for gene-silencing, developing an
CC siRNA algorithm for selecting siRNA, selecting an siRNA with improved
CC functionality, selecting hyperfunctional siRNA, an siRNA molecule
CC effective at silencing Bcl-2, and a kit for gene silencing comprising the
CC siRNA. The siRNA molecule comprises a sequence substantially similar to a
CC sequence consisting of GGGAGAUAGUGAUGAAGUA; GAAGUACAUCCAUUAUAAG;
CC GUACGACAACCGGGAGAUA; AGAUAGUGAUGAAGUACAU; UGAAGACUCUGCUCAGUUU;
CC CAUGCGGCCUCUGUUUGA; UGCGGCCUCUGUUUGAUUU; GAGAUAGUGAUGAAGUACA;
CC GGAGAUAGUGAUGAAGUAC; and GAAGACUCUGCUCAGUUUG. The siRNA molecule
CC comprises a sense strand and an anti-sense strand. The siRNA molecule
CC comprises a hairpin. The siRNA molecule comprises between 18 and 30 base
CC pairs. The kit comprises at least two siRNA, comprising a first optimised
CC siRNA and a second optimised siRNA. The method is useful in selecting
CC siRNA for generating a gene silencing reagent. The present sequence is
CC used in the exemplification of the invention.
XX
SQ Sequence 19 BP; 6 A; 2 C; 5 G; 0 T; 6 U; 0 Other;

Query Match 57.0%; Score 11.4; DB 12; Length 19;
Best Local Similarity 92.3%; Pred. No. 4.3e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ATAGACTTCTCAG 19
||||||.||||||
Db 14 ATAGACCTCTCAG 2

RESULT 40
AAX77133/c
ID AAX77133 standard; DNA; 20 BP.
XX
AC AAX77133;
XX
DT 03-AUG-1999 (first entry)
XX
DE PCR primer 92-5'.
XX
KW Cellular senescence; modulator; GC6 gene; senescent gene expression;
KW pGC6; human; PCR primer; ss.
XX
OS Synthetic.
XX
PN WO9925878-A2.
XX
PD 27-MAY-1999.
XX
PF 19-NOV-1998; 98WO-US024996.
XX
PR 19-NOV-1997; 97US-00974180.
XX
PA (GERO-) GERON CORP.
XX
PI Funk W;
XX
DR WPI; 1999-347496/29.
XX
PT New human GC6 gene, useful for identifying agents for treating diseases
PT and/or conditions associated with cell senescence.
XX
PS Example 5; Page 74; 79pp; English.
XX
CC The invention relates to methods for modulating and identifying cellular
CC senescence. Recombinant expression vectors comprising a recombinant
CC polynucleotide corresponding to a polynucleotide in a human GC6 gene, are
CC useful for altering senescent gene expression. The vectors and host cells
CC comprising the vectors are useful for identifying agents that prevent or
CC modulate senescent gene expression. The polynucleotides are useful for
CC producing the protein, pGC6 and nucleic acid derivatives. The proteins
CC encoded are useful for raising antibodies specific for pGC6, which are
CC useful for isolating pGC6, and for detecting cells comprising pGC6 in
CC complex cell mixtures. The characterization of the polynucleotides enable
CC the identification of therapeutic agents that identify and distinguish
CC between young and senescent cells. This enables treatment of aging
CC diseases induced or exacerbated by cellular senescence
XX
SQ Sequence 20 BP; 7 A; 6 C; 4 G; 3 T; 0 U; 0 Other;

Query Match 57.0%; Score 11.4; DB 2; Length 20;
Best Local Similarity 92.3%; Pred. No. 4.4e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCATAGACTTCTC 17
||||.|||||||
Db 13 GCATTGACTTCTC 1

Search completed: August 12, 2005, 11:15:32
Job time : 244 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 12, 2005, 11:05:14 ; Search time 96 Seconds
(without alignments)
340.891 Million cell updates/sec

Title: US-09-743-825-10
Perfect score: 20
Sequence: 1 gaccgcatagacttctcaga 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 401682

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued_Patents_NA:*
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	13.8	69.0	20	4	US-09-198-452A-2812	Sequence 2812, Ap
c	2	13.2	66.0	20	4	US-10-007-010-48	Sequence 48, Appl
c	3	12.2	61.0	18	3	US-09-106-038A-75	Sequence 75, Appl
	4	12	60.0	20	1	US-07-922-723A-60	Sequence 60, Appl
	5	12	60.0	20	1	US-07-799-828C-60	Sequence 60, Appl
	6	12	60.0	20	2	US-07-952-277A-60	Sequence 60, Appl
	7	12	60.0	20	3	US-09-038-637-113	Sequence 113, App
c	8	11.8	59.0	18	1	US-08-716-459-1	Sequence 1, Appli
	9	11.8	59.0	20	1	US-08-819-912-8	Sequence 8, Appli
	10	11.4	57.0	15	1	US-08-291-932A-289	Sequence 289, App
c	11	11.4	57.0	17	3	US-08-434-511-4	Sequence 4, Appli
c	12	11.4	57.0	17	3	US-08-229-150-4	Sequence 4, Appli
c	13	11.4	57.0	17	6	5401629-5	Patent No. 5401629
c	14	11.4	57.0	17	6	5401629-5	Patent No. 5401629
c	15	11.4	57.0	19	4	US-09-696-791-1238	Sequence 1238, Ap
c	16	11.4	57.0	19	4	US-09-696-791-1239	Sequence 1239, Ap
c	17	11.4	57.0	20	3	US-08-974-180-35	Sequence 35, Appl
c	18	11.4	57.0	20	4	US-10-148-806-20	Sequence 20, Appl
	19	11.4	57.0	20	4	US-10-148-806-21	Sequence 21, Appl
	20	11.2	56.0	18	4	US-09-422-978-4697	Sequence 4697, Ap
	21	11.2	56.0	20	1	US-07-977-284A-113	Sequence 113, App
	22	11.2	56.0	20	2	US-08-256-426B-113	Sequence 113, App
c	23	11.2	56.0	20	3	US-09-249-730-204	Sequence 204, App
c	24	11.2	56.0	20	3	US-09-359-756-36	Sequence 36, Appl
c	25	11.2	56.0	20	4	US-09-198-452A-3744	Sequence 3744, Ap
c	26	11.2	56.0	20	4	US-09-249-247-204	Sequence 204, App
c	27	11.2	56.0	20	4	US-09-975-123-28	Sequence 28, Appl
c	28	11	55.0	18	4	US-09-544-398B-32	Sequence 32, Appl
c	29	11	55.0	18	4	US-09-544-398B-629	Sequence 629, App
c	30	11	55.0	18	4	US-09-543-771B-32	Sequence 32, Appl
c	31	11	55.0	18	4	US-09-543-771B-629	Sequence 629, App
	32	11	55.0	20	1	US-08-357-791-4	Sequence 4, Appli.
	33	10.8	54.0	15	3	US-09-081-646-202	Sequence 202, App
	34	10.8	54.0	15	3	US-09-081-646-743	Sequence 743, App
	35	10.8	54.0	18	4	US-09-124-398-5	Sequence 5, Appli
c	36	10.8	54.0	20	3	US-09-659-791A-37	Sequence 37, Appl
	37	10.6	53.0	17	3	US-08-985-162-399	Sequence 399, App
c	38	10.6	53.0	17	3	US-08-584-040-5340	Sequence 5340, Ap
c	39	10.6	53.0	17	4	US-09-371-772B-2242	Sequence 2242, Ap
	40	10.6	53.0	17	4	US-09-401-063-399	Sequence 399, App
c	41	10.6	53.0	17	4	US-09-685-664B-2242	Sequence 2242, Ap
	42	10.6	53.0	18	4	US-09-663-834A-48	Sequence 48, Appl
	43	10.6	53.0	19	3	US-09-113-309-6	Sequence 6, Appli
	44	10.6	53.0	19	3	US-09-521-109-6	Sequence 6, Appli
c	45	10.6	53.0	19	3	US-09-407-818-36	Sequence 36, Appl
	46	10.6	53.0	19	3	US-09-562-332-6	Sequence 6, Appli
c	47	10.6	53.0	20	3	US-09-067-284-6	Sequence 6, Appli
	48	10.6	53.0	20	3	US-09-178-973B-12	Sequence 12, Appl
	49	10.6	53.0	20	3	US-09-419-568F-12	Sequence 12, Appl
	50	10.6	53.0	20	3	US-09-354-243B-12	Sequence 12, Appl
	51	10.6	53.0	20	3	US-09-470-443-16	Sequence 16, Appl
c	52	10.6	53.0	20	4	US-09-305-856B-80	Sequence 80, Appl
c	53	10.6	53.0	20	4	US-09-422-978-9198	Sequence 9198, Ap
c	54	10.6	53.0	20	4	US-09-843-376-54	Sequence 54, Appl
	55	10.4	52.0	15	1	US-08-291-932A-290	Sequence 290, App
c	56	10.4	52.0	18	4	US-08-747-562-4	Sequence 4, Appli
c	57	10.4	52.0	19	4	US-09-422-978-11557	Sequence 11557, A
c	58	10.4	52.0	19	4	US-09-696-791-2106	Sequence 2106, Ap
c	59	10.4	52.0	20	2	US-08-680-326-19	Sequence 19, Appl
	60	10.4	52.0	20	3	US-09-658-687A-41	Sequence 41, Appl
c	61	10.4	52.0	20	4	US-09-198-452A-6604	Sequence 6604, Ap
c	62	10.4	52.0	20	4	US-09-601-144-10	Sequence 10, Appl
	63	10.2	51.0	16	4	US-09-744-154-7	Sequence 7, Appli
c	64	10.2	51.0	16	4	US-09-563-794B-76	Sequence 76, Appl
c	65	10.2	51.0	17	2	US-08-480-994-17	Sequence 17, Appl
c	66	10.2	51.0	17	2	US-08-616-844-17	Sequence 17, Appl
c	67	10.2	51.0	17	2	US-08-599-654-17	Sequence 17, Appl
c	68	10.2	51.0	17	2	US-08-485-573-17	Sequence 17, Appl
c	69	10.2	51.0	17	3	US-08-944-868A-17	Sequence 17, Appl
c	70	10.2	51.0	17	3	US-08-944-423A-17	Sequence 17, Appl
c	71	10.2	51.0	17	3	US-08-925-743-17	Sequence 17, Appl
c	72	10.2	51.0	17	3	US-08-944-496-17	Sequence 17, Appl
c	73	10.2	51.0	17	3	US-08-925-767-17	Sequence 17, Appl
c	74	10.2	51.0	17	4	US-09-866-108A-6243	Sequence 6243, Ap
c	75	10.2	51.0	17	4	US-09-866-108A-6244	Sequence 6244, Ap
c	76	10.2	51.0	17	4	US-09-866-108A-6245	Sequence 6245, Ap
	77	10.2	51.0	18	2	US-08-928-692-55	Sequence 55, Appl
	78	10.2	51.0	18	3	US-09-256-465-20	Sequence 20, Appl
	79	10.2	51.0	18	3	US-09-339-972-55	Sequence 55, Appl
c	80	10.2	51.0	18	4	US-09-422-978-8829	Sequence 8829, Ap
c	81	10.2	51.0	18	4	US-09-548-797B-130	Sequence 130, App
c	82	10.2	51.0	19	3	US-08-688-376-7	Sequence 7, Appli
c	83	10.2	51.0	19	4	US-08-705-477E-66	Sequence 66, Appl
c	84	10.2	51.0	19	4	US-09-585-174-20	Sequence 20, Appl
c	85	10.2	51.0	19	4	US-09-261-104-12	Sequence 12, Appl
c	86	10.2	51.0	19	4	US-09-696-791-4025	Sequence 4025, Ap
c	87	10.2	51.0	19	4	US-09-696-791-4026	Sequence 4026, Ap
c	88	10.2	51.0	19	4	US-09-696-791-4027	Sequence 4027, Ap
c	89	10.2	51.0	19	4	US-09-696-791-4028	Sequence 4028, Ap
c	90	10.2	51.0	20	2	US-08-669-284B-8	Sequence 8, Appli
c	91	10.2	51.0	20	3	US-09-078-317-7	Sequence 7, Appli
c	92	10.2	51.0	20	3	US-09-166-186-98	Sequence 98, Appl
	93	10.2	51.0	20	3	US-09-517-584A-64	Sequence 64, Appl
c	94	10.2	51.0	20	3	US-09-313-932-98	Sequence 98, Appl
c	95	10.2	51.0	20	3	US-09-313-932-445	Sequence 445, App
c	96	10.2	51.0	20	3	US-09-454-818-7	Sequence 7, Appli
c	97	10.2	51.0	20	3	US-09-420-786A-6	Sequence 6, Appli
c	98	10.2	51.0	20	3	US-09-518-914-36	Sequence 36, Appl
	99	10.2	51.0	20	3	US-09-658-679A-13	Sequence 13, Appl
	100	10.2	51.0	20	3	US-09-517-467B-119	Sequence 119, App

ALIGNMENTS

```
RESULT 1
US-09-198-452A-2812
; Sequence 2812, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, preve
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/09/198,452A
;  CURRENT FILING DATE:  1998-11-24
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 2812
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
US-09-198-452A-2812

  Query Match             69.0%;  Score 13.8;  DB 4;  Length 20;
  Best Local Similarity   88.2%;  Pred. No. 6e+02;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GACCGCATAGACTTCTC 17
              ||||||||| |||| ||
Db          3 GACCGCATAAACTTATC 19


RESULT 2
US-10-007-010-48/c
; Sequence 48, Application US/10007010
; Patent No. 6828151
; GENERAL INFORMATION:
;  APPLICANT: Alexander H. Borchers
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF HCK EXPRESSION
;  FILE REFERENCE: RTS-0345
;  CURRENT APPLICATION NUMBER: US/10/007,010
;  CURRENT FILING DATE:  2001-12-04
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 48
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-007-010-48

  Query Match             66.0%;  Score 13.2;  DB 4;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 1.3e+03;
  Matches   15;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 ACCGCATAGACTTCTCAG 19
              | | ||| ||||||||||
Db         20 AACTCATTGACTTCTCAG 3


RESULT 3
US-09-106-038A-75/c
; Sequence 75, Application US/09106038A
; Patent No. 6007995
;  GENERAL INFORMATION:
;    APPLICANT:  Brenda F. Baker and Lex M. Cowsert
;    TITLE OF INVENTION:  ANTISENSE MODULATION OF TNFR1
;    TITLE OF INVENTION:  EXPRESSION
;    NUMBER OF SEQUENCES:  91
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Isis Pharmaceuticals, Inc.
;      STREET:  2292 Faraday Avenue
;      CITY:  Carlsbad
;      STATE:  CA
;      COUNTRY:  U.S.A.
;      ZIP:  92008
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch disk, 1.44 Mb
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  Windows NT
;      SOFTWARE:  Microsoft Word 97
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/106,038A
;      FILING DATE:  June 26, 1998
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Laurel Spear Bernstein
;      REGISTRATION NUMBER:  37,280
;      REFERENCE/DOCKET NUMBER:  RTS-0004
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (760) 931-9200
;      TELEFAX:  (760) 603-3820
;  INFORMATION FOR SEQ ID NO:  75:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-106-038A-75

  Query Match             61.0%;  Score 12.2;  DB 3;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 4.2e+03;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 CGCATAGACTTCTCAGA 20
              |||  ||  |||||||||
Db         18 CGCCCAGTCTTCTCAGA 2


RESULT 4
US-07-922-723A-60
; Sequence 60, Application US/07922723A
; Patent No. 5369004
;  GENERAL INFORMATION:
;    APPLICANT:  Drs. Mihael H. Polymeropoulos
;    APPLICANT:  and Carl R. Merril
;    TITLE OF INVENTION:  FIVE HIGHLY INFORMATIVE
;    TITLE OF INVENTION:  REPEAT POLYMORPHIC DNA MARKERS
;    NUMBER OF SEQUENCES:  73
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lowe, Price, LeBlanc & Becker
;      STREET:  Suite 300, 99 Canal Center Plaza
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22314
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  DOS Text File
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/922,723A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  D.J. Mills
;      REGISTRATION NUMBER:  34506
;      REFERENCE/DOCKET NUMBER:  717081B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703 684 1111
;  INFORMATION FOR SEQ ID NO:  60:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20
```

```
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-922-723A-60

  Query Match             60.0%;  Score 12;  DB 1;  Length 20;
  Best Local Similarity   75.0%;  Pred. No. 5.5e+03;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GACCGCATAGACTTCTCAGA 20
              |||| || || ||  |||||
Db          1 GACCCCACAGCCTATTCAGA 20


RESULT 5
US-07-799-828C-60
; Sequence 60, Application US/07799828C
; Patent No. 5378602
;  GENERAL INFORMATION:
;    APPLICANT:  Drs. Carl R. Merril and
;    APPLICANT:  Mihael H. Polymeropoulos
;    TITLE OF INVENTION:  TWENTY SEVEN HIGHLY INFORMATIVE
;    TITLE OF INVENTION:  MICROSATELLITE REPEAT
;    TITLE OF INVENTION:  POLYMORPHIC DNA MARKERS
;    NUMBER OF SEQUENCES:  63
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lowe, Price, LeBlanc & Becker
;      STREET:  Suite 300, 99 Canal Center Plaza
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22314
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  DOS Text File
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/799,828C
;      FILING DATE:  19911127
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  D.J. Mills
;      REGISTRATION NUMBER:  34,506
;      REFERENCE/DOCKET NUMBER:  717081A
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703 684 1111
;  INFORMATION FOR SEQ ID NO:  60:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-799-828C-60

  Query Match             60.0%;  Score 12;  DB 1;  Length 20;
  Best Local Similarity   75.0%;  Pred. No. 5.5e+03;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GACCGCATAGACTTCTCAGA 20
              |||| || || ||  |||||
Db          1 GACCCCACAGCCTATTCAGA 20


RESULT 6
US-07-952-277A-60
; Sequence 60, Application US/07952277A
; Patent No. 5861504
;  GENERAL INFORMATION:
;    APPLICANT:  Drs. Mihael H. Polymeropoulos
;    APPLICANT:  and Carl R. Merril
;    TITLE OF INVENTION:  ELEVEN HIGHLY INFORMATIVE
;    TITLE OF INVENTION:  REPEAT POLYMORPHIC DNA MARKERS
;    NUMBER OF SEQUENCES:  85
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lowe, Price, LeBlanc & Becker
;      STREET:  Suite 300, 99 Canal Center Plaza
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22314
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  DOS Text File
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/952,277A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  D.J. Mills
;      REGISTRATION NUMBER:  34506
;      REFERENCE/DOCKET NUMBER:  717081C
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  703 684 1111
;  INFORMATION FOR SEQ ID NO:  60:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
US-07-952-277A-60

  Query Match             60.0%;  Score 12;  DB 2;  Length 20;
  Best Local Similarity   75.0%;  Pred. No. 5.5e+03;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GACCGCATAGACTTCTCAGA 20
              |||| || || ||  |||||
Db          1 GACCCCACAGCCTATTCAGA 20


RESULT 7
US-09-038-637-113
; Sequence 113, Application US/09038637
; Patent No. 6235470
;  GENERAL INFORMATION:
;    APPLICANT:  Sidransky, David
;    TITLE OF INVENTION:  DETECTION OF NEOPLASIM BY ANALYSIS OF SALIVA
;    NUMBER OF SEQUENCES:  195
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fish & Richardson P.C.
;      STREET:  4225 Executive Square, Suite 1400
;      CITY:  La Jolla
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92037
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows 95
;      SOFTWARE:  FastSEQ for Windows Version 2.0b
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/038,637
;      FILING DATE:  10-MAR-1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/579,233
;      FILING DATE:  28-DEC-1995
;      APPLICATION NUMBER:  08/152,313
;      FILING DATE:  12-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Haile, Lisa A.
```

```
;      REGISTRATION NUMBER:  38,347
;      REFERENCE/DOCKET NUMBER:  07265/146001
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619/678-5070
;      TELEFAX:  619/678-5099
;  INFORMATION FOR SEQ ID NO:  113:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
US-09-038-637-113

  Query Match             60.0%;  Score 12;  DB 3;  Length 20;
  Best Local Similarity   75.0%;  Pred. No. 5.5e+03;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GACCGCATAGACTTCTCAGA 20
              |||| || || ||  |||||
Db          1 GACCCCACAGCCTATTCAGA 20


RESULT 8
US-08-716-459-1/c
; Sequence 1, Application US/08716459
; Patent No. 5821062
;  GENERAL INFORMATION:
;    APPLICANT:  KOMAI, Koichiro
;    APPLICANT:  KANEKO, Hideo
;    APPLICANT:  NAKATSUKA, Iwao
;    TITLE OF INVENTION:  OLIGONUCLEOTIDE FOR USE IN CHECKING
;    TITLE OF INVENTION:  PRESENCE OR ABSENCE OF MUTATION IN
;    TITLE OF INVENTION:  HUMAN-DERIVED CYTOCHROME P450IIC18 GENE
;    NUMBER OF SEQUENCES:  13
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Birch, Stewart, Kolasch & Birch, LLP
;      STREET:  P.O. Box 747
;      CITY:  Falls Church
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22040-0747
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 Mb
;      COMPUTER:  IBM PC
;      OPERATING SYSTEM:  IBM DOS Version 5.00
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/716,459
;      FILING DATE:  27 SEPTEMBER 1996
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP-059385/1994
;      APPLICATION NUMBER:  JP-059386/1994
;      FILING DATE:  29-03-1994
;      FILING DATE:  29-03-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SVENSSON, Leonard R.
;      REGISTRATION NUMBER:  30,330
;      REFERENCE/DOCKET NUMBER:  20-4081PCT
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 205-8000
;      TELEFAX:  (703) 205-8050
;      TELEX:  248345
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  18
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Other nucleic acid   synthetic DNA
US-08-716-459-1

  Query Match             59.0%;  Score 11.8;  DB 1;  Length 18;
  Best Local Similarity   86.7%;  Pred. No. 6.9e+03;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 CATAGACTTCTCAGA 20
              ||||||||| | |||
Db         16 CATAGACTTTGAGA 2


RESULT 9
US-08-819-912-8
; Sequence 8, Application US/08819912
; Patent No. 5795722
;  GENERAL INFORMATION:
;    APPLICANT:  Lacroix, Jean-Michel
;    APPLICANT:  Dunn, James M.
;    TITLE OF INVENTION:  METHOD AND KIT FOR QUANTITATION AND
;    TITLE OF INVENTION:  NUCLEIC ACID SEQUENCING OF NUCLEIC ACID ANALYTES IN A SAMPLE
;    NUMBER OF SEQUENCES:  15
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Oppedahl & Larson
;      STREET:  1992 Commerce Street Suite 309
;      CITY:  Yorktown
;      STATE:  NY
;      COUNTRY:  US
;      ZIP:  10598
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette - 3.5 inch, 1.44 Mb storage
;      COMPUTER:  IBM compatible
;      OPERATING SYSTEM:  MS DOS
;      SOFTWARE:  Word Perfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/819,912
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Larson, Marina T.
;      REGISTRATION NUMBER:  32,038
;      REFERENCE/DOCKET NUMBER:  VGEN.P-039US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (914) 245-3252
;      TELEFAX:  (914) 962-4330
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  other nucleic acid
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  yes
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
;      ORGANISM:  Chlamydia trachomatis
;    FEATURE:
;      OTHER INFORMATION:  amplification primer CT1431F for cryptic
;      OTHER INFORMATION:  plasmid
US-08-819-912-8

  Query Match             59.0%;  Score 11.8;  DB 1;  Length 20;
  Best Local Similarity   86.7%;  Pred. No. 7e+03;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 GCATAGACTTCTCAG 19
              ||||| |||||| ||
Db          3 GCATAAACTTCTGAG 17


RESULT 10
```

```
US-08-291-932A-289
; Sequence 289, Application US/08291932A
; Patent No. 5658780
;  GENERAL INFORMATION:
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Draper, Kenneth G.
;    APPLICANT:  McSwiggen, James
;    TITLE OF INVENTION:  RIBOZYME TREATMENT OF
;    TITLE OF INVENTION:  DISEASES OR CONDITIONS
;    TITLE OF INVENTION:  RELATED TO LEVELS OF
;    TITLE OF INVENTION:  NF-KB
;    NUMBER OF SEQUENCES:  830
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/291,932A
;      FILING DATE:  August 15, 1994
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;    PRIOR APPLICATION DATA:  including application
;    PRIOR APPLICATION DATA:  described below:                    Two
;      APPLICATION NUMBER:  08/245,466
;      FILING DATE:  May 18, 1994
;      APPLICATION NUMBER:  07/987,132
;      FILING DATE:  December 7, 1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  208/157
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  289:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  15 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-291-932A-289

  Query Match             57.0%;  Score 11.4;  DB 1;  Length 15;
  Best Local Similarity   61.5%;  Pred. No. 1.1e+04;
  Matches    8;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 ATAGACTTCTCAG 19
              |: |||::|:|||
Db          1 AUGGACUUCUCAG 13


RESULT 11
US-08-434-511-4/c
; Sequence 4, Application US/08434511
; Patent No. 6057114
;  GENERAL INFORMATION:
;    APPLICANT:  Akong, Anthony
;    APPLICANT:  Harpold, Michael
;    APPLICANT:  Velicelebi, Gonul
;    APPLICANT:  Brust, Paul
;    TITLE OF INVENTION:  AUTOMATED ANALYSIS EQUIPMENT AND ASSAY
;    TITLE OF INVENTION:  METHOD FOR DETECTING CELL SURFACE PROTEIN FUNCTION USING SAME
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Brown, Martin, Haller & McClain
;      STREET:  1660 Union Street
;      CITY:  San Diego
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  92101-2926
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/434,511
;      FILING DATE:  04-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/244,985
;      FILING DATE:  20-JUN-1994
;      APPLICATION NUMBER:  PCT/US92/11090
;      FILING DATE:  18-DEC-1992
;      APPLICATION NUMBER:  07/812,254
;      FILING DATE:  20-DEC-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Seidman, Stephanie L
;      REGISTRATION NUMBER:  33,779
;      REFERENCE/DOCKET NUMBER:  6362-9738
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  619-238-0999
;      TELEFAX:  619-238-0062
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:
;    ORIGINAL SOURCE:
US-08-434-511-4

  Query Match             57.0%;  Score 11.4;  DB 3;  Length 17;
  Best Local Similarity   92.3%;  Pred. No. 1.1e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 ATAGACTTCTCAG 19
              ||||| |||||||
Db         13 ATAGAATTCTCAG 1


RESULT 12
US-08-229-150-4/c
; Sequence 4, Application US/08229150
; Patent No. 6127133
; GENERAL INFORMATION:
;  APPLICANT: Akong, Michael A.
;  APPLICANT: Harpold, Michael M.
;  APPLICANT: Velicelebi, G.
;  APPLICANT: Brust, Paul
;  TITLE OF INVENTION: AUTOMATED ANALYSIS EQUIPMENT AND ASSAY METHOD FOR DETECTING CELL S
;  TITLE OF INVENTION: PROTEIN FUNCTION USING SAME
;  FILE REFERENCE: 24735-51505B
;  CURRENT APPLICATION NUMBER: US/08/229,150
;  CURRENT FILING DATE: 1994-04-18
;  EARLIER APPLICATION NUMBER: 07/812,254
;  EARLIER FILING DATE: 1991-12-20
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
```

```
;   LENGTH: 17
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:
;   OTHER INFORMATION: Oligonucleotide used for screening of products having
;   OTHER INFORMATION: EcoRI site adjacent to initiation codon of human
;   OTHER INFORMATION: HM1 coding region
US-08-229-150-4

  Query Match             57.0%;  Score 11.4;  DB 3;  Length 17;
  Best Local Similarity   92.3%;  Pred. No. 1.1e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 ATAGACTTCTCAG 19
              ||||| |||||||
Db         13 ATAGAATTCTCAG 1


RESULT 13
5401629-5/c
;Patent No. 5401629
;    APPLICANT: HARPOLD, MICHAEL M.;BRUST, PAUL
;    TITLE OF INVENTION: ASSAY METHODS AND COMPOSITIONS USEFUL
;FOR MEASURING THE TRANSDUCTION OF AN INTRACELLULAR SIGNAL
;    NUMBER OF SEQUENCES: 5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/563,751
;      FILING DATE: 07-AUG-1990
;SEQ ID NO:5:
;      LENGTH: 17
5401629-5

  Query Match             57.0%;  Score 11.4;  DB 6;  Length 17;
  Best Local Similarity   92.3%;  Pred. No. 1.1e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 ATAGACTTCTCAG 19
              ||||| |||||||
Db         13 ATAGAATTCTCAG 1


RESULT 14
5401629-5/c
;Patent No. 5401629
;    APPLICANT: HARPOLD, MICHAEL M.;BRUST, PAUL
;    TITLE OF INVENTION: ASSAY METHODS AND COMPOSITIONS USEFUL
;FOR MEASURING THE TRANSDUCTION OF AN INTRACELLULAR SIGNAL
;    NUMBER OF SEQUENCES: 5
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/563,751
;      FILING DATE: 07-AUG-1990
;SEQ ID NO:5:
;      LENGTH: 17
5401629-5

  Query Match             57.0%;  Score 11.4;  DB 6;  Length 17;
  Best Local Similarity   92.3%;  Pred. No. 1.1e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 ATAGACTTCTCAG 19
              ||||| |||||||
Db         13 ATAGAATTCTCAG 1


RESULT 15
US-09-696-791-1238/c
; Sequence 1238, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
;  APPLICANT:  Robbins, Joan M.
;  APPLICANT:  Tritz, Richard
;  TITLE OF INVENTION:  RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
;  TITLE OF INVENTION:  SKIN AND EYE DISEASES
;  FILE REFERENCE:  480124.407
;  CURRENT APPLICATION NUMBER: US/09/696,791
;  CURRENT FILING DATE:  2000-10-25
;  NUMBER OF SEQ ID NOS:  4523
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 1238
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Cdk-we-hu ribozyme binding site
US-09-696-791-1238

  Query Match             57.0%;  Score 11.4;  DB 4;  Length 19;
  Best Local Similarity   92.3%;  Pred. No. 1.1e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GCATAGACTTCTC 17
              ||||| |||||||
Db         15 GCATATACTTCTC 3


RESULT 16
US-09-696-791-1239/c
; Sequence 1239, Application US/09696791
; Patent No. 6770633
; GENERAL INFORMATION:
;  APPLICANT:  Robbins, Joan M.
;  APPLICANT:  Tritz, Richard
;  TITLE OF INVENTION:  RIBOZYME THERAPY FOR THE TREATMENT OF PROLIFERATIVE
;  TITLE OF INVENTION:  SKIN AND EYE DISEASES
;  FILE REFERENCE:  480124.407
;  CURRENT APPLICATION NUMBER: US/09/696,791
;  CURRENT FILING DATE:  2000-10-25
;  NUMBER OF SEQ ID NOS:  4523
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 1239
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: Cdk-we-hu ribozyme binding site
US-09-696-791-1239

  Query Match             57.0%;  Score 11.4;  DB 4;  Length 19;
  Best Local Similarity   92.3%;  Pred. No. 1.1e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GCATAGACTTCTC 17
              ||||| |||||||
Db         13 GCATATACTTCTC 1


RESULT 17
US-08-974-180-35/c
; Sequence 35, Application US/08974180
; Patent No. 6025194
;  GENERAL INFORMATION:
;    APPLICANT:  Funk, Walter
;    TITLE OF INVENTION:  Methods for Modulating and Identifying
;    TITLE OF INVENTION:  Cellular Senescence
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Geron Corporation
;      STREET:  230 Constitution Drive
;      CITY:  Menlo Park
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94025
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
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```
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/974,180
;       FILING DATE:  19-NOV-1997
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Kaster, Kevin R.
;       REGISTRATION NUMBER:  32,704
;       REFERENCE/DOCKET NUMBER:  206
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (650) 473-7779
;       TELEFAX:  (650) 473-8654
;   INFORMATION FOR SEQ ID NO:  35:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  20 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA
;     FEATURE:
;       NAME/KEY:  -
;       LOCATION:  1..20
;       OTHER INFORMATION:  /note= "primer 92-5'"
US-08-974-180-35

  Query Match             57.0%;  Score 11.4;  DB 3;  Length 20;
  Best Local Similarity   92.3%;  Pred. No. 1.1e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GCATAGACTTCTC 17
              |||| ||||||||
Db         13 GCATTGACTTCTC 1


RESULT 18
US-10-148-806-20/c
; Sequence 20, Application US/10148806
; Patent No. 6762042
; GENERAL INFORMATION:
;  APPLICANT: Bai, Chang
;  APPLICANT:  Metzger, Michael
;  APPLICANT:  Liu, Xiaomei
;  TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN NHL, A DNA
;  TITLE OF INVENTION:  HELICASE
;  FILE REFERENCE: 20585P
;  CURRENT APPLICATION NUMBER: US/10/148,806
;  CURRENT FILING DATE:  2002-06-05
;  PRIOR APPLICATION NUMBER: US00/33065
;  PRIOR FILING DATE: 2000-12-09
;  PRIOR APPLICATION NUMBER: 60/169,970
;  PRIOR FILING DATE: 1999-12-09
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: oligonucleotide
US-10-148-806-20

  Query Match             57.0%;  Score 11.4;  DB 4;  Length 20;
  Best Local Similarity   92.3%;  Pred. No. 1.1e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 TAGACTTCTCAGA 20
              | ||||||||||||
Db         17 TGGACTTCTCAGA 5


RESULT 19
US-10-148-806-21
; Sequence 21, Application US/10148806
; Patent No. 6762042
; GENERAL INFORMATION:
;  APPLICANT: Bai, Chang
;  APPLICANT:  Metzger, Michael
;  APPLICANT:  Liu, Xiaomei
;  TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN NHL, A DNA
;  TITLE OF INVENTION:  HELICASE
;  FILE REFERENCE: 20585P
;  CURRENT APPLICATION NUMBER: US/10/148,806
;  CURRENT FILING DATE:  2002-06-05
;  PRIOR APPLICATION NUMBER: US00/33065
;  PRIOR FILING DATE: 2000-12-09
;  PRIOR APPLICATION NUMBER: 60/169,970
;  PRIOR FILING DATE: 1999-12-09
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: oligonucleotide
US-10-148-806-21

  Query Match             57.0%;  Score 11.4;  DB 4;  Length 20;
  Best Local Similarity   92.3%;  Pred. No. 1.1e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 TAGACTTCTCAGA 20
              | ||||||||||||
Db          4 TGGACTTCTCAGA 16


RESULT 20
US-09-422-978-4697
; Sequence 4697, Application US/09422978
; Patent No. 6537751
; GENERAL INFORMATION:
;  APPLICANT: Cohen, Daniel
;  APPLICANT: Blumenfeld, Marta
;  APPLICANT: Chumakov, Ilya
;  TITLE OF INVENTION: Biallelic markers for use in constructing a high density...
;  FILE REFERENCE: GENSET.020CP1
;  CURRENT APPLICATION NUMBER: US/09/422,978
;  CURRENT FILING DATE: 1999-10-20
;  EARLIER APPLICATION NUMBER: US 09/298,850
;  EARLIER FILING DATE: 1999-04-21
;  EARLIER APPLICATION NUMBER: US 60/109,732
;  EARLIER FILING DATE: 1998-11-23
;  EARLIER APPLICATION NUMBER: US 60/082,614
;  EARLIER FILING DATE: 1998-04-21
;  NUMBER OF SEQ ID NOS: 11796
; SEQ ID NO 4697
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Homo Sapiens
;   FEATURE:
;   NAME/KEY: primer_bind
;   LOCATION: 1..18
;   OTHER INFORMATION: upstream amplification primer 99-17105 for SEQ 763,
US-09-422-978-4697

  Query Match             56.0%;  Score 11.2;  DB 4;  Length 18;
  Best Local Similarity   81.2%;  Pred. No. 1.4e+04;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 GCATAGACTTCTCAGA 20
              ||| |||||||  |||
Db          1 GCACAGACTTCAAAGA 16


RESULT 21
```

```
US-07-977-284A-113
; Sequence 113, Application US/07977284A
; Patent No. 5558988
;  GENERAL INFORMATION:
;    APPLICANT:  Prockop, Darwin J.
;    APPLICANT:  Ala-Kokko, Leena
;    APPLICANT:  Williams, Charlene J.
;    APPLICANT:  Ritvaniemi, Pertti
;    APPLICANT:  Baldwin, Clinton
;    APPLICANT:  Hopkinson, Ian
;    APPLICANT:  Ahmad, Nilofer Nina
;    TITLE OF INVENTION:  METHODS OF DETECTING A GENETIC
;    TITLE OF INVENTION:  PREDISPOSITION FOR OSTEOARTHRITIS
;    NUMBER OF SEQUENCES:  261
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock, Washburn, Kurtz, Mackiewicz & No. 5558988ris
;      STREET:  One Liberty Place, 46th floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/977,284A
;      FILING DATE:  13-NOV-1992
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  DeLuca, Mark
;      REGISTRATION NUMBER:  33,229
;      REFERENCE/DOCKET NUMBER:  TJU-0697
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-3100
;      TELEFAX:  (215) 568-3439,
;  INFORMATION FOR SEQ ID NO:  113:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  LINEAR
;    ANTI-SENSE:  NO
US-07-977-284A-113

  Query Match             56.0%;  Score 11.2;  DB 1;  Length 20;
  Best Local Similarity   81.2%;  Pred. No. 1.5e+04;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 ACCGCATAGACTTCTC 17
              || |||  ||||||||
Db          4 ACTGCAGGGACTTCTC 19


RESULT 22
US-08-256-426B-113
; Sequence 113, Application US/08256426B
; Patent No. 5948611
;  GENERAL INFORMATION:
;    APPLICANT:  Prockop, Darwin J.
;    APPLICANT:  Ala-Kokko, Leena
;    APPLICANT:  Williams, Charlene J.
;    APPLICANT:  Ritvaniemi, Pertti
;    APPLICANT:  Baldwin, Clinton
;    APPLICANT:  Hopkinson, Ian
;    APPLICANT:  Ahmad, Nilofer Nina
;    TITLE OF INVENTION:  Methods of Detecting A Genetic
;    NUMBER OF SEQUENCES:  293
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Woodcock Washburn Kurtz Mackiewicz & No. 5948611ris
;      STREET:  One Liberty Place - 46th Floor
;      CITY:  Philadelphia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  DISKETTE, 3.5 INCH
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  Windows 3.1
;      SOFTWARE:  WORDPERFECT 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/256,426B
;      FILING DATE:  03-FEB-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US93/10964
;      FILING DATE:  12-NOV-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/977,284
;      FILING DATE:  13-NOV-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Mark DeLuca
;      REGISTRATION NUMBER:  33,229
;      REFERENCE/DOCKET NUMBER:  TJU-1082
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 568-3100
;      TELEFAX:  (215) 568-3439
;  INFORMATION FOR SEQ ID NO:  113:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  20
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  LINEAR
;    ANTI-SENSE:  NO
US-08-256-426B-113

  Query Match             56.0%;  Score 11.2;  DB 2;  Length 20;
  Best Local Similarity   81.2%;  Pred. No. 1.5e+04;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 ACCGCATAGACTTCTC 17
              || |||  ||||||||
Db          4 ACTGCAGGGACTTCTC 19


RESULT 23
US-09-249-730-204/c
; Sequence 204, Application US/09249730
; Patent No. 6121000
; GENERAL INFORMATION:
;  APPLICANT: WRIGHT, Jim A.
;  APPLICANT: YOUNG, Aiping H.
;  TITLE OF INVENTION: Antitumor Antisense Sequences Directed Against R1 and
;  TITLE OF INVENTION: R2 Components of Ribonucleotide Reductase
;  FILE REFERENCE: 032396-040
;  CURRENT APPLICATION NUMBER: US/09/249,730
;  CURRENT FILING DATE: 1999-02-11
;  NUMBER OF SEQ ID NOS: 220
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 204
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Human
US-09-249-730-204

  Query Match             56.0%;  Score 11.2;  DB 3;  Length 20;
  Best Local Similarity   81.2%;  Pred. No. 1.5e+04;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 CGCATAGACTTCTCAG 19
              |||| || ||| ||||
Db         20 CGCAGAGTCTTGTCAG 5
```

```
RESULT 24
US-09-359-756-36/c
; Sequence 36, Application US/09359756
; Patent No. 6168950
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT: William Gaarde
;  APPLICANT: Donna T. Ward
;  APPLICANT: Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF MEKK1 EXPRESSION
;  FILE REFERENCE: RTS-0077
;  CURRENT APPLICATION NUMBER: US/09/359,756
;  CURRENT FILING DATE: 1999-07-23
;  NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 36
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-359-756-36

  Query Match             56.0%;  Score 11.2;  DB 3;  Length 20;
  Best Local Similarity   81.2%;  Pred. No. 1.5e+04;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 GCATAGACTTCTCAGA 20
              ||||||||||||   ||
Db         19 GCATAGACTTCAGGGA 4


RESULT 25
US-09-198-452A-3744/c
; Sequence 3744, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
;  APPLICANT: Griffais, R.
;  TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
;  TITLE OF INVENTION:  thereof and uses thereof, in particular for the diagnosis, preve
;  TITLE OF INVENTION:  and treatment of infection
;  FILE REFERENCE: 9710-003-999
;  CURRENT APPLICATION NUMBER: US/09/198,452A
;  CURRENT FILING DATE:  1998-11-24
;  NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 3744
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Chlamydia pneumoniae
US-09-198-452A-3744

  Query Match             56.0%;  Score 11.2;  DB 4;  Length 20;
  Best Local Similarity   81.2%;  Pred. No. 1.5e+04;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          2 ACCGCATAGACTTCTC 17
              | | ||  |||||||||
Db         20 ATCTCAGAGACTTCTC 5


RESULT 26
US-09-249-247-204/c
; Sequence 204, Application US/09249247
; Patent No. 6593305
; GENERAL INFORMATION:
;  APPLICANT: WRIGHT, Jim A.
;  APPLICANT: YOUNG, Aiping H.
;  TITLE OF INVENTION: Antitumor Antisense Sequences Directed Against R1 and
;  TITLE OF INVENTION: R2 Components of Ribonucleotide Reductase
;  FILE REFERENCE: 032396-023
;  CURRENT APPLICATION NUMBER: US/09/249,247
;  CURRENT FILING DATE: 1999-02-11
;  EARLIER APPLICATION NUMBER: US 60/023,040
;  EARLIER FILING DATE: 1996-08-02
;  EARLIER APPLICATION NUMBER: US 60/039,959
;  EARLIER FILING DATE: 1997-03-07
;  EARLIER APPLICATION NUMBER: US 08/904,901
;  EARLIER FILING DATE: 1997-08-01
;  NUMBER OF SEQ ID NOS: 220
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 204
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Human
US-09-249-247-204

  Query Match             56.0%;  Score 11.2;  DB 4;  Length 20;
  Best Local Similarity   81.2%;  Pred. No. 1.5e+04;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 CGCATAGACTTCTCAG 19
              |||| || ||| ||||
Db         20 CGCAGAGTCTTGTCAG 5


RESULT 27
US-09-975-123-28/c
; Sequence 28, Application US/09975123
; Patent No. 6750019
; GENERAL INFORMATION:
;  APPLICANT: Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: RTS-0253
;  CURRENT APPLICATION NUMBER: US/09/975,123
;  CURRENT FILING DATE:  2001-10-09
;  NUMBER OF SEQ ID NOS: 43
; SEQ ID NO 28
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-975-123-28

  Query Match             56.0%;  Score 11.2;  DB 4;  Length 20;
  Best Local Similarity   81.2%;  Pred. No. 1.5e+04;
  Matches   13;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GACCGCATAGACTTCT 16
              ||||||| ||  ||||
Db         17 GACCGCAAAGGATTCT 2


RESULT 28
US-09-544-398B-32/c
; Sequence 32, Application US/09544398B
; Patent No. 6770461
; GENERAL INFORMATION:
;  APPLICANT: Carulli, John P.
;  APPLICANT:  Little, Randall D.
;  APPLICANT:  Recker, Robert R.
;  APPLICANT:  Johnson, Mark L.
;  TITLE OF INVENTION: High bone mass gene of 11q13.3
;  FILE REFERENCE: 032796-013
;  CURRENT APPLICATION NUMBER: US/09/544,398B
;  CURRENT FILING DATE:  2002-06-10
;  PRIOR APPLICATION NUMBER: US 09/229,319
;  PRIOR FILING DATE: 1999-01-13
;  PRIOR APPLICATION NUMBER: US 60/071,449
;  PRIOR FILING DATE: 1998-01-13
;  PRIOR APPLICATION NUMBER: US 60/105,511
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 641
;  SOFTWARE: FastSEQ for Windows Version 4.0
```

```
; SEQ ID NO 32
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Artificial sequence is a primer.
US-09-544-398B-32

  Query Match             55.0%;  Score 11;  DB 4;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GACTTCTCAGA 20
              ||||||||||
Db         17 GACTTCTCAGA 7


RESULT 29
US-09-544-398B-629/c
; Sequence 629, Application US/09544398B
; Patent No. 6770461
; GENERAL INFORMATION:
;  APPLICANT: Carulli, John P.
;  APPLICANT:  Little, Randall D.
;  APPLICANT:  Recker, Robert R.
;  APPLICANT:  Johnson, Mark L.
;  TITLE OF INVENTION: High bone mass gene of 11q13.3
;  FILE REFERENCE: 032796-013
;  CURRENT APPLICATION NUMBER: US/09/544,398B
;  CURRENT FILING DATE:  2002-06-10
;  PRIOR APPLICATION NUMBER: US 09/229,319
;  PRIOR FILING DATE: 1999-01-13
;  PRIOR APPLICATION NUMBER: US 60/071,449
;  PRIOR FILING DATE: 1998-01-13
;  PRIOR APPLICATION NUMBER: US 60/105,511
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 641
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 629
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Artificial Sequence is a primer.
; Patent No. 6770461
US-09-544-398B-629

  Query Match             55.0%;  Score 11;  DB 4;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GACTTCTCAGA 20
              ||||||||||
Db         17 GACTTCTCAGA 7


RESULT 30
US-09-543-771B-32/c
; Sequence 32, Application US/09543771B
; Patent No. 6780609
; GENERAL INFORMATION:
;  APPLICANT: Carulli, John P.
;  APPLICANT:  Little, Randall D.
;  APPLICANT:  Recker, Robert R.
;  APPLICANT:  Johnson, Mark L.
;  TITLE OF INVENTION: High bone mass gene of 11q13.3
;  FILE REFERENCE: 032796-014
;  CURRENT APPLICATION NUMBER: US/09/543,771B
;  CURRENT FILING DATE:  2000-04-05
;  PRIOR APPLICATION NUMBER: US 09/229,319
;  PRIOR FILING DATE: 1999-01-13
;  PRIOR APPLICATION NUMBER: US 60/071,449
;  PRIOR FILING DATE: 1998-01-13
;  PRIOR APPLICATION NUMBER: US 60/105,511
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 641
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 32
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Artificial sequence is a primer.
US-09-543-771B-32

  Query Match             55.0%;  Score 11;  DB 4;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GACTTCTCAGA 20
              ||||||||||
Db         17 GACTTCTCAGA 7


RESULT 31
US-09-543-771B-629/c
; Sequence 629, Application US/09543771B
; Patent No. 6780609
; GENERAL INFORMATION:
;  APPLICANT: Carulli, John P.
;  APPLICANT:  Little, Randall D.
;  APPLICANT:  Recker, Robert R.
;  APPLICANT:  Johnson, Mark L.
;  TITLE OF INVENTION: High bone mass gene of 11q13.3
;  FILE REFERENCE: 032796-014
;  CURRENT APPLICATION NUMBER: US/09/543,771B
;  CURRENT FILING DATE:  2000-04-05
;  PRIOR APPLICATION NUMBER: US 09/229,319
;  PRIOR FILING DATE: 1999-01-13
;  PRIOR APPLICATION NUMBER: US 60/071,449
;  PRIOR FILING DATE: 1998-01-13
;  PRIOR APPLICATION NUMBER: US 60/105,511
;  PRIOR FILING DATE: 1998-10-23
;  NUMBER OF SEQ ID NOS: 641
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 629
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Artificial Sequence is a primer.
; Patent No. 6780609
US-09-543-771B-629

  Query Match             55.0%;  Score 11;  DB 4;  Length 18;
  Best Local Similarity   100.0%;  Pred. No. 1.8e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         10 GACTTCTCAGA 20
              ||||||||||
Db         17 GACTTCTCAGA 7


RESULT 32
US-08-357-791-4
; Sequence 4, Application US/08357791
; Patent No. 5652102
;  GENERAL INFORMATION:
;    APPLICANT:  Fratamico, Pina M.
;    APPLICANT:  Sackitey, Soloman K.
;    APPLICANT:  Wiedmann, Martin
;    TITLE OF INVENTION:  Assay for Enterohemorrhagic Escherichia
;    TITLE OF INVENTION:  coli 0157:H7 by the Polymerase Chain Reaction
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Janelle S. Graeter
```

```
;       STREET:  Bldg. 005, Rm 411, BARC-West
;       CITY:  Beltsville
;       STATE:  Maryland
;       COUNTRY:  U.S.A.
;       ZIP:  20705
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/357,791
;       FILING DATE:
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Graeter, Janelle S.
;       REGISTRATION NUMBER:  35,024
;       REFERENCE/DOCKET NUMBER:  D.N. 0079.94
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  301-504-5676
;       TELEFAX:  301-504-5060
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  20 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  circular
;     MOLECULE TYPE:  DNA (genomic)
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  NO
;     ORIGINAL SOURCE:
;       ORGANISM:  Escherichia coli
;       STRAIN:  0157:H7
US-08-357-791-4

  Query Match             55.0%;  Score 11;  DB 1;  Length 20;
  Best Local Similarity   100.0%;  Pred. No. 1.9e+04;
  Matches   11;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 ATAGACTTCTC 17
              ||||||||||
Db          7 ATAGACTTCTC 17


RESULT 33
US-09-081-646-202
; Sequence 202, Application US/09081646
; Patent No. 6333152
; GENERAL INFORMATION:
;  APPLICANT: Kinzler, Kenneth
;  APPLICANT: Vogelstein, Bert
;  APPLICANT: Zhang, Lin
;  APPLICANT: Zhou, Wei
;  TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
;  TITLE OF INVENTION: Cancer Cells
;  FILE REFERENCE: 01107.74664
;  CURRENT APPLICATION NUMBER: US/09/081,646
;  CURRENT FILING DATE: 1998-05-20
;  EARLIER APPLICATION NUMBER: 60/047,352
;  EARLIER FILING DATE: 1997-05-21
;  NUMBER OF SEQ ID NOS: 871
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 202
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-081-646-202

  Query Match             54.0%;  Score 10.8;  DB 3;  Length 15;
  Best Local Similarity   85.7%;  Pred. No. 2.3e+04;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 CATAGACTTCTCAG 19
              ||| || |||||||
Db          1 CATGGATTTCTCAG 14


RESULT 34
US-09-081-646-743
; Sequence 743, Application US/09081646
; Patent No. 6333152
; GENERAL INFORMATION:
;  APPLICANT: Kinzler, Kenneth
;  APPLICANT: Vogelstein, Bert
;  APPLICANT: Zhang, Lin
;  APPLICANT: Zhou, Wei
;  TITLE OF INVENTION: Gene Expression Profiles in No. 6333152mal and
;  TITLE OF INVENTION: Cancer Cells
;  FILE REFERENCE: 01107.74664
;  CURRENT APPLICATION NUMBER: US/09/081,646
;  CURRENT FILING DATE: 1998-05-20
;  EARLIER APPLICATION NUMBER: 60/047,352
;  EARLIER FILING DATE: 1997-05-21
;  NUMBER OF SEQ ID NOS: 871
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 743
;   LENGTH: 15
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-081-646-743

  Query Match             54.0%;  Score 10.8;  DB 3;  Length 15;
  Best Local Similarity   85.7%;  Pred. No. 2.3e+04;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 CATAGACTTCTCAG 19
              ||| || |||||||
Db          1 CATGGATTTCTCAG 14


RESULT 35
US-09-124-398-5
; Sequence 5, Application US/09124398A
; Patent No. 6770456
; GENERAL INFORMATION:
;  APPLICANT: Coulie, Pierre
;  APPLICANT: Boon-Falleur, Thierry
;  TITLE OF INVENTION: ENDOGENOUS RETROVIRUS TUMOR ASSOCIATED NUCLEIC ACIDS AND ANTIGENS
;  FILE REFERENCE: L0461/7033
;  CURRENT APPLICATION NUMBER: US/09/124,398A
;  CURRENT FILING DATE: 1998-07-29
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: FastSEQ for Window Version 3.0
; SEQ ID NO 5
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-124-398-5

  Query Match             54.0%;  Score 10.8;  DB 4;  Length 18;
  Best Local Similarity   85.7%;  Pred. No. 2.3e+04;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 CCGCATAGACTTCT 16
              || |||||||| ||
Db          4 CCACATAGACTCCT 17


RESULT 36
US-09-659-791A-37/c
; Sequence 37, Application US/09659791A
; Patent No. 6383808
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Susan M. Freier
;  TITLE OF INVENTION: ANTISENSE MODULATION OF CLUSTERIN EXPRESSION
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;  FILE REFERENCE: RTS-0156
;  CURRENT APPLICATION NUMBER: US/09/659,791A
;  CURRENT FILING DATE:  2000-09-11
;  NUMBER OF SEQ ID NOS: 90
; SEQ ID NO 37
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-791A-37

  Query Match             54.0%;  Score 10.8;  DB 3;  Length 20;
  Best Local Similarity   85.7%;  Pred. No. 2.4e+04;
  Matches   12;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 ACCGCATAGACTTC 15
              ||||||| |||| |
Db         20 ACCGCATCGACTCC 7


RESULT 37
US-08-985-162-399
; Sequence 399, Application US/08985162
; Patent No. 6057156
;  GENERAL INFORMATION:
;    APPLICANT:  Akhtar, Saghir
;    APPLICANT:  Fell, Patricia
;    APPLICANT:  McSwiggen, James
;    TITLE OF INVENTION:  ENZYMATIC NUCLEIC ACID TREATMENT
;    TITLE OF INVENTION:  OF DISEASES OR CONDITIONS RELATED
;    TITLE OF INVENTION:  TO LEVELS OF EPIDERMAL GROWTH
;    TITLE OF INVENTION:  FACTOR RECEPTORS
;    NUMBER OF SEQUENCES:  1877
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/985,162
;      FILING DATE:  04 December 1997
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/036,476
;      FILING DATE:  31 January 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  230/107
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213)  955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  399:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-985-162-399

  Query Match             53.0%;  Score 10.6;  DB 3;  Length 17;
  Best Local Similarity   70.6%;  Pred. No. 3e+04;
  Matches   12;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GACCGCATAGACTTCTC 17
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Db          1 GACAGCAUAGACGACAC 17


RESULT 38
US-08-584-040-5340/c
; Sequence 5340, Application US/08584040
; Patent No. 6346398
;  GENERAL INFORMATION:
;    APPLICANT:  Pavco, Pamela
;    APPLICANT:  McSwiggen, James
;    APPLICANT:  Stinchcomb, Dan T.
;    APPLICANT:  Escobedo, Jaime
;    TITLE OF INVENTION:  METHOD AND REAGENT FOR THE
;    TITLE OF INVENTION:  TREATMENT OF DISEASES OR
;    TITLE OF INVENTION:  CONDITIONS RELATED TO LEVELS
;    TITLE OF INVENTION:  OF VASCULAR ENDOTHELIAL
;    TITLE OF INVENTION:  GROWTH FACTOR
;    NUMBER OF SEQUENCES:  8502
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  Word Perfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/584,040
;      FILING DATE:  January 11, 1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/005,974
;      FILING DATE:  October 26, 1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  218/064
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213) 955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  5340:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-584-040-5340

  Query Match             53.0%;  Score 10.6;  DB 3;  Length 17;
  Best Local Similarity   76.5%;  Pred. No. 3e+04;
  Matches   13;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 CCGCATAGACTTCTCAG 19
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Db         17 CCGCAAAGAAGTCACAG 1


RESULT 39
US-09-371-772B-2242/c
; Sequence 2242, Application US/09371772B
; Patent No. 6566127
; GENERAL INFORMATION:
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;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Pavco, Pam
;  APPLICANT:  McSwiggen, Jim
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Escobedo, Jaime
;  TITLE OF INVENTION: Method and Reagent for the Treatment of Diseases or Conditions Re
;  TITLE OF INVENTION:  Levels of Vascular Endothelial Growth Factor Receptor
;  FILE REFERENCE: MBHB00,876-J (237/198)
;  CURRENT APPLICATION NUMBER: US/09/371,772B
;  CURRENT FILING DATE:  1999-08-10
;  PRIOR APPLICATION NUMBER: US 60/005,974
;  PRIOR FILING DATE: 1995-10-26
;  PRIOR APPLICATION NUMBER: US 08/584,040
;  PRIOR FILING DATE: 1996-01-08
;  NUMBER OF SEQ ID NOS: 14225
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2242
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Mus sp.
US-09-371-772B-2242

  Query Match             53.0%;  Score 10.6;  DB 4;  Length 17;
  Best Local Similarity   76.5%;  Pred. No. 3e+04;
  Matches   13;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 CCGCATAGACTTCTCAG 19
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Db         17 CCGCAAAGAAGTCACAG 1


RESULT 40
US-09-401-063-399
; Sequence 399, Application US/09401063
; Patent No. 6623962
;  GENERAL INFORMATION:
;    APPLICANT:  Akhtar, Saghir
;    APPLICANT:  Fell, Patricia
;    APPLICANT:  McSwiggen, James
;    TITLE OF INVENTION:  ENZYMATIC NUCLEIC ACID TREATMENT
;    TITLE OF INVENTION:  OF DISEASES OR CONDITIONS RELATED
;    TITLE OF INVENTION:  TO LEVELS OF EPIDERMAL GROWTH
;    TITLE OF INVENTION:  FACTOR RECEPTORS
;    NUMBER OF SEQUENCES:  1877
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Lyon & Lyon
;      STREET:  633 West Fifth Street
;      STREET:  Suite 4700
;      CITY:  Los Angeles
;      STATE:  California
;      COUNTRY:  U.S.A.
;      ZIP:  90071-2066
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5" Diskette, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  IBM P.C. DOS 5.0
;      SOFTWARE:  FastSEQ for Windows 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/401,063
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/985,162
;      FILING DATE:  04 December 1997
;      APPLICATION NUMBER:  60/036,476
;      FILING DATE:  31 January 1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Warburg, Richard J.
;      REGISTRATION NUMBER:  32,327
;      REFERENCE/DOCKET NUMBER:  230/107
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (213) 489-1600
;      TELEFAX:  (213)  955-0440
;      TELEX:  67-3510
;  INFORMATION FOR SEQ ID NO:  399:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  17 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-401-063-399

  Query Match             53.0%;  Score 10.6;  DB 4;  Length 17;
  Best Local Similarity   70.6%;  Pred. No. 3e+04;
  Matches   12;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GACCGCATAGACTTCTC 17
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Db          1 GACAGCAUAGACGACAC 17


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GenCore version 5.1.6

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Perfect score: 20
Sequence: 1 gaccgcatagacttctcaga 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7305758 seqs, 3244068913 residues

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Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	13.8	69.0	20	17	US-10-289-762-2812	Sequence 2812, Ap
c	2	13.2	66.0	20	15	US-10-007-010-48	Sequence 48, Appl
	3	12.6	63.0	20	21	US-10-956-250-12	Sequence 12, Appl
	4	12.4	62.0	17	9	US-09-864-785-499	Sequence 499, App
	5	12.4	62.0	17	9	US-09-864-785-2106	Sequence 2106, Ap
c	6	12.2	61.0	18	22	US-10-702-817-75	Sequence 75, Appl
	7	12.2	61.0	19	17	US-10-365-742-187	Sequence 187, App
	8	12.2	61.0	19	21	US-10-741-600-73759	Sequence 73759, A
c	9	12.2	61.0	20	17	US-10-190-366-196	Sequence 196, App
	10	12.2	61.0	20	17	US-10-190-366-389	Sequence 389, App
	11	12.2	61.0	20	21	US-10-956-250-11	Sequence 11, Appl
	12	12	60.0	20	9	US-09-863-806-113	Sequence 113, App
	13	12	60.0	20	21	US-10-754-478-113	Sequence 113, App
c	14	11.8	59.0	19	22	US-10-923-329-137	Sequence 137, App
	15	11.8	59.0	19	22	US-10-923-329-333	Sequence 333, App
	16	11.6	58.0	18	21	US-10-741-600-73758	Sequence 73758, A
c	17	11.6	58.0	19	9	US-09-768-436-31	Sequence 31, Appl
c	18	11.6	58.0	19	22	US-10-888-226-46	Sequence 46, Appl
	19	11.6	58.0	19	22	US-10-888-226-460	Sequence 460, App
	20	11.6	58.0	20	9	US-09-731-457B-14	Sequence 14, Appl
	21	11.6	58.0	20	16	US-10-345-092-51	Sequence 51, Appl
	22	11.4	57.0	15	14	US-10-056-414-289	Sequence 289, App
	23	11.4	57.0	17	9	US-09-864-785-2881	Sequence 2881, Ap
	24	11.4	57.0	20	9	US-09-795-668-43	Sequence 43, Appl
	25	11.4	57.0	20	9	US-09-795-686-43	Sequence 43, Appl
	26	11.4	57.0	20	9	US-09-946-807-43	Sequence 43, Appl
c	27	11.4	57.0	20	15	US-10-148-806-20	Sequence 20, Appl
	28	11.4	57.0	20	15	US-10-148-806-21	Sequence 21, Appl
c	29	11.4	57.0	20	17	US-10-174-319-35	Sequence 35, Appl
	30	11.4	57.0	20	17	US-10-174-319-101	Sequence 101, App
	31	11.4	57.0	20	19	US-10-304-111-24	Sequence 24, Appl
c	32	11.4	57.0	20	21	US-10-831-901A-2082	Sequence 2082, Ap
c	33	11.4	57.0	20	21	US-10-831-901A-2083	Sequence 2083, Ap
c	34	11.4	57.0	20	21	US-10-831-901A-2084	Sequence 2084, Ap
c	35	11.4	57.0	20	21	US-10-831-901A-2085	Sequence 2085, Ap
c	36	11.4	57.0	20	21	US-10-831-901A-2086	Sequence 2086, Ap
c	37	11.4	57.0	20	21	US-10-831-901A-2087	Sequence 2087, Ap
c	38	11.4	57.0	20	21	US-10-831-901A-2088	Sequence 2088, Ap
c	39	11.4	57.0	20	21	US-10-831-901A-2089	Sequence 2089, Ap
c	40	11.4	57.0	20	22	US-10-859-792-20	Sequence 20, Appl
	41	11.4	57.0	20	22	US-10-859-792-21	Sequence 21, Appl
c	42	11.2	56.0	17	16	US-10-157-305A-99	Sequence 99, Appl
c	43	11.2	56.0	17	16	US-10-157-391-99	Sequence 99, Appl
c	44	11.2	56.0	17	16	US-10-157-096-99	Sequence 99, Appl
c	45	11.2	56.0	17	16	US-10-157-302-99	Sequence 99, Appl
c	46	11.2	56.0	17	16	US-10-157-215A-99	Sequence 99, Appl
c	47	11.2	56.0	17	16	US-10-157-299-99	Sequence 99, Appl
c	48	11.2	56.0	17	16	US-10-154-951B-99	Sequence 99, Appl
c	49	11.2	56.0	17	16	US-10-156-831-99	Sequence 99, Appl
c	50	11.2	56.0	17	16	US-10-157-147-99	Sequence 99, Appl
c	51	11.2	56.0	17	16	US-10-157-166-99	Sequence 99, Appl
c	52	11.2	56.0	17	16	US-10-156-902-99	Sequence 99, Appl
c	53	11.2	56.0	17	16	US-10-157-318-99	Sequence 99, Appl
c	54	11.2	56.0	17	17	US-10-157-178-99	Sequence 99, Appl
c	55	11.2	56.0	17	17	US-10-156-792A-99	Sequence 99, Appl
c	56	11.2	56.0	17	17	US-10-157-213-99	Sequence 99, Appl
	57	11.2	56.0	17	17	US-10-260-638-191	Sequence 191, App
c	58	11.2	56.0	17	17	US-10-260-638-192	Sequence 192, App
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c	60	11.2	56.0	17	17	US-10-157-073-99	Sequence 99, Appl
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c	63	11.2	56.0	17	17	US-10-157-418A-99	Sequence 99, Appl
c	64	11.2	56.0	17	17	US-10-157-171-99	Sequence 99, Appl
c	65	11.2	56.0	17	17	US-10-157-491-99	Sequence 99, Appl
c	66	11.2	56.0	17	17	US-10-157-317-99	Sequence 99, Appl
c	67	11.2	56.0	17	17	US-10-157-339-99	Sequence 99, Appl
	68	11.2	56.0	18	17	US-10-349-143-4697	Sequence 4697, Ap
c	69	11.2	56.0	19	18	US-10-333-429-452	Sequence 452, App
c	70	11.2	56.0	20	10	US-09-975-123-28	Sequence 28, Appl
c	71	11.2	56.0	20	10	US-09-915-814-88	Sequence 88, Appl
c	72	11.2	56.0	20	14	US-10-104-919-44	Sequence 44, Appl
c	73	11.2	56.0	20	16	US-10-240-046A-81	Sequence 81, Appl
c	74	11.2	56.0	20	16	US-10-240-046A-82	Sequence 82, Appl
c	75	11.2	56.0	20	17	US-10-289-762-3744	Sequence 3744, Ap
c	76	11.2	56.0	20	17	US-10-447-136-204	Sequence 204, App
c	77	11.2	56.0	20	17	US-10-395-741B-45	Sequence 45, Appl
c	78	11.2	56.0	20	20	US-10-807-837-17	Sequence 17, Appl
	79	11.2	56.0	20	20	US-10-632-581-8	Sequence 8, Appli
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c	82	11.2	56.0	20	22	US-10-516-505-108	Sequence 108, App
	83	11.2	56.0	20	22	US-10-516-505-185	Sequence 185, App
c	84	11	55.0	18	17	US-10-374-979-32	Sequence 32, Appl
c	85	11	55.0	18	18	US-10-182-936A-32	Sequence 32, Appl
c	86	11	55.0	18	19	US-10-731-739-32	Sequence 32, Appl
c	87	11	55.0	18	19	US-10-731-739-629	Sequence 629, App
c	88	11	55.0	18	20	US-10-477-238A-32	Sequence 32, Appl
c	89	11	55.0	18	20	US-10-477-238A-629	Sequence 629, App
c	90	11	55.0	18	20	US-10-680-287A-32	Sequence 32, Appl
c	91	11	55.0	18	20	US-10-680-287A-629	Sequence 629, App
c	92	11	55.0	18	21	US-10-477-173-32	Sequence 32, Appl
c	93	11	55.0	18	21	US-10-477-173-629	Sequence 629, App
c	94	11	55.0	18	21	US-10-477-173-855	Sequence 855, App
c	95	11	55.0	18	22	US-10-834-377-32	Sequence 32, Appl
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	97	11	55.0	19	21	US-10-485-999-81	Sequence 81, Appl
	98	11	55.0	19	21	US-10-813-747-19	Sequence 19, Appl
	99	11	55.0	20	19	US-10-688-706-705	Sequence 705, App
	100	11	55.0	20	19	US-10-688-706-1211	Sequence 1211, Ap

ALIGNMENTS

RESULT 1
US-10-289-762-2812
; Sequence 2812, Application US/10289762
; Publication No. US20040006218A1
; GENERAL INFORMATION:
; APPLICANT: Griffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/10/289,762
; CURRENT FILING DATE: 2003-03-27
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 2812
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-289-762-2812

Query Match 69.0%; Score 13.8; DB 17; Length 20;
Best Local Similarity 88.2%; Pred. No. 2.4e+03;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 GACCGCATAGACTTCTC 17
              ||||||||| |||| ||
Db          3 GACCGCATAAACTTATC 19
```

RESULT 2
US-10-007-010-48/c
; Sequence 48, Application US/10007010
; Publication No. US20030125275A1
; GENERAL INFORMATION:
; APPLICANT: Alexander H. Borchers
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF HCK EXPRESSION
; FILE REFERENCE: RTS-0345
; CURRENT APPLICATION NUMBER: US/10/007,010
; CURRENT FILING DATE: 2001-12-04
; NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 48
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-007-010-48

Query Match 66.0%; Score 13.2; DB 15; Length 20;
Best Local Similarity 83.3%; Pred. No. 5.1e+03;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```
Qy          2 ACCGCATAGACTTCTCAG 19
              | | ||| ||||||||||
Db         20 AACTCATTGACTTCTCAG 3
```

RESULT 3
US-10-956-250-12
; Sequence 12, Application US/10956250
; Publication No. US20050090430A1
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; Schatzman, Randall C.
; Tsuchihashi, Zenta
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; DIAGNOSIS AND TREATMENT OF IRON MISREGULATION D
; ISEASES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSEQ for Windows Version 2.0b
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/956,250
; FILING DATE: 01-Oct-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/920,559
; FILING DATE: 27-Aug-1997
; APPLICATION NUMBER: US 08/652,265
; FILING DATE: 23-MAY-1996
; APPLICATION NUMBER: US 08/834,497
; FILING DATE: 04-APR-1997
; APPLICATION NUMBER: US 08/866,211
; FILING DATE: 13-JUN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Poissant, Brian M
; REGISTRATION NUMBER: 28,462
; REFERENCE/DOCKET NUMBER: 8907-0062-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-956-250-12

Query Match 63.0%; Score 12.6; DB 21; Length 20;
Best Local Similarity 78.9%; Pred. No. 1.1e+04;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
Qy          1 GACCGCATAGACTTCTCAG 19
              ||| ||| ||||||| | |
Db          2 GACAGCACAGACTTCACCG 20
```

RESULT 4

```
US-09-864-785-499
; Sequence 499, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Draper, Ken
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Levels of NF-Kappa B
;  FILE REFERENCE: 400/022 (MBHB00-812-D)
;  CURRENT APPLICATION NUMBER: US/09/864,785
;  CURRENT FILING DATE:  2001-05-23
;  NUMBER OF SEQ ID NOS: 3929
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 499
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Nucleic Acid
US-09-864-785-499

  Query Match             62.0%;  Score 12.4;  DB 9;  Length 17;
  Best Local Similarity   64.3%;  Pred. No. 1.4e+04;
  Matches    9;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CATAGACTTCTCAG 19
              ||: |||::|:|||
Db          2 CAUGGACUUCUCAG 15


RESULT 5
US-09-864-785-2106
; Sequence 2106, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Draper, Ken
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Levels of NF-Kappa B
;  FILE REFERENCE: 400/022 (MBHB00-812-D)
;  CURRENT APPLICATION NUMBER: US/09/864,785
;  CURRENT FILING DATE:  2001-05-23
;  NUMBER OF SEQ ID NOS: 3929
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2106
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Nucleic Acid
US-09-864-785-2106

  Query Match             62.0%;  Score 12.4;  DB 9;  Length 17;
  Best Local Similarity   64.3%;  Pred. No. 1.4e+04;
  Matches    9;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CATAGACTTCTCAG 19
              ||: |||::|:|||
Db          4 CAUGGACUUCUCAG 17


RESULT 6
US-10-702-817-75/c
; Sequence 75, Application US/10702817
; Publication No. US20040147471A1
; GENERAL INFORMATION:
;  APPLICANT: Hong Zhang
;  TITLE OF INVENTION: ANTISENSE MODULATION OF TNFR1 EXPRESSION
;  FILE REFERENCE: ISPH-0797
;  CURRENT APPLICATION NUMBER: US/10/702,817
;  CURRENT FILING DATE:  2003-11-06
;  PRIOR APPLICATION NUMBER: US 09/106,038
;  PRIOR FILING DATE: 1998-06-26
;  PRIOR APPLICATION NUMBER: PCT/US99/13763
;  PRIOR FILING DATE: 1999-06-17
;  PRIOR APPLICATION NUMBER: 09/695,451
;  PRIOR FILING DATE: 2000-10-24
;  NUMBER OF SEQ ID NOS: 247
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 75
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-702-817-75

  Query Match             61.0%;  Score 12.2;  DB 22;  Length 18;
  Best Local Similarity   82.4%;  Pred. No. 1.8e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 CGCATAGACTTCTCAGA 20
              |||  || |||||||||
Db         18 CGCCCAGTCTTCTCAGA 2


RESULT 7
US-10-365-742-187
; Sequence 187, Application US/10365742
; Publication No. US20030204868A1
; GENERAL INFORMATION:
;  APPLICANT: Collmer, Alan
;  APPLICANT:  Alfano, James R.
;  APPLICANT:  Cartinhour, Samuel W.
;  APPLICANT:  Schneider, David J.
;  APPLICANT:  Tang, Xiaoyan
;  TITLE OF INVENTION: PSEUDOMONAS AVR AND HOP PROTEINS, THEIR ENCODING
;  TITLE OF INVENTION:  NUCLEIC ACIDS, AND USE THEREOF
;  FILE REFERENCE: 19603/4112
;  CURRENT APPLICATION NUMBER: US/10/365,742
;  CURRENT FILING DATE:  2002-02-12
;  PRIOR APPLICATION NUMBER: 60/356,408
;  PRIOR FILING DATE: 2002-02-12
;  PRIOR APPLICATION NUMBER: 60/380,185
;  PRIOR FILING DATE: 2002-05-10
;  NUMBER OF SEQ ID NOS: 209
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 187
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  primer
US-10-365-742-187

  Query Match             61.0%;  Score 12.2;  DB 17;  Length 19;
  Best Local Similarity   82.4%;  Pred. No. 1.8e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 CCGCATAGACTTCTCAG 19
              |||||||||| | || |
Db          3 CCGCATAGACCTGTCTG 19


RESULT 8
US-10-741-600-73759
; Sequence 73759, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
```

```
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73759
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-73759

  Query Match             61.0%;  Score 12.2;  DB 21;  Length 19;
  Best Local Similarity   82.4%;  Pred. No. 1.8e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GACCGCATAGACTTCTC 17
              ||| ||| ||||||| |
Db          1 GACAGCACAGACTTCAC 17


RESULT 9
US-10-190-366-196/c
; Sequence 196, Application US/10190366
; Publication No. US20040006031A1
; GENERAL INFORMATION:
;  APPLICANT: Nicholas M. Dean
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF HMG-COA REDUCTASE EXPRESSION
;  FILE REFERENCE: PTS-0023
;  CURRENT APPLICATION NUMBER: US/10/190,366
;  CURRENT FILING DATE:  2002-07-02
;  NUMBER OF SEQ ID NOS: 409
; SEQ ID NO 196
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-190-366-196

  Query Match             61.0%;  Score 12.2;  DB 17;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 1.8e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 CGCATAGACTTCTCAGA 20
              | || ||||| ||||||
Db         18 CACAGAGACTCCTCAGA 2


RESULT 10
US-10-190-366-389
; Sequence 389, Application US/10190366
; Publication No. US20040006031A1
; GENERAL INFORMATION:
;  APPLICANT: Nicholas M. Dean
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF HMG-COA REDUCTASE EXPRESSION
;  FILE REFERENCE: PTS-0023
;  CURRENT APPLICATION NUMBER: US/10/190,366
;  CURRENT FILING DATE:  2002-07-02
;  NUMBER OF SEQ ID NOS: 409
; SEQ ID NO 389
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: M. musculus
;   FEATURE:
US-10-190-366-389

  Query Match             61.0%;  Score 12.2;  DB 17;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 1.8e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 CGCATAGACTTCTCAGA 20
              | || ||||| ||||||
Db          3 CACAGAGACTCCTCAGA 19


RESULT 11
US-10-956-250-11
; Sequence 11, Application US/10956250
; Publication No. US20050090430A1
;   GENERAL INFORMATION:
;        APPLICANT: Feder, John N.
;                   Schatzman, Randall C.
;                   Tsuchihashi, Zenta
;        TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
;                            DIAGNOSIS AND TREATMENT OF IRON MISREGULATION D
;                            ISEASES
;        NUMBER OF SEQUENCES: 13
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Pennie & Edmonds LLP
;             STREET: 1155 Avenue of the Americas
;             CITY: New York
;             STATE: NY
;             COUNTRY: USA
;             ZIP: 10036-2811
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: Windows
;             SOFTWARE: FastSEQ for Windows Version 2.0b
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/956,250
;             FILING DATE: 01-Oct-2004
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/920,559
;             FILING DATE: 27-Aug-1997
;             APPLICATION NUMBER: US 08/652,265
;             FILING DATE: 23-MAY-1996
;             APPLICATION NUMBER: US 08/834,497
;             FILING DATE: 04-APR-1997
;             APPLICATION NUMBER: US 08/866,211
;             FILING DATE: 13-JUN-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Poissant, Brian M
;             REGISTRATION NUMBER: 28,462
;             REFERENCE/DOCKET NUMBER: 8907-0062-999
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 650-493-4935
;             TELEFAX: 650-493-5556
;             TELEX: 66141 PENNIE
;   INFORMATION FOR SEQ ID NO: 11:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 20 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-956-250-11

  Query Match             61.0%;  Score 12.2;  DB 21;  Length 20;
  Best Local Similarity   82.4%;  Pred. No. 1.8e+04;
  Matches   14;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GACCGCATAGACTTCTC 17
              ||| ||| ||||||| |
Db          2 GACAGCACAGACTTCAC 18


RESULT 12
US-09-863-806-113
; Sequence 113, Application US/09863806
; Publication No. US20020197608A1
```

```
;   GENERAL INFORMATION:
;        APPLICANT: Sidransky, David
;        TITLE OF INVENTION: DETECTION OF NEOPLASIM BY ANALYSIS OF SALIVA
;        NUMBER OF SEQUENCES: 195
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Fish & Richardson P.C.
;             STREET: 4225 Executive Square, Suite 1400
;             CITY: La Jolla
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 92037
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: Windows 95
;             SOFTWARE: FastSEQ for Windows Version 2.0b
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/863,806
;             FILING DATE: 22-May-2001
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/038,637
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: 08/152,313
;             FILING DATE: 12-NOV-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Haile, Lisa A.
;             REGISTRATION NUMBER: 38,347
;             REFERENCE/DOCKET NUMBER: 07265/146001
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 619/678-5070
;             TELEFAX: 619/678-5099
;   INFORMATION FOR SEQ ID NO: 113:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 20 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: Genomic DNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-09-863-806-113

  Query Match             60.0%;  Score 12;  DB 9;  Length 20;
  Best Local Similarity   75.0%;  Pred. No. 2.3e+04;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GACCGCATAGACTTCTCAGA 20
              |||| || || ||  |||||
Db          1 GACCCCACAGCCTATTCAGA 20


RESULT 13
US-10-754-478-113
; Sequence 113, Application US/10754478
; Publication No. US20050009040A1
;   GENERAL INFORMATION:
;        APPLICANT: Sidransky, David
;        TITLE OF INVENTION: DETECTION OF NEOPLASIM BY ANALYSIS OF SALIVA
;        NUMBER OF SEQUENCES: 195
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Fish & Richardson P.C.
;             STREET: 4225 Executive Square, Suite 1400
;             CITY: La Jolla
;             STATE: CA
;             COUNTRY: USA
;             ZIP: 92037
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: Windows 95
;             SOFTWARE: FastSEQ for Windows Version 2.0b
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/754,478
;             FILING DATE: 09-Jan-2004
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/038,637
;             FILING DATE: 10-MAR-1998
;             APPLICATION NUMBER: 08/579,233
;             FILING DATE: 28-DEC-1995
;             APPLICATION NUMBER: 08/152,313
;             FILING DATE: 12-NOV-1993
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Haile, Lisa A.
;             REGISTRATION NUMBER: 38,347
;             REFERENCE/DOCKET NUMBER: 07265/146001
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 619/678-5070
;             TELEFAX: 619/678-5099
;   INFORMATION FOR SEQ ID NO: 113:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 20 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: Genomic DNA
;        SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-10-754-478-113

  Query Match             60.0%;  Score 12;  DB 21;  Length 20;
  Best Local Similarity   75.0%;  Pred. No. 2.3e+04;
  Matches   15;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GACCGCATAGACTTCTCAGA 20
              |||| || || ||  |||||
Db          1 GACCCCACAGCCTATTCAGA 20


RESULT 14
US-10-923-329-137/c
; Sequence 137, Application US/10923329
; Publication No. US20050164968A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  Richards, Ivan
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of ADAM33 Gene Expression
;  TITLE OF INVENTION:  Using Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/225 (MBHB04-672)
;  CURRENT APPLICATION NUMBER: US/10/923,329
;  CURRENT FILING DATE:  2004-08-20
;  PRIOR APPLICATION NUMBER: PCT/US04/16390
;  PRIOR FILING DATE: 2004-05-24
;  PRIOR APPLICATION NUMBER: US 10/826,966
;  PRIOR FILING DATE: 2004-04-16
;  PRIOR APPLICATION NUMBER: PCT/US04/13456
;  PRIOR FILING DATE: 2004-04-30
;  PRIOR APPLICATION NUMBER: US 10/780,447
;  PRIOR FILING DATE: 2004-02-13
;  PRIOR APPLICATION NUMBER: US 60/292,217
;  PRIOR FILING DATE: 2001-05-18
;  PRIOR APPLICATION NUMBER: US 60/362,016
;  PRIOR FILING DATE: 2002-03-06
;  PRIOR APPLICATION NUMBER: US 60/363,883
;  PRIOR FILING DATE: 2001-07-20
;  PRIOR APPLICATION NUMBER: US 60/311,865
;  PRIOR FILING DATE: 2001-08-13
;  PRIOR APPLICATION NUMBER: US 10/727,780
;  PRIOR FILING DATE: 2003-12-03
;  PRIOR APPLICATION NUMBER: US 60/543,480
;  PRIOR FILING DATE: 2004-02-10
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 514
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 137
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
```

```
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target Sequence/siNA sense r
US-10-923-329-137

  Query Match             59.0%;  Score 11.8;  DB 22;  Length 19;
  Best Local Similarity   86.7%;  Pred. No. 2.9e+04;
  Matches   13;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 GCATAGACTTCTCAG 19
              ||| || ||||||||
Db         17 GCAGAGGCTTCTCAG 3


RESULT 15
US-10-923-329-333
; Sequence 333, Application US/10923329
; Publication No. US20050164968A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  Richards, Ivan
;  APPLICANT:  McSwiggen, James
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of ADAM33 Gene Expression
;  TITLE OF INVENTION:  Using Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400/225 (MBHB04-672)
;  CURRENT APPLICATION NUMBER: US/10/923,329
;  CURRENT FILING DATE:  2004-08-20
;  PRIOR APPLICATION NUMBER: PCT/US04/16390
;  PRIOR FILING DATE: 2004-05-24
;  PRIOR APPLICATION NUMBER: US 10/826,966
;  PRIOR FILING DATE: 2004-04-16
;  PRIOR APPLICATION NUMBER: PCT/US04/13456
;  PRIOR FILING DATE: 2004-04-30
;  PRIOR APPLICATION NUMBER: US 10/780,447
;  PRIOR FILING DATE: 2004-02-13
;  PRIOR APPLICATION NUMBER: US 60/292,217
;  PRIOR FILING DATE: 2001-05-18
;  PRIOR APPLICATION NUMBER: US 60/362,016
;  PRIOR FILING DATE: 2002-03-06
;  PRIOR APPLICATION NUMBER: US 60/363,883
;  PRIOR FILING DATE: 2001-07-20
;  PRIOR APPLICATION NUMBER: US 60/311,865
;  PRIOR FILING DATE: 2001-08-13
;  PRIOR APPLICATION NUMBER: US 10/727,780
;  PRIOR FILING DATE: 2003-12-03
;  PRIOR APPLICATION NUMBER: US 60/543,480
;  PRIOR FILING DATE: 2004-02-10
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 514
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 333
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  siNA antisense region
US-10-923-329-333

  Query Match             59.0%;  Score 11.8;  DB 22;  Length 19;
  Best Local Similarity   66.7%;  Pred. No. 2.9e+04;
  Matches   10;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 GCATAGACTTCTCAG 19
              ||| || |::|:|||
Db          3 GCAGAGGCUUCUCAG 17


RESULT 16
US-10-741-600-73758
; Sequence 73758, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
;  APPLICANT: CARGILL, Michele et al.
;  TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
;  TITLE OF INVENTION:  MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001499
;  CURRENT APPLICATION NUMBER: US/10/741,600
;  CURRENT FILING DATE:  2003-12-22
;  NUMBER OF SEQ ID NOS: 73997
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73758
;   LENGTH: 18
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-741-600-73758

  Query Match             58.0%;  Score 11.6;  DB 21;  Length 18;
  Best Local Similarity   77.8%;  Pred. No. 3.7e+04;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 ACCGCATAGACTTCTCAG 19
              || ||| ||||||| | |
Db          1 ACAGCACAGACTTCACCG 18


RESULT 17
US-09-768-436-31/c
; Sequence 31, Application US/09768436
; Patent No. US20020006639A1
; GENERAL INFORMATION:
;  APPLICANT:  Paul Andrew Whittaker et al
;  TITLE OF INVENTION:  Disease-Associated Gene
;  FILE REFERENCE:  Case No. US20020006639A1 4-31306A/HO 25
;  CURRENT APPLICATION NUMBER: US/09/768,436
;  CURRENT FILING DATE:  2001-01-24
;  NUMBER OF SEQ ID NOS:  70
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 31
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-768-436-31

  Query Match             58.0%;  Score 11.6;  DB 9;  Length 19;
  Best Local Similarity   77.8%;  Pred. No. 3.7e+04;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GACCGCATAGACTTCTCA 18
              ||| |||  ||| |||||
Db         18 GACGGCAGCGACATCTCA 1


RESULT 18
US-10-888-226-46/c
; Sequence 46, Application US/10888226
; Publication No. US20050124568A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Usman, Nassim
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Acetyl-CoA-Carboxylase
;  TITLE OF INVENTION:  Gene Expression Using Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400-199 (MBHB03-710-A)
;  CURRENT APPLICATION NUMBER: US/10/888,226
;  CURRENT FILING DATE:  2004-07-09
;  PRIOR APPLICATION NUMBER: US 60/486,729
;  PRIOR FILING DATE: 2003-07-11
;  PRIOR APPLICATION NUMBER: PCT/US04/16390
;  PRIOR FILING DATE: 2004-05-24
;  PRIOR APPLICATION NUMBER: US 10/826,966
;  PRIOR FILING DATE: 2004-04-16
;  PRIOR APPLICATION NUMBER: US 10/757,803
;  PRIOR FILING DATE: 2004-01-14
;  PRIOR APPLICATION NUMBER: US 10/720,448
;  PRIOR FILING DATE: 2003-11-24
;  PRIOR APPLICATION NUMBER: US 10/693,059
;  PRIOR FILING DATE: 2003-10-23
```

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;  PRIOR APPLICATION NUMBER: US 10/444,853
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: PCT/US03/05346
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: PCT/US03/05028
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US 60/358580
;  PRIOR FILING DATE: 2002-02-20
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 955
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 46
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Target Sequence/siNA sense r
US-10-888-226-46

  Query Match           58.0%;  Score 11.6;  DB 22;  Length 19;
  Best Local Similarity  77.8%;  Pred. No. 3.7e+04;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GACCGCATAGACTTCTCA 18
              || ||||| |||||| ||
Db         18 GAGCGCATGCACTTCACA 1


RESULT 19
US-10-888-226-460
; Sequence 460, Application US/10888226
; Publication No. US20050124568A1
; GENERAL INFORMATION:
;  APPLICANT: Sirna Therapeutics, Inc.
;  APPLICANT:  McSwiggen, James
;  APPLICANT:  Usman, Nassim
;  TITLE OF INVENTION: RNA Interference Mediated Inhibition of Acetyl-CoA-Carboxylase
;  TITLE OF INVENTION:  Gene Expression Using Short Interfering Nucleic Acid (siNA)
;  FILE REFERENCE: 400-199 (MBHB03-710-A)
;  CURRENT APPLICATION NUMBER: US/10/888,226
;  CURRENT FILING DATE:  2004-07-09
;  PRIOR APPLICATION NUMBER: US 60/486,729
;  PRIOR FILING DATE: 2003-07-11
;  PRIOR APPLICATION NUMBER: PCT/US04/16390
;  PRIOR FILING DATE: 2004-05-24
;  PRIOR APPLICATION NUMBER: US 10/826,966
;  PRIOR FILING DATE: 2004-04-16
;  PRIOR APPLICATION NUMBER: US 10/757,803
;  PRIOR FILING DATE: 2004-01-14
;  PRIOR APPLICATION NUMBER: US 10/720,448
;  PRIOR FILING DATE: 2003-11-24
;  PRIOR APPLICATION NUMBER: US 10/693,059
;  PRIOR FILING DATE: 2003-10-23
;  PRIOR APPLICATION NUMBER: US 10/444,853
;  PRIOR FILING DATE: 2003-05-23
;  PRIOR APPLICATION NUMBER: PCT/US03/05346
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: PCT/US03/05028
;  PRIOR FILING DATE: 2003-02-20
;  PRIOR APPLICATION NUMBER: US 60/358580
;  PRIOR FILING DATE: 2002-02-20
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 955
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 460
;   LENGTH: 19
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  siNA antisense region
US-10-888-226-460

  Query Match           58.0%;  Score 11.6;  DB 22;  Length 19;
  Best Local Similarity  61.1%;  Pred. No. 3.7e+04;
  Matches   11;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GACCGCATAGACTTCTCA 18
              || ||||:  ||::| ||
Db          2 GAGCGCAUGCACUUCACA 19


RESULT 20
US-09-731-457B-14
; Sequence 14, Application US/09731457B
; Patent No. US20020103146A1
; GENERAL INFORMATION:
;  APPLICANT: Ian Popoff
;  APPLICANT:  Jacqueline Wyatt
;  TITLE OF INVENTION: ANTISENSE MODULATION OF DAMAGE-SPECIFIC DNA BINDING PROTEIN 1, P1
;  TITLE OF INVENTION:  EXPRESSION
;  FILE REFERENCE: RTS-0182
;  CURRENT APPLICATION NUMBER: US/09/731,457B
;  CURRENT FILING DATE:  2000-12-06
;  NUMBER OF SEQ ID NOS: 87
; SEQ ID NO 14
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-09-731-457B-14

  Query Match           58.0%;  Score 11.6;  DB 9;  Length 20;
  Best Local Similarity  77.8%;  Pred. No. 3.7e+04;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GACCGCATAGACTTCTCA 18
              |||| |||||| ||| |
Db          2 GACCACATAGATCTCTAA 19


RESULT 21
US-10-345-092-51
; Sequence 51, Application US/10345092
; Publication No. US20030165506A1
; GENERAL INFORMATION:
;  APPLICANT: Vlaams Interuniversitair Instituut voor Biotechnol
;  TITLE OF INVENTION: No. US20030165506A1el alpha-catenin expressed in heart and testis
;  FILE REFERENCE: FVR/aTc/V067
;  CURRENT APPLICATION NUMBER: US/10/345,092
;  CURRENT FILING DATE:  2003-01-13
;  PRIOR APPLICATION NUMBER: 00202472.7
;  PRIOR FILING DATE: 2000-07-12
;  PRIOR APPLICATION NUMBER: US 60/218,309
;  PRIOR FILING DATE: 2000-07-14
;  NUMBER OF SEQ ID NOS: 134
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: upper primer
;   OTHER INFORMATION: FVR2521
US-10-345-092-51

  Query Match           58.0%;  Score 11.6;  DB 16;  Length 20;
  Best Local Similarity  77.8%;  Pred. No. 3.7e+04;
  Matches   14;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1'GACCGCATAGACTTCTCA 18
              ||| | | || |||||||
Db          2 GACTGAACAGGCTTCTCA 19


RESULT 22
```

```
US-10-056-414-289
; Sequence 289, Application US/10056414
; Publication No. US20030003469A1
;   GENERAL INFORMATION:
;        APPLICANT: Stinchcomb, Dan T.
;                   Draper, Kenneth G.
;                   McSwiggen, James
;        TITLE OF INVENTION: RIBOZYME TREATMENT OF
;                            DISEASES OR CONDITIONS
;                            RELATED TO LEVELS OF
;                            NF-KB
;        NUMBER OF SEQUENCES: 830
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Lyon & Lyon
;             STREET: 633 West Fifth Street
;                     Suite 4700
;             CITY: Los Angeles
;             STATE: California
;             COUNTRY: U.S.A.
;             ZIP: 90071-2066
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
;                          storage
;             COMPUTER: IBM Compatible
;             OPERATING SYSTEM: IBM P.C. DOS 5.0
;             SOFTWARE: Word Perfect 5.1
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/056,414
;             FILING DATE: 23-Jan-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/291,932A
;             FILING DATE: August 15, 1994
;             APPLICATION NUMBER: 08/245,466
;             FILING DATE: May 18, 1994
;             APPLICATION NUMBER: 07/987,132
;             FILING DATE: December 7, 1992
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Warburg, Richard J.
;             REGISTRATION NUMBER: 32,327
;             REFERENCE/DOCKET NUMBER: 208/157
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (213) 489-1600
;             TELEFAX: (213) 955-0440
;             TELEX: 67-3510
;   INFORMATION FOR SEQ ID NO: 289:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 15 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 289:
US-10-056-414-289

  Query Match             57.0%;  Score 11.4;  DB 14;  Length 15;
  Best Local Similarity   61.5%;  Pred. No. 4.7e+04;
  Matches    8;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 ATAGACTTCTCAG 19
              |: |||::|:|||
Db          1 AUGGACUUCUCAG 13


RESULT 23
US-09-864-785-2881
; Sequence 2881, Application US/09864785
; Patent No. US20020177568A1
; GENERAL INFORMATION:
;  APPLICANT: Ribozyme Pharmaceuticals, Inc.
;  APPLICANT:  Stinchcomb, Dan
;  APPLICANT:  Draper, Ken
;  APPLICANT:  McSwiggen, Jim
;  TITLE OF INVENTION: Enzymatic Nucleic Acid Treatment of Diseases or Conditions Relate
;  TITLE OF INVENTION:  Levels of NF-Kappa B
;  FILE REFERENCE: 400/022 (MBHB00-812-D)
;  CURRENT APPLICATION NUMBER: US/09/864,785
;  CURRENT FILING DATE:  2001-05-23
;  NUMBER OF SEQ ID NOS: 3929
;  SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2881
;   LENGTH: 17
;   TYPE: RNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:  Nucleic Acid
US-09-864-785-2881

  Query Match             57.0%;  Score 11.4;  DB 9;  Length 17;
  Best Local Similarity   61.5%;  Pred. No. 4.7e+04;
  Matches    8;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CATAGACTTCTCA 18
              ||: |||::|:||
Db          5 CAUGGACUUCUCA 17


RESULT 24
US-09-795-668-43
; Sequence 43, Application US/09795668
; Patent No. US20020045577A1
; GENERAL INFORMATION:
;  APPLICANT: Stefansson, Hreinn
;  APPLICANT:  Steinthorsdottir, Valgerdur
;  APPLICANT:  Gulcher, Jeffrey R.
;  TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
;  FILE REFERENCE: 2345.2004-001
;  CURRENT APPLICATION NUMBER: US/09/795,668
;  CURRENT FILING DATE:  2001-02-28
;  PRIOR APPLICATION NUMBER: US 09/515,716
;  PRIOR FILING DATE: 2000-02-28
;  NUMBER OF SEQ ID NOS: 1531
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 43
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-795-668-43

  Query Match             57.0%;  Score 11.4;  DB 9;  Length 20;
  Best Local Similarity   92.3%;  Pred. No. 4.8e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          5 GCATAGACTTCTC 17
              ||||||| |||||
Db          6 GCATAGAATTCTC 18


RESULT 25
US-09-795-686-43
; Sequence 43, Application US/09795686
; Patent No. US20020094954A1
; GENERAL INFORMATION:
;  APPLICANT: Stefansson, Hreinn
;  APPLICANT:  Steinthorsdottir, Valgerdur
;  APPLICANT:  Gulcher, Jeffrey R.
;  TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
;  FILE REFERENCE: 2345.2005-001
;  CURRENT APPLICATION NUMBER: US/09/795,686
;  CURRENT FILING DATE:  2001-02-28
;  PRIOR APPLICATION NUMBER: US 09/515,715
;  PRIOR FILING DATE: 2000-02-28
;  NUMBER OF SEQ ID NOS: 1531
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 43
;   LENGTH: 20
;   TYPE: DNA
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; ORGANISM: Homo sapiens
US-09-795-686-43

  Query Match 57.0%; Score 11.4; DB 9; Length 20;
  Best Local Similarity 92.3%; Pred. No. 4.8e+04;
  Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCATAGACTTCTC 17
      ||||||| |||||
Db 6 GCATAGAATTCTC 18

RESULT 26
US-09-946-807-43
; Sequence 43, Application US/09946807
; Patent No. US20020165144A1
; GENERAL INFORMATION:
; APPLICANT: Stefansson, Hreinn
; APPLICANT: Steinthorsdottir, Valgerdur
; APPLICANT: Gulcher, Jeffrey R.
; TITLE OF INVENTION: HUMAN SCHIZOPHRENIA GENE
; FILE REFERENCE: 2345.2004-001
; CURRENT APPLICATION NUMBER: US/09/946,807
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US/09/795,668
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 09/515,716
; PRIOR FILING DATE: 2000-02-28
; NUMBER OF SEQ ID NOS: 1531
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-946-807-43

  Query Match 57.0%; Score 11.4; DB 9; Length 20;
  Best Local Similarity 92.3%; Pred. No. 4.8e+04;
  Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GCATAGACTTCTC 17
      ||||||| |||||
Db 6 GCATAGAATTCTC 18

RESULT 27
US-10-148-806-20/c
; Sequence 20, Application US/10148806
; Publication No. US20030138933A1
; GENERAL INFORMATION:
; APPLICANT: Bai, Chang
; APPLICANT: Metzger, Michael
; APPLICANT: Liu, Xiaomei
; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN NHL, A DNA
; TITLE OF INVENTION: HELICASE
; FILE REFERENCE: 20585P
; CURRENT APPLICATION NUMBER: US/10/148,806
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US00/33065
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: 60/169,970
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-148-806-20

  Query Match 57.0%; Score 11.4; DB 15; Length 20;
  Best Local Similarity 92.3%; Pred. No. 4.8e+04;
  Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 TAGACTTCTCAGA 20
      | ||||||||||||
Db 17 TGGACTTCTCAGA 5

RESULT 28
US-10-148-806-21
; Sequence 21, Application US/10148806
; Publication No. US20030138933A1
; GENERAL INFORMATION:
; APPLICANT: Bai, Chang
; APPLICANT: Metzger, Michael
; APPLICANT: Liu, Xiaomei
; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN NHL, A DNA
; TITLE OF INVENTION: HELICASE
; FILE REFERENCE: 20585P
; CURRENT APPLICATION NUMBER: US/10/148,806
; CURRENT FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US00/33065
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: 60/169,970
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-148-806-21

  Query Match 57.0%; Score 11.4; DB 15; Length 20;
  Best Local Similarity 92.3%; Pred. No. 4.8e+04;
  Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 TAGACTTCTCAGA 20
      | ||||||||||||
Db 4 TGGACTTCTCAGA 16

RESULT 29
US-10-174-319-35/c
; Sequence 35, Application US/10174319
; Publication No. US20030232771A1
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Susan M. Freier
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTISENSE MODULATION OF MARK3 EXPRESSION
; FILE REFERENCE: PTS-0018
; CURRENT APPLICATION NUMBER: US/10/174,319
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 121
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-10-174-319-35

  Query Match 57.0%; Score 11.4; DB 17; Length 20;
  Best Local Similarity 92.3%; Pred. No. 4.8e+04;
  Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 8 TAGACTTCTCAGA 20
      ||||| |||||||
Db 19 TAGACATCTCAGA 7

```
RESULT 30
US-10-174-319-101
; Sequence 101, Application US/10174319
; Publication No. US20030232771A1
; GENERAL INFORMATION:
;  APPLICANT: Donna T. Ward
;  APPLICANT:  Susan M. Freier
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: ANTISENSE MODULATION OF MARK3 EXPRESSION
;  FILE REFERENCE: PTS-0018
;  CURRENT APPLICATION NUMBER: US/10/174,319
;  CURRENT FILING DATE:  2002-06-17
;  NUMBER OF SEQ ID NOS: 121
; SEQ ID NO 101
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: H. sapiens
;   FEATURE:
US-10-174-319-101

  Query Match             57.0%;  Score 11.4;  DB 17;  Length 20;
  Best Local Similarity   92.3%;  Pred. No. 4.8e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          8 TAGACTTCTCAGA 20
              ||||| |||||||
Db          2 TAGACATCTCAGA 14


RESULT 31
US-10-304-111-24
; Sequence 24, Application US/10304111
; Publication No. US20040102403A1
; GENERAL INFORMATION:
;  APPLICANT: C. Frank Bennett
;  APPLICANT:  Nicholas M. Dean
;  APPLICANT:  Kenneth W. Dobie
;  TITLE OF INVENTION: MODULATION OF FIBRILLARIN EXPRESSION
;  FILE REFERENCE: HTS-0075
;  CURRENT APPLICATION NUMBER: US/10/304,111
;  CURRENT FILING DATE:  2002-11-21
;  NUMBER OF SEQ ID NOS: 71
; SEQ ID NO 24
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense Oligonucleotide
US-10-304-111-24

  Query Match             57.0%;  Score 11.4;  DB 19;  Length 20;
  Best Local Similarity   92.3%;  Pred. No. 4.8e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GACCGCATAGACT 13
              ||| |||||||||
Db          2 GACTGCATAGACT 14


RESULT 32
US-10-831-901A-2082/c
; Sequence 2082, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
;  APPLICANT: Crooke, Stanley T.
;  APPLICANT:  Ecker, David J.
;  APPLICANT:  Sampath, Rangarajan
;  APPLICANT:  Freier, Susan M.
;  APPLICANT:  Massire, Christian
;  APPLICANT:  Hofstadler, Steven A.
;  APPLICANT:  Lowery, Kristin Sannes
;  APPLICANT:  Swayze, Eric
;  APPLICANT:  Baker, Brenda F.
;  APPLICANT:  Bennett, C. Frank
;  TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
;  TITLE OF INVENTION:  Acute Respiratory Syndrome (SARS)
;  FILE REFERENCE: ISIS0083-100 (BIOL0008US)
;  CURRENT APPLICATION NUMBER: US/10/831,901A
;  CURRENT FILING DATE:  2004-04-26
;  PRIOR APPLICATION NUMBER: 60/466,426
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: 60/468,562
;  PRIOR FILING DATE: 2003-05-06
;  PRIOR APPLICATION NUMBER: 60/467,770
;  PRIOR FILING DATE: 2003-04-30
;  PRIOR APPLICATION NUMBER: 60/468,627
;  PRIOR FILING DATE: 2003-05-06
;  PRIOR APPLICATION NUMBER: 60/477,637
;  PRIOR FILING DATE: 2003-06-10
;  PRIOR APPLICATION NUMBER: 60/483,579
;  PRIOR FILING DATE: 2003-06-27
;  NUMBER OF SEQ ID NOS: 30063
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2082
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense compound
US-10-831-901A-2082

  Query Match             57.0%;  Score 11.4;  DB 21;  Length 20;
  Best Local Similarity   92.3%;  Pred. No. 4.8e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 ATAGACTTCTCAG 19
              | ||||||||||||
Db         13 ACAGACTTCTCAG 1


RESULT 33
US-10-831-901A-2083/c
; Sequence 2083, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
;  APPLICANT: Crooke, Stanley T.
;  APPLICANT:  Ecker, David J.
;  APPLICANT:  Sampath, Rangarajan
;  APPLICANT:  Freier, Susan M.
;  APPLICANT:  Massire, Christian
;  APPLICANT:  Hofstadler, Steven A.
;  APPLICANT:  Lowery, Kristin Sannes
;  APPLICANT:  Swayze, Eric
;  APPLICANT:  Baker, Brenda F.
;  APPLICANT:  Bennett, C. Frank
;  TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
;  TITLE OF INVENTION:  Acute Respiratory Syndrome (SARS)
;  FILE REFERENCE: ISIS0083-100 (BIOL0008US)
;  CURRENT APPLICATION NUMBER: US/10/831,901A
;  CURRENT FILING DATE:  2004-04-26
;  PRIOR APPLICATION NUMBER: 60/466,426
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: 60/468,562
;  PRIOR FILING DATE: 2003-05-06
;  PRIOR APPLICATION NUMBER: 60/467,770
;  PRIOR FILING DATE: 2003-04-30
;  PRIOR APPLICATION NUMBER: 60/468,627
;  PRIOR FILING DATE: 2003-05-06
;  PRIOR APPLICATION NUMBER: 60/477,637
;  PRIOR FILING DATE: 2003-06-10
;  PRIOR APPLICATION NUMBER: 60/483,579
;  PRIOR FILING DATE: 2003-06-27
;  NUMBER OF SEQ ID NOS: 30063
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2083
```

```
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense compound
US-10-831-901A-2083

  Query Match             57.0%;  Score 11.4;  DB 21;  Length 20;
  Best Local Similarity   92.3%;  Pred. No. 4.8e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 ATAGACTTCTCAG 19
              | ||||||||||||
Db         14 ACAGACTTCTCAG 2


RESULT 34
US-10-831-901A-2084/c
; Sequence 2084, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
;  APPLICANT: Crooke, Stanley T.
;  APPLICANT:  Ecker, David J.
;  APPLICANT:  Sampath, Rangarajan
;  APPLICANT:  Freier, Susan M.
;  APPLICANT:  Massire, Christian
;  APPLICANT:  Hofstadler, Steven A.
;  APPLICANT:  Lowery, Kristin Sannes
;  APPLICANT:  Swayze, Eric
;  APPLICANT:  Baker, Brenda F.
;  APPLICANT:  Bennett, C. Frank
;  TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
;  TITLE OF INVENTION:  Acute Respiratory Syndrome (SARS)
;  FILE REFERENCE: ISIS0083-100 (BIOL0008US)
;  CURRENT APPLICATION NUMBER: US/10/831,901A
;  CURRENT FILING DATE:  2004-04-26
;  PRIOR APPLICATION NUMBER: 60/466,426
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: 60/468,562
;  PRIOR FILING DATE: 2003-05-06
;  PRIOR APPLICATION NUMBER: 60/467,770
;  PRIOR FILING DATE: 2003-04-30
;  PRIOR APPLICATION NUMBER: 60/468,627
;  PRIOR FILING DATE: 2003-05-06
;  PRIOR APPLICATION NUMBER: 60/477,637
;  PRIOR FILING DATE: 2003-06-10
;  PRIOR APPLICATION NUMBER: 60/483,579
;  PRIOR FILING DATE: 2003-06-27
;  NUMBER OF SEQ ID NOS: 30063
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2084
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense compound
US-10-831-901A-2084

  Query Match             57.0%;  Score 11.4;  DB 21;  Length 20;
  Best Local Similarity   92.3%;  Pred. No. 4.8e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 ATAGACTTCTCAG 19
              | ||||||||||||
Db         15 ACAGACTTCTCAG 3


RESULT 35
US-10-831-901A-2085/c
; Sequence 2085, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
;  APPLICANT: Crooke, Stanley T.
;  APPLICANT:  Ecker, David J.
;  APPLICANT:  Sampath, Rangarajan
;  APPLICANT:  Freier, Susan M.
;  APPLICANT:  Massire, Christian
;  APPLICANT:  Hofstadler, Steven A.
;  APPLICANT:  Lowery, Kristin Sannes
;  APPLICANT:  Swayze, Eric
;  APPLICANT:  Baker, Brenda F.
;  APPLICANT:  Bennett, C. Frank
;  TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
;  TITLE OF INVENTION:  Acute Respiratory Syndrome (SARS)
;  FILE REFERENCE: ISIS0083-100 (BIOL0008US)
;  CURRENT APPLICATION NUMBER: US/10/831,901A
;  CURRENT FILING DATE:  2004-04-26
;  PRIOR APPLICATION NUMBER: 60/466,426
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: 60/468,562
;  PRIOR FILING DATE: 2003-05-06
;  PRIOR APPLICATION NUMBER: 60/467,770
;  PRIOR FILING DATE: 2003-04-30
;  PRIOR APPLICATION NUMBER: 60/468,627
;  PRIOR FILING DATE: 2003-05-06
;  PRIOR APPLICATION NUMBER: 60/477,637
;  PRIOR FILING DATE: 2003-06-10
;  PRIOR APPLICATION NUMBER: 60/483,579
;  PRIOR FILING DATE: 2003-06-27
;  NUMBER OF SEQ ID NOS: 30063
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2085
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense compound
US-10-831-901A-2085

  Query Match             57.0%;  Score 11.4;  DB 21;  Length 20;
  Best Local Similarity   92.3%;  Pred. No. 4.8e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 ATAGACTTCTCAG 19
              | ||||||||||||
Db         16 ACAGACTTCTCAG 4


RESULT 36
US-10-831-901A-2086/c
; Sequence 2086, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
;  APPLICANT: Crooke, Stanley T.
;  APPLICANT:  Ecker, David J.
;  APPLICANT:  Sampath, Rangarajan
;  APPLICANT:  Freier, Susan M.
;  APPLICANT:  Massire, Christian
;  APPLICANT:  Hofstadler, Steven A.
;  APPLICANT:  Lowery, Kristin Sannes
;  APPLICANT:  Swayze, Eric
;  APPLICANT:  Baker, Brenda F.
;  APPLICANT:  Bennett, C. Frank
;  TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
;  TITLE OF INVENTION:  Acute Respiratory Syndrome (SARS)
;  FILE REFERENCE: ISIS0083-100 (BIOL0008US)
;  CURRENT APPLICATION NUMBER: US/10/831,901A
;  CURRENT FILING DATE:  2004-04-26
;  PRIOR APPLICATION NUMBER: 60/466,426
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: 60/468,562
;  PRIOR FILING DATE: 2003-05-06
;  PRIOR APPLICATION NUMBER: 60/467,770
;  PRIOR FILING DATE: 2003-04-30
;  PRIOR APPLICATION NUMBER: 60/468,627
;  PRIOR FILING DATE: 2003-05-06
```

```
;  PRIOR APPLICATION NUMBER: 60/477,637
;  PRIOR FILING DATE: 2003-06-10
;  PRIOR APPLICATION NUMBER: 60/483,579
;  PRIOR FILING DATE: 2003-06-27
;  NUMBER OF SEQ ID NOS: 30063
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2086
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense compound
US-10-831-901A-2086

  Query Match             57.0%;  Score 11.4;  DB 21;  Length 20;
  Best Local Similarity   92.3%;  Pred. No. 4.8e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 ATAGACTTCTCAG 19
              | ||||||||||||
Db         17 ACAGACTTCTCAG 5


RESULT 37
US-10-831-901A-2087/c
; Sequence 2087, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
;  APPLICANT: Crooke, Stanley T.
;  APPLICANT:  Ecker, David J.
;  APPLICANT:  Sampath, Rangarajan
;  APPLICANT:  Freier, Susan M.
;  APPLICANT:  Massire, Christian
;  APPLICANT:  Hofstadler, Steven A.
;  APPLICANT:  Lowery, Kristin Sannes
;  APPLICANT:  Swayze, Eric
;  APPLICANT:  Baker, Brenda F.
;  APPLICANT:  Bennett, C. Frank
;  TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
;  TITLE OF INVENTION:  Acute Respiratory Syndrome (SARS)
;  FILE REFERENCE: ISIS0083-100 (BIOL0008US)
;  CURRENT APPLICATION NUMBER: US/10/831,901A
;  CURRENT FILING DATE:  2004-04-26
;  PRIOR APPLICATION NUMBER: 60/466,426
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: 60/468,562
;  PRIOR FILING DATE: 2003-05-06
;  PRIOR APPLICATION NUMBER: 60/467,770
;  PRIOR FILING DATE: 2003-04-30
;  PRIOR APPLICATION NUMBER: 60/468,627
;  PRIOR FILING DATE: 2003-05-06
;  PRIOR APPLICATION NUMBER: 60/477,637
;  PRIOR FILING DATE: 2003-06-10
;  PRIOR APPLICATION NUMBER: 60/483,579
;  PRIOR FILING DATE: 2003-06-27
;  NUMBER OF SEQ ID NOS: 30063
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2087
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense compound
US-10-831-901A-2087

  Query Match             57.0%;  Score 11.4;  DB 21;  Length 20;
  Best Local Similarity   92.3%;  Pred. No. 4.8e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 ATAGACTTCTCAG 19
              | ||||||||||||
Db         18 ACAGACTTCTCAG 6


RESULT 38
US-10-831-901A-2088/c
; Sequence 2088, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
;  APPLICANT: Crooke, Stanley T.
;  APPLICANT:  Ecker, David J.
;  APPLICANT:  Sampath, Rangarajan
;  APPLICANT:  Freier, Susan M.
;  APPLICANT:  Massire, Christian
;  APPLICANT:  Hofstadler, Steven A.
;  APPLICANT:  Lowery, Kristin Sannes
;  APPLICANT:  Swayze, Eric
;  APPLICANT:  Baker, Brenda F.
;  APPLICANT:  Bennett, C. Frank
;  TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
;  TITLE OF INVENTION:  Acute Respiratory Syndrome (SARS)
;  FILE REFERENCE: ISIS0083-100 (BIOL0008US)
;  CURRENT APPLICATION NUMBER: US/10/831,901A
;  CURRENT FILING DATE:  2004-04-26
;  PRIOR APPLICATION NUMBER: 60/466,426
;  PRIOR FILING DATE: 2003-04-28
;  PRIOR APPLICATION NUMBER: 60/468,562
;  PRIOR FILING DATE: 2003-05-06
;  PRIOR APPLICATION NUMBER: 60/467,770
;  PRIOR FILING DATE: 2003-04-30
;  PRIOR APPLICATION NUMBER: 60/468,627
;  PRIOR FILING DATE: 2003-05-06
;  PRIOR APPLICATION NUMBER: 60/477,637
;  PRIOR FILING DATE: 2003-06-10
;  PRIOR APPLICATION NUMBER: 60/483,579
;  PRIOR FILING DATE: 2003-06-27
;  NUMBER OF SEQ ID NOS: 30063
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2088
;   LENGTH: 20
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Antisense compound
US-10-831-901A-2088

  Query Match             57.0%;  Score 11.4;  DB 21;  Length 20;
  Best Local Similarity   92.3%;  Pred. No. 4.8e+04;
  Matches   12;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          7 ATAGACTTCTCAG 19
              | ||||||||||||
Db         19 ACAGACTTCTCAG 7


RESULT 39
US-10-831-901A-2089/c
; Sequence 2089, Application US/10831901A
; Publication No. US20050100885A1
; GENERAL INFORMATION:
;  APPLICANT: Crooke, Stanley T.
;  APPLICANT:  Ecker, David J.
;  APPLICANT:  Sampath, Rangarajan
;  APPLICANT:  Freier, Susan M.
;  APPLICANT:  Massire, Christian
;  APPLICANT:  Hofstadler, Steven A.
;  APPLICANT:  Lowery, Kristin Sannes
;  APPLICANT:  Swayze, Eric
;  APPLICANT:  Baker, Brenda F.
;  APPLICANT:  Bennett, C. Frank
;  TITLE OF INVENTION: Compositions And Methods For The Treatment Of Severe
;  TITLE OF INVENTION:  Acute Respiratory Syndrome (SARS)
;  FILE REFERENCE: ISIS0083-100 (BIOL0008US)
;  CURRENT APPLICATION NUMBER: US/10/831,901A
;  CURRENT FILING DATE:  2004-04-26
;  PRIOR APPLICATION NUMBER: 60/466,426
```

; PRIOR FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: 60/468,562
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/467,770
; PRIOR FILING DATE: 2003-04-30
; PRIOR APPLICATION NUMBER: 60/468,627
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/477,637
; PRIOR FILING DATE: 2003-06-10
; PRIOR APPLICATION NUMBER: 60/483,579
; PRIOR FILING DATE: 2003-06-27
; NUMBER OF SEQ ID NOS: 30063
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2089
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense compound
US-10-831-901A-2089

Query Match 57.0%; Score 11.4; DB 21; Length 20;
Best Local Similarity 92.3%; Pred. No. 4.8e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          7 ATAGACTTCTCAG 19
              | ||||||||||||
Db         20 ACAGACTTCTCAG 8
```

RESULT 40
US-10-859-792-20/c
; Sequence 20, Application US/10859792
; Publication No. US20050136425A1
; GENERAL INFORMATION:
; APPLICANT: Bai, Chang
; APPLICANT: Metzger, Michael
; APPLICANT: Liu, Xiaomei
; TITLE OF INVENTION: DNA MOLECULES ENCODING HUMAN NHL, A DNA
; TITLE OF INVENTION: HELICASE
; FILE REFERENCE: 20585P
; CURRENT APPLICATION NUMBER: US/10/859,792
; CURRENT FILING DATE: 2004-06-03
; PRIOR APPLICATION NUMBER: US/10/148,806
; PRIOR FILING DATE: 2002-06-05
; PRIOR APPLICATION NUMBER: US00/33065
; PRIOR FILING DATE: 2000-12-09
; PRIOR APPLICATION NUMBER: 60/169,970
; PRIOR FILING DATE: 1999-12-09
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-859-792-20

Query Match 57.0%; Score 11.4; DB 22; Length 20;
Best Local Similarity 92.3%; Pred. No. 4.8e+04;
Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy          8 TAGACTTCTCAGA 20
              | ||||||||||||
Db         17 TGGACTTCTCAGA 5
```

Search completed: August 12, 2005, 12:19:44
Job time : 376 secs

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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: August 12, 2005, 11:03:34 ; Search time 1779 Seconds
(without alignments)
427.929 Million cell updates/sec

Title: US-09-743-825-10
Perfect score: 20
Sequence: 1 gaccgcatagacttctcaga 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 12452

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	10.2	51.0	19	7	CO792214	NT014C_A1
	2	9.8	49.0	19	8	AZ309643	AZ309643 1M0016E23
c	3	9.6	48.0	20	8	AZ660128	AZ660128 1M0538G04
c	4	9.2	46.0	17	9	CL681189	PRI0130b_
c	5	9	45.0	18	5	BQ593906	BQ593906 S015504-0
	6	9	45.0	19	1	AJ671616	AJ671616 AJ671616
	7	9	45.0	19	9	CL671780	PRI0165c_
	8	9	45.0	20	9	AG188131	AG188131 Pan trogl
c	9	8.8	44.0	16	5	BQ585512	BQ585512 E012305-0
	10	8.8	44.0	19	8	AZ585898	AZ585898 1M0391L22
c	11	8.8	44.0	20	9	AG187931	AG187931 Pan trogl
c	12	8.8	44.0	20	9	AG200702	AG200702 Pan trogl
c	13	8.6	43.0	16	1	AJ684587	AJ684587 AJ684587
	14	8.6	43.0	19	8	AZ309116	AZ309116 1M0012E23
	15	8.6	43.0	20	7	CO783852	CO783852 BL279A_E0
	16	8.6	43.0	20	8	AZ440002	AZ440002 1M0230E19
	17	8.4	42.0	17	1	AJ648088	AJ648088 AJ648088
c	18	8.4	42.0	19	8	AZ313531	AZ313531 1M0029N07
	19	8.4	42.0	19	8	AZ663240	AZ663240 1M0542H18
c	20	8.4	42.0	20	8	AZ303578	AZ303578 1M0003H07
c	21	8.4	42.0	20	8	AZ771437	AZ771437 1M0573P03
	22	8.2	41.0	16	9	CL423466	CL423466 01S0557-0
c	23	8.2	41.0	19	1	AA916934	AA916934 on14a09.s
c	24	8.2	41.0	19	8	AZ414372	AZ414372 1M0188G18
c	25	8.2	41.0	19	8	AZ436629	AZ436629 1M0224O19
c	26	8.2	41.0	19	8	AZ454430	AZ454430 1M0256F21
c	27	8.2	41.0	19	8	AZ647364	AZ647364 1M0513O16
	28	8.2	41.0	19	8	AZ655870	AZ655870 1M0531N06
	29	8.2	41.0	19	8	AZ783477	AZ783477 2M0025D18
c	30	8	40.0	12	9	AJ594088	AJ594088 Arabidops
	31	8	40.0	20	8	AZ345710	AZ345710 1M0080H05
	32	7.8	39.0	14	9	CL423876	CL423876 01S0750-0
	33	7.8	39.0	14	9	CL438505	CL438505 PST7640-N
	34	7.8	39.0	18	9	AJ587709	AJ587709 Arabidops
	35	7.8	39.0	19	8	AZ355195	AZ355195 1M0094G22
c	36	7.8	39.0	19	8	AZ422531	AZ422531 1M0201E16
	37	7.8	39.0	19	8	AZ875430	AZ875430 2M0189K09
c	38	7.8	39.0	19	9	AJ595189	AJ595189 Arabidops
	39	7.8	39.0	19	9	AJ599121	AJ599121 Arabidops
	40	7.8	39.0	19	9	CL683526	CL683526 PRI0137a_
c	41	7.8	39.0	20	1	AJ808310	AJ808310 AJ808310
	42	7.8	39.0	20	8	AZ480596	AZ480596 1M0302D18
	43	7.8	39.0	20	9	AJ597717	AJ597717 Arabidops
	44	7.8	39.0	20	9	CL423931	CL423931 02S0166-0
	45	7.6	38.0	17	9	AJ587423	AJ587423 Arabidops
	46	7.6	38.0	19	1	AA915433	AA915433 vz30f10.r
c	47	7.6	38.0	19	7	CF328201	CF328201 NACL--02-
	48	7.6	38.0	19	8	AZ442391	AZ442391 1M0236P13
	49	7.6	38.0	19	8	AZ588035	AZ588035 1M0396G17
	50	7.6	38.0	19	8	AZ613058	AZ613058 1M0441C18
c	51	7.6	38.0	19	8	AZ617087	AZ617087 1M0448M12
	52	7.6	38.0	19	8	AZ623412	AZ623412 1M0461A08
c	53	7.6	38.0	20	1	AU258388	AU258388 AU258388
c	54	7.6	38.0	20	4	BF966452	BF966452 602287066
c	55	7.6	38.0	20	4	BM398906	BM398906 5009-0-50
	56	7.6	38.0	20	8	AZ475341	AZ475341 1M0293H11
	57	7.6	38.0	20	8	AZ480598	AZ480598 1M0302E17
c	58	7.6	38.0	20	8	AZ590476	AZ590476 1M0400P06
c	59	7.6	38.0	20	8	AZ786334	AZ786334 2M0031H15
	60	7.6	38.0	20	8	AZ792286	AZ792286 2M0043G08
c	61	7.6	38.0	20	9	AG193233	AG193233 Pan trogl
c	62	7.6	38.0	20	9	AG200990	AG200990 Pan trogl
	63	7.4	37.0	10	9	CL439564	CL439564 PST951-1.
	64	7.4	37.0	17	9	AJ600606	AJ600606 Arabidops
c	65	7.4	37.0	17	9	CL883716	CL883716 abf63c08.
	66	7.4	37.0	18	4	BM393920	BM393920 50072-2-1
	67	7.4	37.0	18	9	AJ588001	AJ588001 Arabidops
	68	7.4	37.0	18	9	AJ592301	AJ592301 Arabidops
	69	7.4	37.0	18	9	CL695736	CL695736 PRI017a_G
	70	7.4	37.0	19	1	AI017940	AI017940 ou24b04.x
	71	7.4	37.0	19	1	AI597783	AI597783 tr92g04.x
	72	7.4	37.0	19	1	AJ647608	AJ647608 AJ647608
c	73	7.4	37.0	19	8	AZ384797	AZ384797 1M0142P19
c	74	7.4	37.0	19	8	AZ636812	AZ636812 1M0495B21
	75	7.4	37.0	19	8	AZ785518	AZ785518 2M0029M23
c	76	7.4	37.0	19	9	CL671134	CL671134 PRI0163d_
	77	7.4	37.0	20	1	AJ683142	AJ683142 AJ683142
c	78	7.4	37.0	20	1	AU013891	AU013891 AU013891
	79	7.4	37.0	20	5	BQ593049	BQ593049 E012375-0
c	80	7.4	37.0	20	8	AZ313204	AZ313204 1M0029P19
c	81	7.4	37.0	20	8	AZ366451	AZ366451 1M0115N07
	82	7.4	37.0	20	8	AZ514604	AZ514604 1M0361K19
	83	7.4	37.0	20	8	AZ581459	AZ581459 1M0370D14
	84	7.4	37.0	20	8	AZ637439	AZ637439 1M0496N13
c	85	7.4	37.0	20	8	AZ656648	AZ656648 1M0532P16
	86	7.4	37.0	20	8	AZ816586	AZ816586 2M0085H22
	87	7.4	37.0	20	8	AZ838929	AZ838929 2M0134O14
c	88	7.2	36.0	13	7	CO778077	CO778077 BL002D_E0
c	89	7.2	36.0	13	9	AJ588190	AJ588190 Arabidops
	90	7.2	36.0	14	2	BE516032	BE516032 WHE0629_B
	91	7.2	36.0	14	4	BM398220	BM398220 5009-0-42
	92	7.2	36.0	14	6	CA798290	CA798290 Cac_BL_61
	93	7.2	36.0	16	1	AJ649083	AJ649083 AJ649083
c	94	7.2	36.0	16	9	AJ596507	AJ596507 Arabidops
c	95	7.2	36.0	17	4	BM397301	BM397301 5009-0-30
	96	7.2	36.0	19	1	AI688430	AI688430 wc89e09.x
c	97	7.2	36.0	19	1	AJ672970	AJ672970 AJ672970

c 98	7.2	36.0	19	4	BM397569	BM397569 5009-0-34
c 99	7.2	36.0	19	4	BM399684	BM399684 5009-0-60
c 100	7.2	36.0	19	6	C01992	C01992 HUMGS000401

ALIGNMENTS

```
RESULT 1
CO792214
LOCUS       CO792214                 19 bp    mRNA    linear   EST 05-AUG-2004
DEFINITION  NT014C_A10 St18-22 Neural tube (NT) Ambystoma mexicanum cDNA 5'
            similar to hypothetical protein, mRNA sequence.
ACCESSION   CO792214
VERSION     CO792214.1  GI:51008185
KEYWORDS    EST.
SOURCE      Ambystoma mexicanum (axolotl)
  ORGANISM  Ambystoma mexicanum
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
            Ambystoma.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Habermann,B., Bebin,A.G., Herklotz,S., Volkmer,M., Eckelt,K.,
            Pehlke,K., Epperlein,H.H., Schackert,H.K., Wiebe,G. and Tanaka,E.M.
  TITLE     An Ambystoma mexicanum EST sequencing project: Analysis of 17,352
            expressed sequence tags from embryonic and regenerating blastema
            cDNA libraries
  JOURNAL   Genome Biol. (2004) In press
COMMENT     Contact: Elly M. Tanaka
            Tanaka Lab
            Max Planck Institute of Molecular Cell Biology and Genetics,
            Dresden
            Pfotenhauerstrasse 108,01307 Dresden, Germany
            Tel: 0049 351 210 2620
            Fax: 0049 351 210 1489
            Email: tanaka@mpi-cbg.de
            Plate: NT014C  row: 10  column: A
            Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Ambystoma mexicanum"
                     /mol_type="mRNA"
                     /db_xref="taxon:8296"
                     /tissue_type="Neural Tube, Notochord, Somites"
                     /cell_type="Includes Neural tube, notochord, somites"
                     /dev_stage="Stage 18-22"
                     /clone_lib="St18-22 Neural tube (NT)"
                     /note="Vector: pCMVSport6; Site_1: NotI; Site_2: SalI;
                     Unnormalized cDNA plasmid library prepared by Invitrogen.
                     Size fractionated mRNA was polydT primed and cloned into
                     NotI-SalI site of pCMVSport6. Bacterial host is
                     EMDH10B-TONA. Average insert size is 1.5 kB.
                     TAG_LIB=NT"
ORIGIN

  Query Match             51.0%;  Score 10.2;  DB 7;  Length 19;
  Best Local Similarity   80.0%;  Pred. No. 1.4e+06;
  Matches   12;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 CCGCATAGACTTCTC 17
              ||||| || |||| |
Db          1 CCGCAGAGGCTTCAC 15


RESULT 2
AZ309643
LOCUS       AZ309643                 19 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0016E23F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0016E23 F, genomic survey sequence.
ACCESSION   AZ309643
VERSION     AZ309643.1  GI:10350661
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0016  row: E  column: 23
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0016E23"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             49.0%;  Score 9.8;  DB 8;  Length 19;
  Best Local Similarity   84.6%;  Pred. No. 2.3e+06;
  Matches   11;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 GCATAGACTTCTC 17
              ||| ||| |||||
Db          3 GCACAGAGTTCTC 15


RESULT 3
AZ660128/c
LOCUS       AZ660128                 20 bp    DNA     linear   GSS 14-DEC-2000
DEFINITION  1M0538G04F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0538G04 F, genomic survey sequence.
ACCESSION   AZ660128
VERSION     AZ660128.1  GI:11797274
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
```

```
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0538  row: G  column: 04
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0538G04"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             48.0%;  Score 9.6;  DB 8;  Length 20;
  Best Local Similarity   75.0%;  Pred. No. 3e+06;
  Matches   12;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          5 GCATAGACTTCTCAGA 20
              ||||||| | ||| |
Db         20 GCATAGATATATCATA 5


RESULT 4
CL681189/c
LOCUS       CL681189                  17 bp    DNA     linear   GSS 09-JUL-2004
DEFINITION  PRI0130b_G06_2 - PRI0130b.BR (17) Mixed stage fosmid library of P.
            pacificus var. California Pristionchus pacificus genomic, genomic
            survey sequence.
ACCESSION   CL681189
VERSION     CL681189.1  GI:50188197
KEYWORDS    GSS.
SOURCE      Pristionchus pacificus
  ORGANISM  Pristionchus pacificus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
            Neodiplogasteridae; Pristionchus.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
  TITLE     AppaDB: an AcedB database for the nematode satellite organism
            Pristionchus pacificus
  JOURNAL   Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT     Contact: Sommer RJ
            Evolutionary Biology
            Max-Planck-Institute for Developmental Biology
            Spemannstr. 37-39, Tuebingen D-72076, Germany
            Tel: 00497071601371
            Fax: 00497071601498
            Email: ralf.sommer@tuebingen.mpg.de
            This library was generated at Caltech, Pasadena, USA and end
            sequenced at Vancouver, Canada.
            Seq primer: T7
            Class: fosmid ends.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Pristionchus pacificus"
                     /mol_type="genomic DNA"
                     /strain="California"
                     /db_xref="taxon:54126"
                     /clone_lib="Mixed stage fosmid library of P. pacificus
                     var. California"
                     /note="Vector: pEpifos-5 Fosmid vector"
ORIGIN

  Query Match             46.0%;  Score 9.2;  DB 9;  Length 17;
  Best Local Similarity   78.6%;  Pred. No. 4.8e+06;
  Matches   11;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          3 CCGCATAGACTTCT 16
              | ||| | ||||||
Db         15 CTGCAGATACTTCT 2


RESULT 5
BQ593906/c
LOCUS       BQ593906                  18 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  S015504-024-025-M13-SP6 MPIZ-ADIS-024-developing root Beta vulgaris
            cDNA clone 024-025-M13 5-PRIME, mRNA sequence.
ACCESSION   BQ593906
VERSION     BQ593906.1  GI:26123489
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 18)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 18   Std Error: 0.00
            Plate: 25  row: M  column: 13
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .18
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                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:192944"
                     /db_xref="taxon:161934"
                     /clone="024-025-M13"
                     /tissue_type="developing root"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-developing root"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN

  Query Match            45.0%;  Score 9;  DB 5;  Length 18;
  Best Local Similarity   70.6%;  Pred. No. 6.2e+06;
  Matches   12;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GACCGCATAGACTTCTC 17
              |||| |||  |||  ||
Db         18 GACCACATCCACTCTTC 2


RESULT 6
AJ671616
LOCUS       AJ671616                 19 bp    mRNA    linear   EST 28-JUN-2004
DEFINITION  AJ671616 KN224 Bos taurus cDNA clone KN224-006_N20, mRNA sequence.
ACCESSION   AJ671616
VERSION     AJ671616.1  GI:49356473
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
  TITLE     Development of cDNA and EST resources for studying reproduction and
            embryo development in pigs and cattle
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Anderson SI
            Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
            Single pass sequencing. Bases called and trimmed with phred
            v0.020425.c. Vector identified by cross_match with the -minscore 20
            and -minmatch 12 options. Vector: pBluescriptII(SK+) R. Site 1:
            EcoRI R. Site 2: NotI 5' Seq primer M13F Description: Normalised
            library constructed from Bovine Uterus tissue. Clones available
            from UK Centre for Functional Genomics in Farm Animals, Roslin
            Institite, Roslin, Midlothian, UK, EH25 9PS, www.arkgenomics.org.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /db_xref="taxon:9913"
                     /clone="KN224-006_N20"
                     /tissue_type="uterus"
                     /clone_lib="KN224"
                     /note="Vector: pBluescriptII(SK+); Site_1: EcoRI; Site_2:
                     NotI; Single pass sequencing. Normalised library
                     constructed from Bovine Uterus tissue."
ORIGIN

  Query Match            45.0%;  Score 9;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 6.3e+06;
  Matches    9;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         12 CTTCTCAGA 20
              |||||||||
Db          5 CTTCTCAGA 13


RESULT 7
CL671780
LOCUS       CL671780                 19 bp    DNA     linear   GSS 09-JUL-2004
DEFINITION  PRI0165c_F12 - PRI0165c.B21 (19) Mixed stage fosmid library of P.
            pacificus var. California Pristionchus pacificus genomic, genomic
            survey sequence.
ACCESSION   CL671780
VERSION     CL671780.1  GI:50171182
KEYWORDS    GSS.
SOURCE      Pristionchus pacificus
  ORGANISM  Pristionchus pacificus
            Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
            Neodiplogasteridae; Pristionchus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
  TITLE     AppaDB: an AcedB database for the nematode satellite organism
            Pristionchus pacificus
  JOURNAL   Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT     Contact: Sommer RJ
            Evolutionary Biology
            Max-Planck-Institute for Developmental Biology
            Spemannstr. 37-39, Tuebingen D-72076, Germany
            Tel: 00497071601371
            Fax: 00497071601498
            Email: ralf.sommer@tuebingen.mpg.de
            This library was generated at Caltech, Pasadena, USA and end
            sequenced at Vancouver, Canada.
            Seq primer: T7
            Class: fosmid ends.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Pristionchus pacificus"
                     /mol_type="genomic DNA"
                     /strain="California"
                     /db_xref="taxon:54126"
                     /clone_lib="Mixed stage fosmid library of P. pacificus
                     var. California"
                     /note="Vector: pEpifos-5 Fosmid vector"
ORIGIN

  Query Match            45.0%;  Score 9;  DB 9;  Length 19;
  Best Local Similarity   70.6%;  Pred. No. 6.3e+06;
  Matches   12;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          4 CGCATAGACTTCTCAGA 20
              |||    |||||| ||
Db          2 CGCTGCAACTTCTCGGA 18


RESULT 8
AG188131
LOCUS       AG188131                 20 bp    DNA     linear   GSS 06-MAR-2004
DEFINITION  Pan troglodytes DNA, clone: RP43-061K12.T7, genomic survey
            sequence.
ACCESSION   AG188131
VERSION     AG188131.1  GI:45220300
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1
  AUTHORS   Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
            Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
  TITLE     BAC end sequences of Library RP-43
```

```
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 20)
  AUTHORS   Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
            Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
            Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
            52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
            (E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,
            Tel:82-42-866-7181, Fax:82-42-860-4409)
COMMENT     Clones are derived from the chimpanzee BAC library RP-43 This BAC
            end was generated during the R&D process and may have higher chance
            of clone tracking errors.
             PRIMERS
                 Sequencing: T7
             LIBRARY
                 Vector    : pBACe3.6
                 R.Site 1  : EcoRI
                 R.Site 2  : EcoRI.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
                     /clone="RP43-061K12.T7"
                     /sex="male"
                     /cell_type="lymphocytes"
                     /clone_lib="RP-43 Chimpanzee Male BAC Library"
ORIGIN

  Query Match             45.0%;  Score 9;  DB 9;  Length 20;
  Best Local Similarity   70.6%;  Pred. No. 6.3e+06;
  Matches   12;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GACCGCATAGACTTCTC 17
              ||||  || || | |||
Db          3 GACCCAATCGATTACTC 19


RESULT 9
BQ585512/c
LOCUS       BQ585512                 16 bp    mRNA    linear   EST 06-DEC-2002
DEFINITION  E012305-024-008-E21-SP6 MPIZ-ADIS-024-inflorescence Beta vulgaris
            cDNA clone 024-008-E21 5-PRIME, mRNA sequence.
ACCESSION   BQ585512
VERSION     BQ585512.1  GI:26115094
KEYWORDS    EST.
SOURCE      Beta vulgaris
  ORGANISM  Beta vulgaris
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            Caryophyllales; Amaranthaceae; Beta.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Herwig,R., Schulz,B., Weisshaar,B., Hennig,S., Steinfath,M.,
            Drungowski,M., Stahl,D., Wruck,W., Menze,A., O'Brien,J., Lehrach,H.
            and Radelof,U.
  TITLE     Construction of a 'unigene' cDNA clone set by oligonucleotide
            fingerprinting allows access to 25 000 potential sugar beet genes
  JOURNAL   Plant J. 32 (5), 845-857 (2002)
  MEDLINE   22362189
   PUBMED   12472698
COMMENT     Contact: Weisshaar B
            ADIS DNA core facility at MPIZ
            Max-Planck-Institute for Plant Breeding Research
            Carl-von-Linne Weg 10, 50829 Koeln, Germany
            Fax: 00492215062851
            Email: weisshaa@mpiz-koeln.mpg.de
            Insert Length: 16   Std Error: 0.00
            Plate: 8  row: E  column: 21
            Seq primer: SP6; CATACGATTTAGGTGACACTATAG.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Beta vulgaris"
                     /mol_type="mRNA"
                     /cultivar="KWS2320 (double haploid, monogerm breeding
                     line)"
                     /db_xref="GABI:184446"
                     /db_xref="taxon:161934"
                     /clone="024-008-E21"
                     /tissue_type="inflorescence"
                     /lab_host="EMDH10B"
                     /clone_lib="MPIZ-ADIS-024-inflorescence"
                     /note="Vector: pCMVSPORT6; Site_1: SalI; Site_2: NotI;
                     cDNA library from sugar beet, library provided by KWS
                     Kleinwanzlebener Saatzucht AG Einbeck, Germany, contact:
                     b.schulz@kws.de; cloning sites SalI-NotI, primer sites and
                     orientation:
                     SP6-SalI-CCACGCGTCCG-5prime-cDNA-polyA-CC-NotI-T7;  Note:
                     Sequencing granted in the context of the GABI-Beet
                     project, local PI: Dr. Katharina Schneider, coordinator:
                     Prof. Christian Jung;  Sequence submission managed by
                     RZPD/GABI-Primary database: http://gabi.rzpd.de"
ORIGIN

  Query Match             44.0%;  Score 8.8;  DB 5;  Length 16;
  Best Local Similarity   83.3%;  Pred. No. 7.8e+06;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          7 ATAGACTTCTCA 18
              |||| ||| |||
Db         16 ATAGGCTTGTCA 5


RESULT 10
AZ585898
LOCUS       AZ585898                 19 bp    DNA     linear   GSS 13-DEC-2000
DEFINITION  1M0391L22F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0391L22 F, genomic survey sequence.
ACCESSION   AZ585898
VERSION     AZ585898.1  GI:11708088
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0391  row: L  column: 22
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0391L22"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
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```
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             44.0%;  Score 8.8;  DB 8;  Length 19;
  Best Local Similarity   83.3%;  Pred. No. 8e+06;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          5 GCATAGACTTCT 16
              ||||  ||||||
Db          3 GCATCTACTTCT 14


RESULT 11
AG187931/c
LOCUS       AG187931                  20 bp    DNA     linear   GSS 06-MAR-2004
DEFINITION  Pan troglodytes DNA, clone: RP43-061C23.TJ, genomic survey
            sequence.
ACCESSION   AG187931
VERSION     AG187931.1  GI:45220100
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1
  AUTHORS   Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
            Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
  TITLE     BAC end sequences of Library RP-43
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 20)
  AUTHORS   Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
            Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
            Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
            52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
            (E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,
            Tel:82-42-866-7181, Fax:82-42-860-4409)
COMMENT     Clones are derived from the chimpanzee BAC library RP-43 This BAC
            end was generated during the R&D process and may have higher chance
            of clone tracking errors.
             PRIMERS
                 Sequencing: TJ
             LIBRARY
                 Vector    : pBACe3.6
                 R.Site 1  : EcoRI
                 R.Site 2  : EcoRI.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
                     /clone="RP43-061C23.TJ"
                     /sex="male"
                     /cell_type="lymphocytes"
                     /clone_lib="RP-43 Chimpanzee Male BAC Library"
ORIGIN

  Query Match             44.0%;  Score 8.8;  DB 9;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 8.1e+06;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          9 AGACTTCTCAGA 20
              ||  ||||||||
Db         13 AGCATTCTCAGA 2


RESULT 12
AG200702/c
LOCUS       AG200702                  20 bp    DNA     linear   GSS 06-MAR-2004
DEFINITION  Pan troglodytes DNA, clone: RP43-082N04.TJ, genomic survey
            sequence.
ACCESSION   AG200702
VERSION     AG200702.1  GI:45232877
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1
  AUTHORS   Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
            Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
  TITLE     BAC end sequences of Library RP-43
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 20)
  AUTHORS   Park,H., Kim,Y., Kim,S., Han,Y., Woo,T., Park,K., Eun,C.J.,
            Hoon,S.T., Chu,M., Kim,H., Joo,S., Kim,C., Song,W. and Yoo,H.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-JAN-2002) Hong-Seog Park, Korea Research Institute of
            Bioscience and Biotechnology (KRIBB), Genome Research Center (GRC);
            52, Oun-dong, Yusong-gu, Daejeon 305-333, Korea
            (E-mail:redstone@mail.kribb.re.kr, URL:http://phs.grc.kribb.re.kr/,
            Tel:82-42-866-7181, Fax:82-42-860-4409)
COMMENT     Clones are derived from the chimpanzee BAC library RP-43 This BAC
            end was generated during the R&D process and may have higher chance
            of clone tracking errors.
             PRIMERS
                 Sequencing: TJ
             LIBRARY
                 Vector    : pBACe3.6
                 R.Site 1  : EcoRI
                 R.Site 2  : EcoRI.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
                     /clone="RP43-082N04.TJ"
                     /sex="male"
                     /cell_type="lymphocytes"
                     /clone_lib="RP-43 Chimpanzee Male BAC Library"
ORIGIN

  Query Match             44.0%;  Score 8.8;  DB 9;  Length 20;
  Best Local Similarity   83.3%;  Pred. No. 8.1e+06;
  Matches   10;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          6 CATAGACTTCTC 17
              ||||||  ||| |
Db         12 CATAGAATTCCC 1


RESULT 13
AJ684587/c
LOCUS       AJ684587                  16 bp    mRNA    linear   EST 29-JUN-2004
DEFINITION  AJ684587 CSEQRAN04 Sus scrofa cDNA clone C0001805_G15, mRNA
            sequence.
ACCESSION   AJ684587
```

```
VERSION     AJ684587.1  GI:49417177
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
  TITLE     Development of cDNA and EST resources for studying reproduction and
            embryo development in pigs and cattle
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Anderson SI
            Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
            Single pass sequencing. Bases called and trimmed with phred
            v0.020425.c. Vector identified by cross_match with the -minscore 20
            and -minmatch 12 options. Vector:pBlueScriptII(KS+) R. Site1: EcoRI
            R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
            from pig uterus. Clones available from UK Centre for Functional
            Genomics in Farm Animals, Roslin Institite, Roslin, Midlothian, UK,
            EH25 9PS, www.arkgenomics.org.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /clone="C0001805_G15"
                     /tissue_type="uterus"
                     /clone_lib="CSEQRAN04"
                     /note="Vector: pBlueScriptII(KS+); Site_1: EcoRI; Site_2:
                     NotI; Single pass sequencing. Normalised library
                     constructed from pig uterus."
ORIGIN

  Query Match             43.0%;  Score 8.6;  DB 1;  Length 16;
  Best Local Similarity   73.3%;  Pred. No. 1e+07;
  Matches   11;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          3 CCGCATAGACTTCTC 17
              | | |||||||  ||
Db         15 CAGAATAGACTCTTC 1


RESULT 14
AZ309116
LOCUS       AZ309116                 19 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0012E23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0012E23 R, genomic survey sequence.
ACCESSION   AZ309116
VERSION     AZ309116.1  GI:10349784
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0012  row: E  column: 23
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0012E23"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             43.0%;  Score 8.6;  DB 8;  Length 19;
  Best Local Similarity   73.3%;  Pred. No. 1e+07;
  Matches   11;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 ACCGCATAGACTTCT 16
              |||  ||  ||||||
Db          5 ACCAAATCTACTTCT 19


RESULT 15
CO783852
LOCUS       CO783852                 20 bp    mRNA    linear   EST 05-AUG-2004
DEFINITION  BL279A_E02 6-Day Axolotl Tail Blastema (6DAxBL) Ambystoma mexicanum
            cDNA 5' similar to hypothetical protein, mRNA sequence.
ACCESSION   CO783852
VERSION     CO783852.1  GI:50999832
KEYWORDS    EST.
SOURCE      Ambystoma mexicanum (axolotl)
  ORGANISM  Ambystoma mexicanum
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomatidae;
            Ambystoma.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Habermann,B., Bebin,A.G., Herklotz,S., Volkmer,M., Eckelt,K.,
            Pehlke,K., Epperlein,H.H., Schackert,H.K., Wiebe,G. and Tanaka,E.M.
  TITLE     An Ambystoma mexicanum EST sequencing project: Analysis of 17,352
            expressed sequence tags from embryonic and regenerating blastema
            cDNA libraries
  JOURNAL   Genome Biol. (2004) In press
COMMENT     Contact: Elly M. Tanaka
            Tanaka Lab
            Max Planck Institute of Molecular Cell Biology and Genetics,
            Dresden
            Pfotenhauerstrasse 108,01307 Dresden, Germany
            Tel: 0049 351 210 2620
            Fax: 0049 351 210 1489
            Email: tanaka@mpi-cbg.de
            Plate: BL279A  row: 02  column: E
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          Seq primer: GCA CAT TAG GCC TAT TTA GGT GAC A.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Ambystoma mexicanum"
                     /mol_type="mRNA"
                     /db_xref="taxon:8296"
                     /tissue_type="Tail Blastema"
                     /cell_type="regenerating tail blastema"
                     /clone_lib="6-Day Axolotl Tail Blastema (6DAxBL)"
                     /note="Vector: pCMVSport6; Site_1: NotI; Site_2: SalI;
                     Unnormalized cDNA plasmid library prepared by Invitrogen.
                     Size fractionated mRNA was polydT primed and cloned into
                     NotI-SalI site of pCMVSport6. Bacterial host is
                     EMDH10B-TONA. Average insert size is 1.67 kB.
                     TAG_LIB=6DAxBL"
ORIGIN

  Query Match             43.0%;  Score 8.6;  DB 7;  Length 20;
  Best Local Similarity   73.3%;  Pred. No. 1e+07;
  Matches   11;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          6 CATAGACTTCTCAGA 20
              ||  || ||| ||||
Db          2 CACTGATTTCACAGA 16


RESULT 16
AZ440002
LOCUS       AZ440002                 20 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0230E19R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0230E19 R, genomic survey sequence.
ACCESSION   AZ440002
VERSION     AZ440002.1  GI:10564015
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0230  row: E  column: 19
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0230E19"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             43.0%;  Score 8.6;  DB 8;  Length 20;
  Best Local Similarity   73.3%;  Pred. No. 1e+07;
  Matches   11;  Conservative    0;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 ACCGCATAGACTTCT 16
              ||| |||   |||||
Db          6 ACCCCATGACCTTCT 20


RESULT 17
AJ648088
LOCUS       AJ648088                 17 bp    mRNA    linear   EST 07-JUL-2004
DEFINITION  AJ648088 CSEQRAN19 Sus scrofa cDNA clone C0003263_J08, mRNA
            sequence.
ACCESSION   AJ648088
VERSION     AJ648088.1  GI:49324933
KEYWORDS    EST.
SOURCE      Sus scrofa (pig)
  ORGANISM  Sus scrofa
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE   1  (bases 1 to 17)
  AUTHORS   Anderson,S.I., Finlayson,H.A. and Archibald,A.L.
  TITLE     Development of cDNA and EST resources for studying reproduction and
            embryo development in pigs and cattle
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Anderson SI
            Genomics and Bioinformatics
            Roslin Institute
            Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
            Single pass sequencing. Bases called and trimmed with phred
            v0.020425.c. Vector identified by cross_match with the -minscore 20
            and -minmatch 12 options. Vector:pBlueScriptII(KS) R. Site1: EcoRI
            R. Site2: NotI 5' Seq Primer M13F Normalised library constructed
            from pooled ovaries. Clones available from UK Centre for Functional
            Genomics in Farm Animals, Roslin Institite, Roslin, Midlothian, UK,
            EH25 9PS, www.ark-genomics.org.
FEATURES             Location/Qualifiers
     source          1. .17
                     /organism="Sus scrofa"
                     /mol_type="mRNA"
                     /db_xref="taxon:9823"
                     /clone="C0003263_J08"
                     /tissue_type="ovary"
                     /clone_lib="CSEQRAN19"
                     /note="Vector: pBlueScript11(KS+); Site_1: EcoRI; Site_2:
                     NotI; Single pass sequencing; Normalised library
                     constructed from pooled ovaries"
ORIGIN

  Query Match             42.0%;  Score 8.4;  DB 1;  Length 17;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+07;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACTTCTCAGA 20
              |||||| |||
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```
Db          5 ACTTCTAAGA 14


RESULT 18
AZ313531/c
LOCUS       AZ313531                 19 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0029N07R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0029N07 R, genomic survey sequence.
ACCESSION   AZ313531
VERSION     AZ313531.1  GI:10358522
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0029  row: N  column: 07
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0029N07"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match           42.0%;  Score 8.4;  DB 8;  Length 19;
  Best Local Similarity   90.0%;  Pred. No. 1.3e+07;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACTTCTCAGA 20
              | ||||||||
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Db         17 ATTTCTCAGA 8


RESULT 19
AZ663240
LOCUS       AZ663240                 19 bp    DNA     linear   GSS 14-DEC-2000
DEFINITION  1M0542H18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0542H18 R, genomic survey sequence.
ACCESSION   AZ663240
VERSION     AZ663240.1  GI:11800386
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0542  row: H  column: 18
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 19.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0542H18"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match           42.0%;  Score 8.4;  DB 8;  Length 19;
  Best Local Similarity   66.7%;  Pred. No. 1.3e+07;
  Matches   12;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 GACCGCATAGACTTCTCA 18
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Db          2 GACAGGATATGACTCTCA 19


RESULT 20
AZ303578/c
LOCUS       AZ303578                 20 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0003H07F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0003H07 F, genomic survey sequence.
ACCESSION   AZ303578
VERSION     AZ303578.1  GI:10338956
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0003  row: H  column: 07
            Seq primer: CGTTGTAAAACGACGGCCAGT
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0003H07"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match            42.0%;  Score 8.4;  DB 8;  Length 20;
  Best Local Similarity  90.0%;  Pred. No. 1.3e+07;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy         11 ACTTCTCAGA 20
              | ||||||||
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Db         19 AATTCTCAGA 10


RESULT 21
AZ771437/c
LOCUS       AZ771437                 20 bp    DNA     linear   GSS 16-FEB-2001
DEFINITION  1M0573P03R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0573P03 R, genomic survey sequence.
ACCESSION   AZ771437
VERSION     AZ771437.1  GI:12893698
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0573  row: P  column: 03
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0573P03"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match            42.0%;  Score 8.4;  DB 8;  Length 20;
  Best Local Similarity  90.0%;  Pred. No. 1.3e+07;
  Matches    9;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          6 CATAGACTTC 15
              |||||| |||
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```
Db         11 CATAGAATTC 2


RESULT 22
CL423466
LOCUS       CL423466                  16 bp    DNA     linear   GSS 16-MAR-2004
DEFINITION  01S0557-03A1-C11 UniformMu MuTAIL Library Zea mays genomic clone
            01S0557-03A1-C11, genomic survey sequence.
ACCESSION   CL423466
VERSION     CL423466.1  GI:45501510
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 16)
  AUTHORS   Latshaw,S., Tan,B-.C., Settles,A.M. and McCarty,D.R.
  TITLE     Sequence tagged transposon insertions from the UniformMu maize
            population
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Donald R. McCarty
            Plant Molecular and Cellular Biology Program
            University of Florida
            PO 110690 Gainesville, FL 32611-0690, USA
            Tel: 352-392-1928 x322
            Email: drm@ufl.edu
            Sequence Sequence flanking probable Mu insertion site in UniformMu
            line: 01S0557-03, Primer set: A
            Class: transposon insertion site.
FEATURES             Location/Qualifiers
     source          1. .16
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="W22 (ACR, bz1-m9)"
                     /cultivar="UniformMu"
                     /db_xref="taxon:4577"
                     /clone="01S0557-03A1-C11"
                     /clone_lib="UniformMu MuTAIL Library"
                     /note="Vector: TOPO-PCR4; DNA flanking Mu transposon
                     insertions in Mu inactive lines were extracted from the
                     UniformMu maize population by the thermo assymmetric
                     interlaced PCR (TAIL) protocol using primers specific for
                     the Mu terminal inverted repeat and a set of 16 arbitrary
                     primers. Amplicons were size enriched using Sepharose 400
                     spin columns and cloned into the TOPO PCR4 vector."
ORIGIN

  Query Match            41.0%;  Score 8.2;  DB 9;  Length 16;
  Best Local Similarity  76.9%;  Pred. No. 1.6e+07;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          5 GCATAGACTTCTC 17
              | | ||||||| |
Db          4 GAACAGACTTCCC 16


RESULT 23
AA916934/c
LOCUS       AA916934                  19 bp    mRNA    linear   EST 17-JUN-1998
DEFINITION  on14a09.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1556632 3'
            similar to SW:BI3_MOUSE P28662 BRAIN PROTEIN I3 ;, mRNA sequence.
ACCESSION   AA916934
VERSION     AA916934.1  GI:3056326
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 444   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1556632"
                     /tissue_type="carcinoid"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Lu5"
                     /note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; 1st strand cDNA was prepared from
                     neuroendocrine lung carcinoid, and was then primed with a
                     Not I - oligo(dT) primer. Double-stranded cDNA was ligated
                     to Eco RI adaptors (Pharmacia), digested with Not I and
                     cloned into the Not I and Eco RI sites of the modified
                     pT7T3 vector.  Library is normalized. Library was
                     constructed by Bento Soares and M. Fatima Bonaldo. "
ORIGIN

  Query Match            41.0%;  Score 8.2;  DB 1;  Length 19;
  Best Local Similarity  76.9%;  Pred. No. 1.7e+07;
  Matches   10;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          7 ATAGACTTCTCAG 19
              ||||| ||  |||
Db         15 ATAGAGTTTGCAG 3


RESULT 24
AZ414372/c
LOCUS       AZ414372                  19 bp    DNA     linear   GSS 03-OCT-2000
DEFINITION  1M0188G18R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0188G18 R, genomic survey sequence.
ACCESSION   AZ414372
VERSION     AZ414372.1  GI:10538385
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
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Plate: 0188 row: G column: 18
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0188G18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 41.0%; Score 8.2; DB 8; Length 19;
Best Local Similarity 76.9%; Pred. No. 1.7e+07;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GCATAGACTTCTC 17
| | ||||| |||
Db 13 GTAAAGACTCCTC 1

RESULT 25
AZ436629/c
LOCUS AZ436629 19 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0224O19F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0224O19 F, genomic survey sequence.
ACCESSION AZ436629
VERSION AZ436629.1 GI:10560642
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0224 row: O column: 19
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0224O19"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 41.0%; Score 8.2; DB 8; Length 19;
Best Local Similarity 76.9%; Pred. No. 1.7e+07;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 CATAGACTTCTCA 18
||| | ||||||
Db 18 CATCAAGTTCTCA 6

RESULT 26
AZ454430/c
LOCUS AZ454430 19 bp DNA linear GSS 04-OCT-2000
DEFINITION 1M0256F21F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0256F21 F, genomic survey sequence.
ACCESSION AZ454430
VERSION AZ454430.1 GI:10612555
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0256 row: F column: 21
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0256F21"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 41.0%; Score 8.2; DB 8; Length 19;
Best Local Similarity 76.9%; Pred. No. 1.7e+07;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 ATAGACTTCTCAG 19
||| | ||| |||
Db 19 ATATAATTCCCAG 7

RESULT 27
AZ647364/c
LOCUS AZ647364 19 bp DNA linear GSS 14-DEC-2000
DEFINITION 1M0513O16R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0513O16 R, genomic survey sequence.
ACCESSION AZ647364
VERSION AZ647364.1 GI:11778756
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0513 row: O column: 16
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0513O16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 41.0%; Score 8.2; DB 8; Length 19;
Best Local Similarity 76.9%; Pred. No. 1.7e+07;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GACCGCATAGACT 13
||| ||| | |||
Db 13 GACAGCACATACT 1

RESULT 28
AZ655870
LOCUS AZ655870 19 bp DNA linear GSS 14-DEC-2000
DEFINITION 1M0531N06F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0531N06 F, genomic survey sequence.
ACCESSION AZ655870
VERSION AZ655870.1 GI:11793016
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0531 row: N column: 06
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0531N06"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 41.0%; Score 8.2; DB 8; Length 19;
Best Local Similarity 76.9%; Pred. No. 1.7e+07;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 ACCGCATAGACTT 14
| ||| ||||||
Db 6 ATCGCTCAGACTT 18

RESULT 29
AZ783477
LOCUS AZ783477 19 bp DNA linear GSS 16-FEB-2001
DEFINITION 2M0025D18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0025D18 F, genomic survey sequence.
ACCESSION AZ783477
VERSION AZ783477.1 GI:12918241
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00

Plate: 0025 row: D column: 18
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0025D18"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 41.0%; Score 8.2; DB 8; Length 19;
Best Local Similarity 76.9%; Pred. No. 1.7e+07;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 CGCATAGACTTCT 16
||||| |||||
Db 7 CGCATTCTCTTCT 19

RESULT 30
AJ594088/c
LOCUS AJ594088 12 bp DNA linear GSS 15-JAN-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 392F11, genomic survey sequence.
ACCESSION AJ594088
VERSION AJ594088.1 GI:37943712
KEYWORDS GSS; left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G., Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE 22363535
PUBMED 12446565
REFERENCE 2 (bases 1 to 12)
AUTHORS Balzergue,S.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from

the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).

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FEATURES             Location/Qualifiers
     source          1. .12
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="392F11"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature    1. .12
                     /note="T-DNA flanking sequence
                     left border"
ORIGIN

  Query Match             40.0%;  Score 8;  DB 9;  Length 12;
  Best Local Similarity   100.0%;  Pred. No. 2e+07;
  Matches    8;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          7 ATAGACTT 14
              ||||||||
Db         10 ATAGACTT 3


RESULT 31
AZ345710
LOCUS       AZ345710                 20 bp    DNA     linear   GSS 29-SEP-2000
DEFINITION  1M0080H05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0080H05 R, genomic survey sequence.
ACCESSION   AZ345710
VERSION     AZ345710.1  GI:10424947
KEYWORDS    GSS.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 20)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
            Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
            Niederhausern,A. and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
            University of Utah
            Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0080  row: H  column: 05
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 20.
FEATURES             Location/Qualifiers
     source          1. .20
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC1M0080H05"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained  from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high  molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN

  Query Match             40.0%;  Score 8;  DB 8;  Length 20;
  Best Local Similarity   68.8%;  Pred. No. 2.2e+07;
  Matches   11;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          2 ACCGCATAGACTTCTC 17
              | |  ||||  |||||
Db          2 AACATATAGTTTCTC 17


RESULT 32
CL423876
LOCUS       CL423876                 14 bp    DNA     linear   GSS 16-MAR-2004
DEFINITION  01S0750-04C1-D08 UniformMu MuTAIL Library Zea mays genomic clone
            01S0750-04C1-D08, genomic survey sequence.
ACCESSION   CL423876
VERSION     CL423876.1  GI:45501920
KEYWORDS    GSS.
SOURCE      Zea mays
  ORGANISM  Zea mays
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
            clade; Panicoideae; Andropogoneae; Zea.
REFERENCE   1  (bases 1 to 14)
  AUTHORS   Latshaw,S., Tan,B-.C., Settles,A.M. and McCarty,D.R.
  TITLE     Sequence tagged transposon insertions from the UniformMu maize
            population
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Donald R. McCarty
            Plant Molecular and Cellular Biology Program
            University of Florida
            PO 110690 Gainesville, FL 32611-0690, USA
            Tel: 352-392-1928 x322
            Email: drm@ufl.edu
            Sequence Sequence flanking probable Mu insertion site in UniformMu
            line: 01S0750-04, Primer set: C
            Class: transposon insertion site.
FEATURES             Location/Qualifiers
     source          1. .14
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="W22 (ACR, bz1-m9)"
                     /cultivar="UniformMu"
                     /db_xref="taxon:4577"
                     /clone="01S0750-04C1-D08"
                     /clone_lib="UniformMu MuTAIL Library"
                     /note="Vector: TOPO-PCR4; DNA flanking Mu transposon
                     insertions in Mu inactive lines were extracted from the
                     UniformMu maize population by the thermo assymmetric
                     interlaced PCR (TAIL) protocol using primers specific for
                     the Mu terminal inverted repeat and a set of 16 arbitrary
                     primers. Amplicons were size enriched using Sepharose 400
```

spin columns and cloned into the TOPO PCR4 vector."
ORIGIN

Query Match 39.0%; Score 7.8; DB 9; Length 14;
Best Local Similarity 81.8%; Pred. No. 2.6e+07;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 8 TAGACTTCTCA 18
| ||| |||||
Db 3 TCGACGTCTCA 13

RESULT 33
CL438505
LOCUS CL438505 14 bp DNA linear GSS 18-MAR-2004
DEFINITION PST7640-NL.Seq MICB1 Mus musculus genomic clone PST7640-NL.Seq similar to Eif4a2, genomic survey sequence.
ACCESSION CL438505
VERSION CL438505.1 GI:45575122
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 14)
AUTHORS Hicks,G.G.
TITLE www.EScells.ca
JOURNAL Unpublished (2002)
COMMENT Contact: Hicks GG
Mammalian Functional Genomics Centre
Manitoba Institute of Cell Biology, Universitry of Manitoba
ON5029, 675 McDermot Ave, Winnipeg, MB R3E 0V9, Canada
Tel: 204 787 2133
Fax: 204 787 2190
Email: hicksgg@cc.umanitoba.ca
U3NeoSV1 gene trap. Tag generated by plasmid rescue. Additional sequence information and target gene cloning can be generated. ES cell line harboring insertion mutation of target gene is available. Sequence analysis available from
http://140.193.242.7/esdb/public_search_frame.php?PST=PST7640-NL.Seq
Class: Gene Trap.
FEATURES Location/Qualifiers
source 1. .14
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="129 sv"
/db_xref="taxon:10090"
/clone="PST7640-NL.Seq"
/sex="Male"
/cell_type="Embryonic stem cell"
/cell_line="D3H (J1 subclone)"
/clone_lib="MICB1"
/note="Vector: U3NeoSV1"
ORIGIN

Query Match 39.0%; Score 7.8; DB 9; Length 14;
Best Local Similarity 81.8%; Pred. No. 2.6e+07;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GCATAGACTTC 15
||||| ||| |
Db 4 GCATAAACTAC 14

RESULT 34
AJ587709
LOCUS AJ587709 18 bp DNA linear GSS 15-JAN-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 312G06, genomic survey sequence.
ACCESSION AJ587709
VERSION AJ587709.1 GI:37937333
KEYWORDS GSS; left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1
AUTHORS Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F., Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G., Lepiniec,L., Caboche,M. and Lecharny,A.
TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)
MEDLINE 22363535
PUBMED 12446565
REFERENCE 2 (bases 1 to 18)
AUTHORS Balzergue,S.
TITLE Direct Submission
JOURNAL Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at http://dbsgap.versailles.inra.fr/publiclines/. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
FEATURES Location/Qualifiers
source 1. .18
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/cultivar="Wassillewskija"
/db_xref="taxon:3702"
/clone="312G06"
/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
misc_feature 1. .18
/note="T-DNA flanking sequence
left border"
ORIGIN

Query Match 39.0%; Score 7.8; DB 9; Length 18;
Best Local Similarity 81.8%; Pred. No. 2.7e+07;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GACCGCATAGA 11
|||| ||| ||
Db 2 GACCTCATCGA 12

RESULT 35
AZ355195
LOCUS AZ355195 19 bp DNA linear GSS 02-OCT-2000
DEFINITION 1M0094G22R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0094G22 R, genomic survey sequence.
ACCESSION AZ355195
VERSION AZ355195.1 GI:10467355
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0094 row: G column: 22
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0094G22"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 39.0%; Score 7.8; DB 8; Length 19;
Best Local Similarity 81.8%; Pred. No. 2.7e+07;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          2 ACCGCATAGAC 12
              || ||||| ||
Db          4 ACAGCATACAC 14
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RESULT 36
AZ422531/c
LOCUS AZ422531 19 bp DNA linear GSS 03-OCT-2000
DEFINITION 1M0201E16F Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC1M0201E16 F, genomic survey sequence.
ACCESSION AZ422531
VERSION AZ422531.1 GI:10546544
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0201 row: E column: 16
Seq primer: CGTTGTAAAACGACGGCCAGT
Class: plasmid ends
High quality sequence stop: 19.

FEATURES Location/Qualifiers
source 1. .19
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0201E16"
/sex="Male"
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gi|4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 39.0%; Score 7.8; DB 8; Length 19;
Best Local Similarity 81.8%; Pred. No. 2.7e+07;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy          7 ATAGACTTCTC 17
              ||| ||||||
Db         19 ATATTCTTCTC 9
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RESULT 37
AZ875430
LOCUS AZ875430 19 bp DNA linear GSS 21-FEB-2001
DEFINITION 2M0189K09R Mouse 10kb plasmid UUGC1M library Mus musculus genomic clone UUGC2M0189K09 R, genomic survey sequence.
ACCESSION AZ875430
VERSION AZ875430.1 GI:13085433
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 19)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss

University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0189 row: K column: 09
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 19.

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FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="UUGC2M0189K09"
                     /sex="Male"
                     /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
                     /note="Vector: PWD42nv; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.jax.org/resources/documents/dnares/). The DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end-repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10-Gold (Stratagene) cells
                     and selected for ampicillin resistance."
ORIGIN
```

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  Query Match             39.0%;  Score 7.8;  DB 8;  Length 19;
  Best Local Similarity   81.8%;  Pred. No. 2.7e+07;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy         10 GACTTCTCAGA 20
              ||||| || ||
Db          2 GACTTGTCTGA 12
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RESULT 38
AJ595189/c
LOCUS       AJ595189                 19 bp    DNA     linear   GSS 15-JAN-2004
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
            412H07, genomic survey sequence.
ACCESSION   AJ595189
VERSION     AJ595189.1  GI:37944813
KEYWORDS    GSS; left border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 19)
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
            http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
            been generated in the framework of the French plant genomics
            program 'Genoplante' (http://www.genoplante.com and
            http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="412H07"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature    1. .19
                     /note="T-DNA flanking sequence
                     left border"
ORIGIN
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  Query Match             39.0%;  Score 7.8;  DB 9;  Length 19;
  Best Local Similarity   81.8%;  Pred. No. 2.7e+07;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 ACCGCATAGAC 12
              |||  ||||||
Db         13 ACCATATAGAC 3
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RESULT 39
AJ599121
LOCUS       AJ599121                 19 bp    DNA     linear   GSS 15-JAN-2004
DEFINITION  Arabidopsis thaliana T-DNA flanking sequence, left border, clone
            481A05, genomic survey sequence.
ACCESSION   AJ599121
VERSION     AJ599121.1  GI:37948749
KEYWORDS    GSS; left border; T-DNA flanking sequence.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE   1
  AUTHORS   Brunaud,V., Balzergue,S., Dubreucq,B., Aubourg,S., Samson,F.,
            Chauvin,S., Bechtold,N., Cruaud,C., DeRose,R., Pelletier,G.,
            Lepiniec,L., Caboche,M. and Lecharny,A.
  TITLE     T-DNA integration into the Arabidopsis genome depends on sequences
            of pre-insertion sites
  JOURNAL   EMBO Rep. 3 (12), 1152-1157 (2002)
  MEDLINE   22363535
   PUBMED   12446565
REFERENCE   2  (bases 1 to 19)
  AUTHORS   Balzergue,S.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-OCT-2003) Balzergue S., UMRGV, INRA/CNRS, 2 rue
            Gaston Cremieux, 91057 Evry cedex, FRANCE
COMMENT     PCR was performed on DNA from transformants of Arabidopsis thaliana
            plants from INRA (Versailles). The DNA fragment(s) resulting from
            the PCR were directly sequenced from the left or the right border
            to determine the genomic sequence flanking the insertion. T-DNA
            derived sequences were removed. Information to order the
            corresponding mutant line and a link to a database providing a
            graphical display of the insertion site are available at
```

```
           http://dbsgap.versailles.inra.fr/publiclines/. This sequence has
           been generated in the framework of the French plant genomics
           program 'Genoplante' (http://www.genoplante.com and
           http://genoplante-info.infobiogen.fr).
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /cultivar="Wassillewskija"
                     /db_xref="taxon:3702"
                     /clone="481A05"
                     /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
     misc_feature    1. .19
                     /note="T-DNA flanking sequence
                     left border"
ORIGIN

  Query Match             39.0%;  Score 7.8;  DB 9;  Length 19;
  Best Local Similarity   81.8%;  Pred. No. 2.7e+07;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          3 CCGCATAGACT 13
              | ||||| |||
Db          4 CAGCATATACT 14


RESULT 40
CL683526
LOCUS       CL683526                 19 bp    DNA     linear   GSS 09-JUL-2004
DEFINITION  PRI0137a_F08_2 - PRI0137a.BR (19) Mixed stage fosmid library of P.
           pacificus var. California Pristionchus pacificus genomic, genomic
           survey sequence.
ACCESSION   CL683526
VERSION     CL683526.1  GI:50191279
KEYWORDS    GSS.
SOURCE      Pristionchus pacificus
  ORGANISM  Pristionchus pacificus
           Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida;
           Neodiplogasteridae; Pristionchus.
REFERENCE   1  (bases 1 to 19)
  AUTHORS   Srinivasan,J., Otto,G.W., Kahlow,U., Geisler,R. and Sommer,R.J.
  TITLE     AppaDB: an AcedB database for the nematode satellite organism
           Pristionchus pacificus
  JOURNAL   Nucleic Acids Res. 32 (1), D421-D422 (2004)
COMMENT     Contact: Sommer RJ
           Evolutionary Biology
           Max-Planck-Institute for Developmental Biology
           Spemannstr. 37-39, Tuebingen D-72076, Germany
           Tel: 00497071601371
           Fax: 00497071601498
           Email: ralf.sommer@tuebingen.mpg.de
           This library was generated at Caltech, Pasadena, USA and end
           sequenced at Vancouver, Canada.
           Seq primer: T7
           Class: fosmid ends.
FEATURES             Location/Qualifiers
     source          1. .19
                     /organism="Pristionchus pacificus"
                     /mol_type="genomic DNA"
                     /strain="California"
                     /db_xref="taxon:54126"
                     /clone_lib="Mixed stage fosmid library of P. pacificus
                     var. California"
                     /note="Vector: pEpifos-5 Fosmid vector"
ORIGIN

  Query Match             39.0%;  Score 7.8;  DB 9;  Length 19;
  Best Local Similarity   81.8%;  Pred. No. 2.7e+07;
  Matches    9;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GACCGCATAGA 11
              | || ||||||
Db          7 GTCCTCATAGA 17
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Search completed: August 12, 2005, 12:11:45
Job time : 1785 secs

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